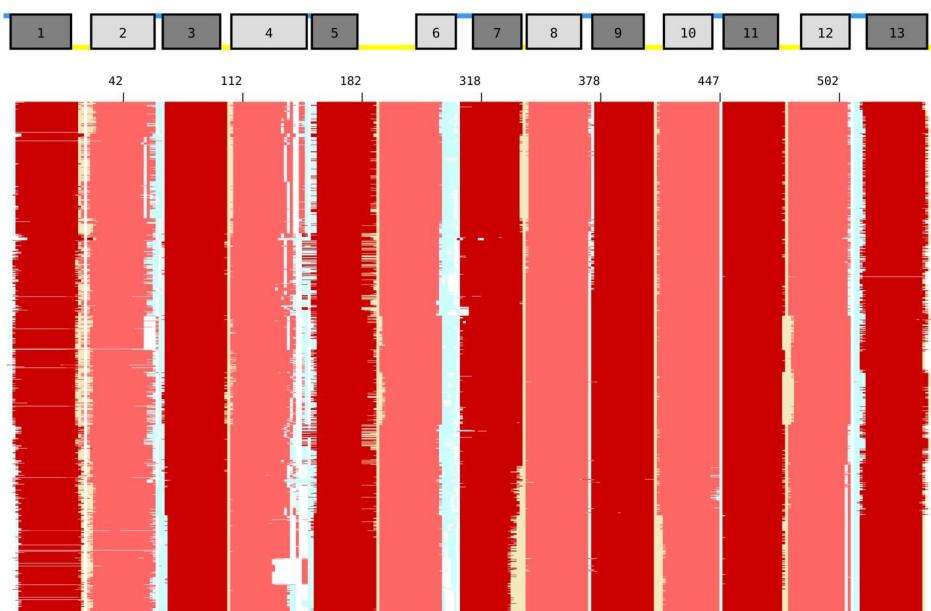
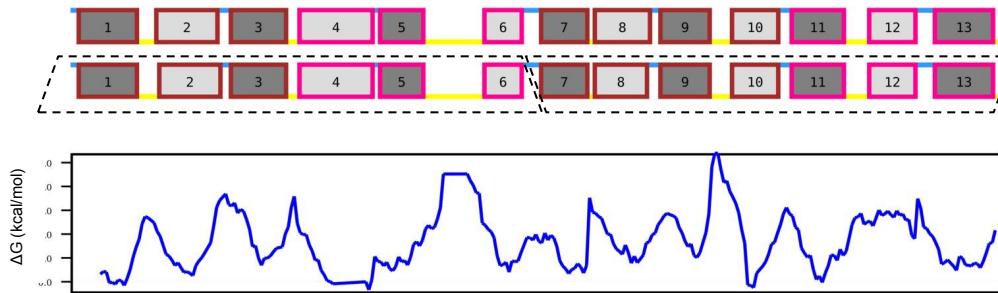


Na_H_Exchanger_1**4CZB****Final topology**

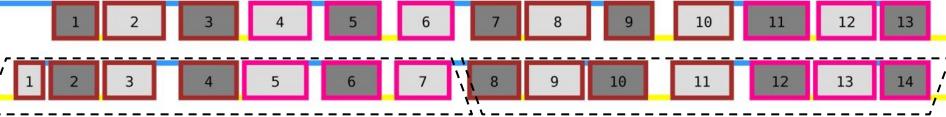
Na_H_Exchanger_2



111 179 242 302 366 421 480

4CZ8

Final topology

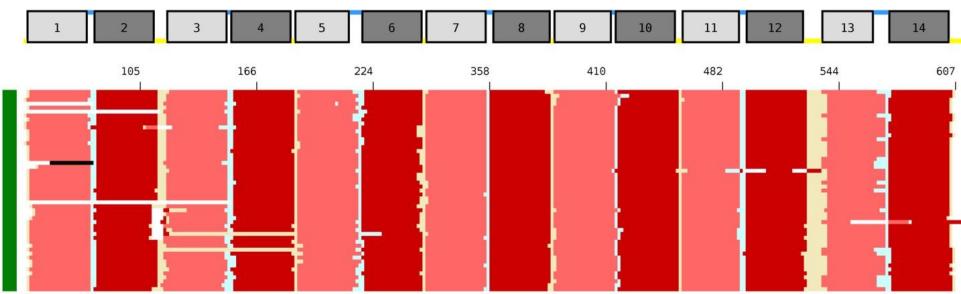


ΔG (kcal/mol)



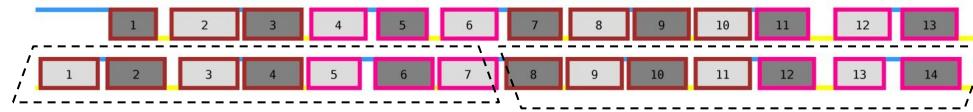
Na_H_Exchanger_2

Initial topology

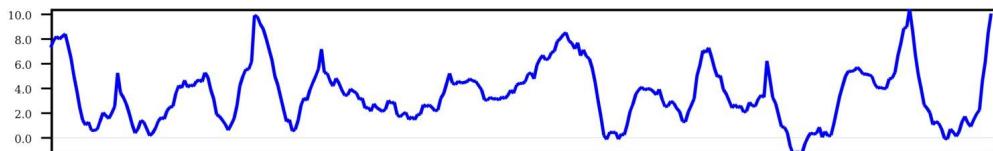


4CZ8

Final topology

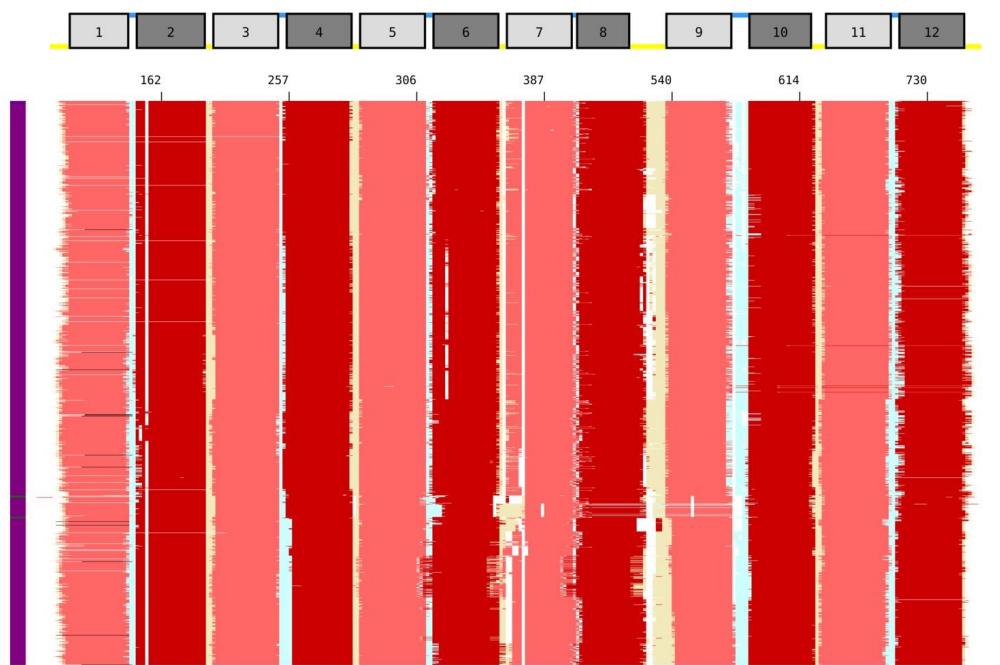


ΔG (kcal/mol)



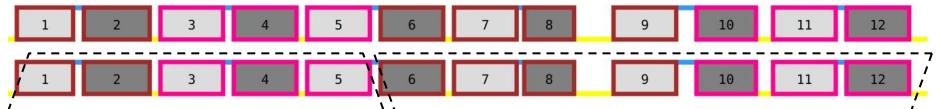
Na_H_antiport_1

Initial topology

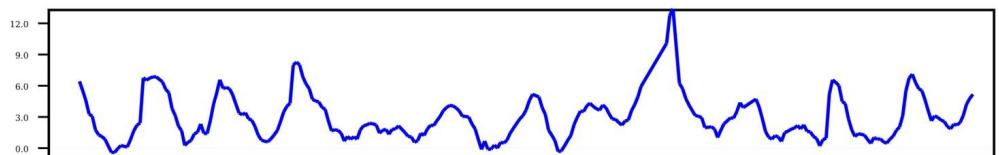


1ZCD

Final topology



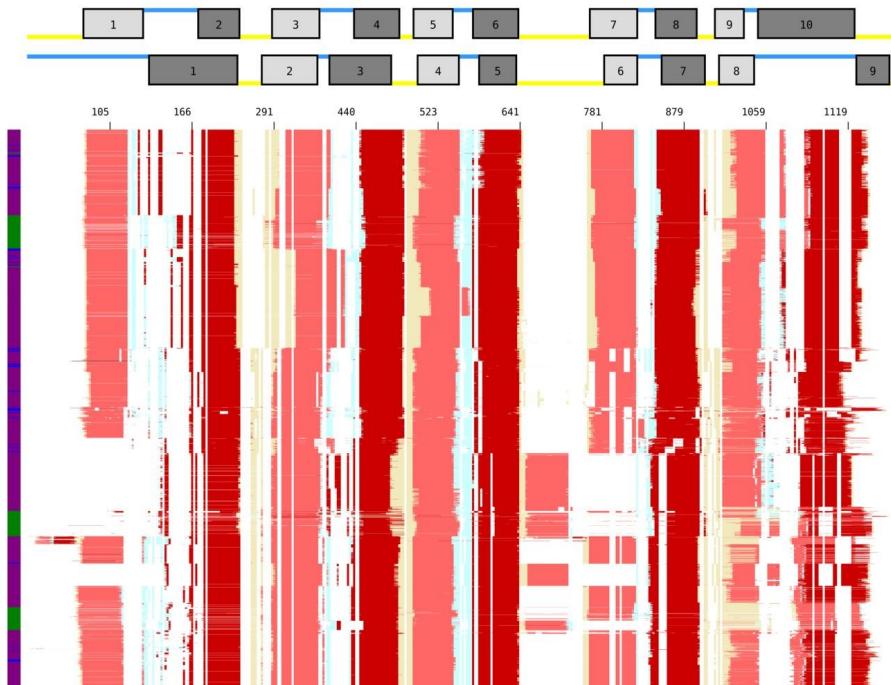
ΔG (kcal/mol)



SBF_1

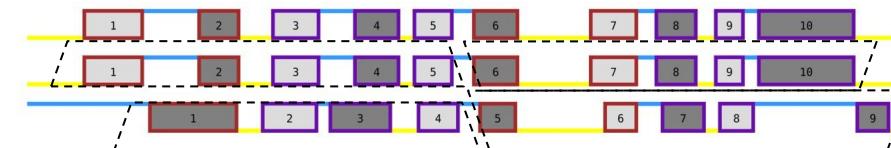
SBF_2

Initial topology

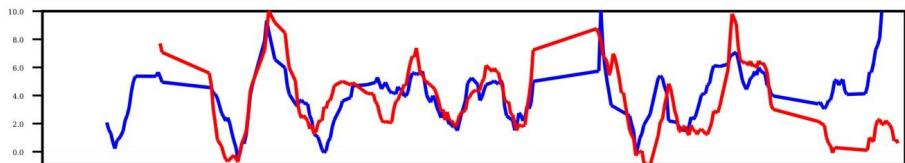


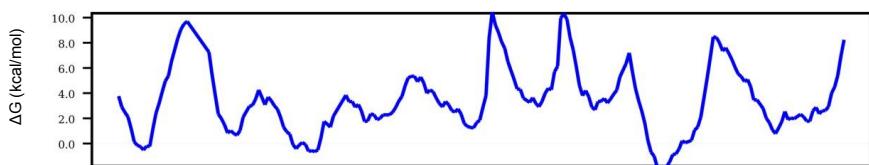
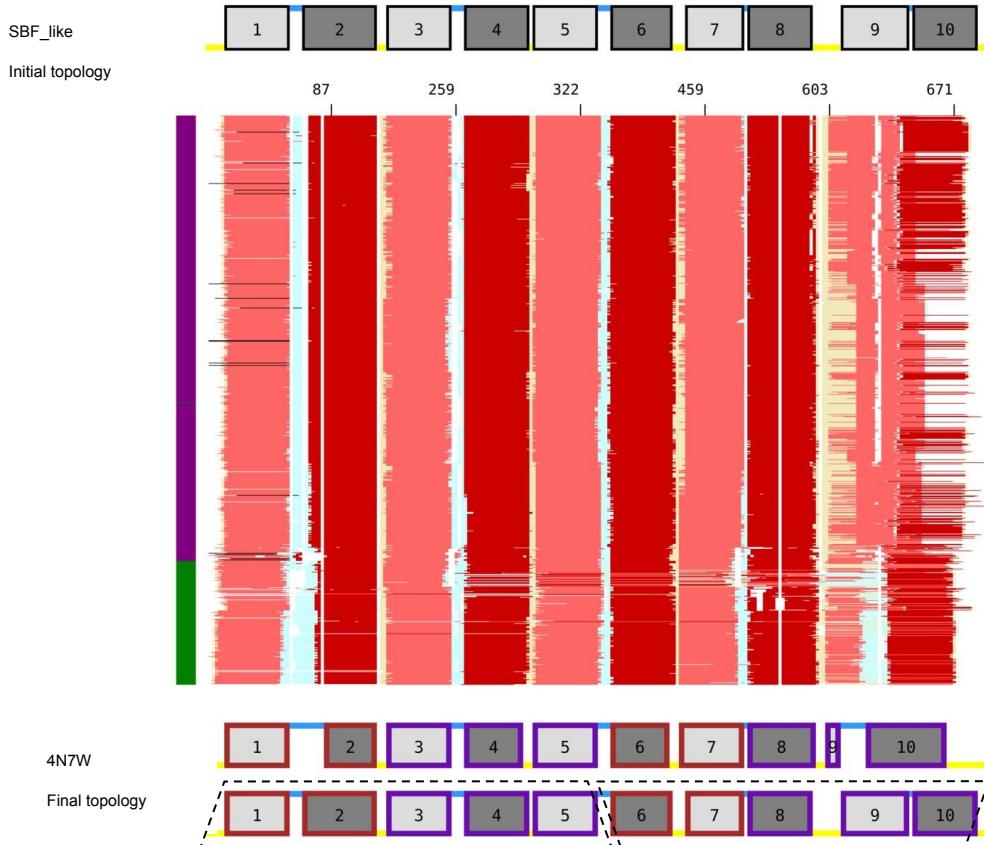
4N7W

Final topology



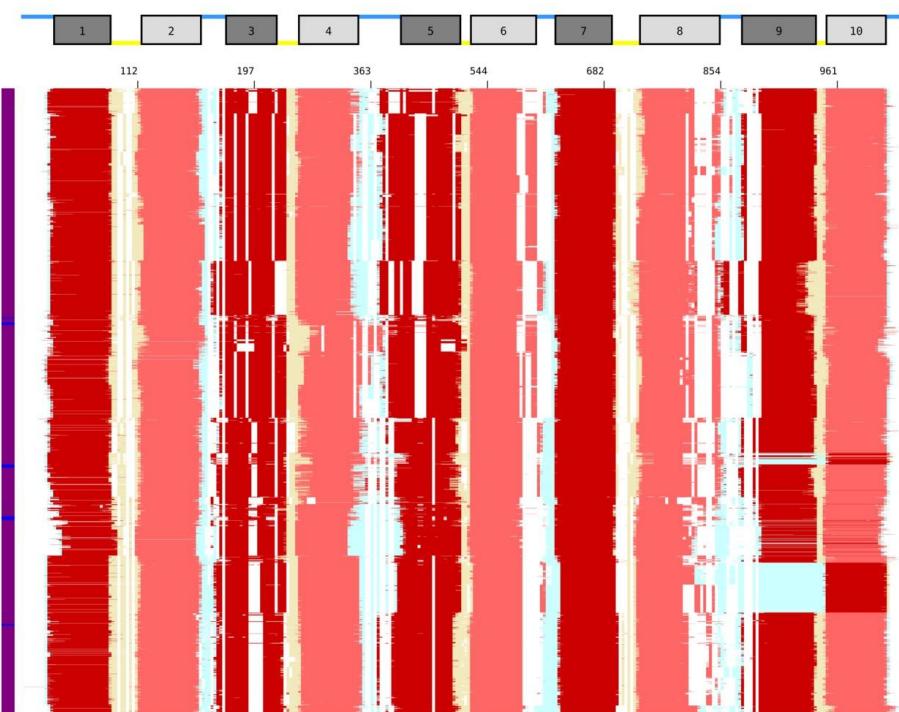
ΔG (kcal/mol)





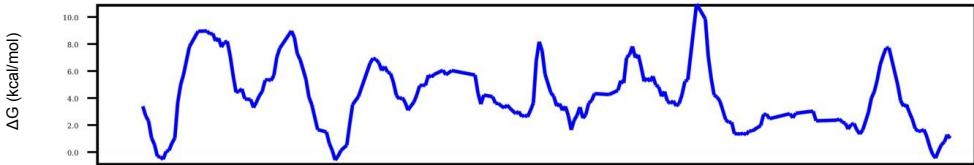
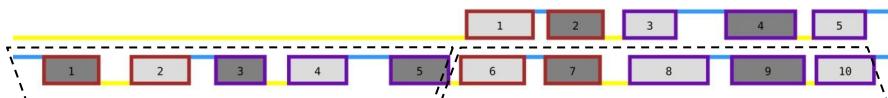
Mem_trans

Initial topology

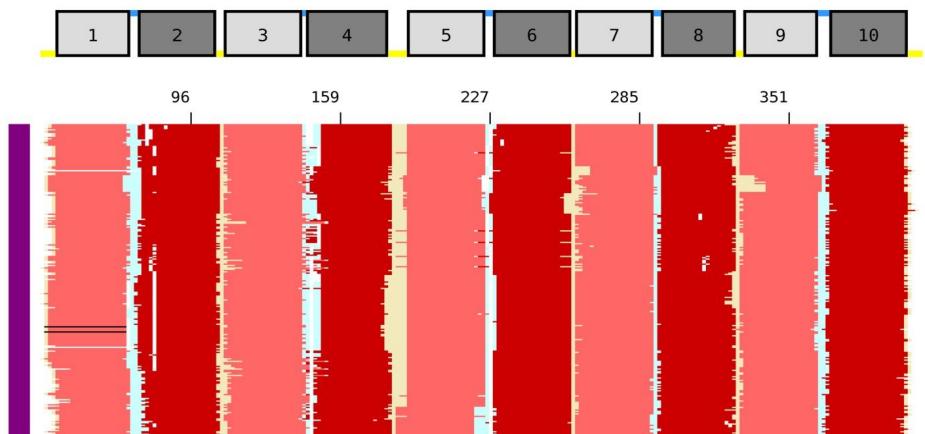


3ZUX

Final topology

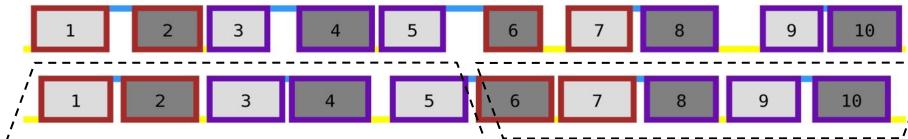


KdgT
Initial topology

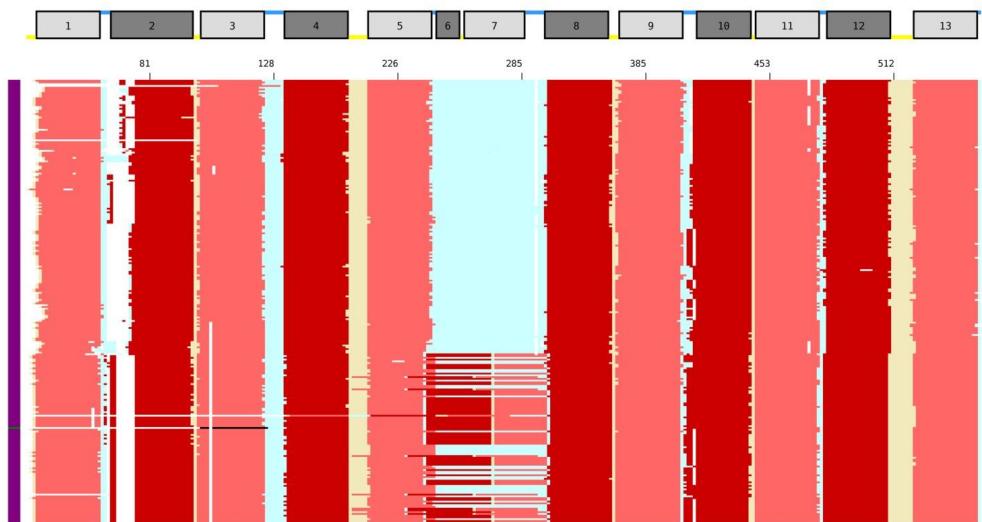


3ZUX

Final topology

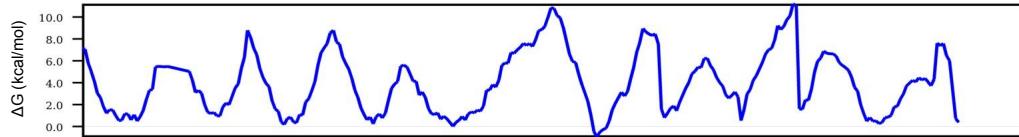
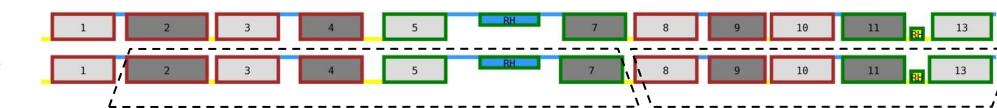


2HCT
Initial topology

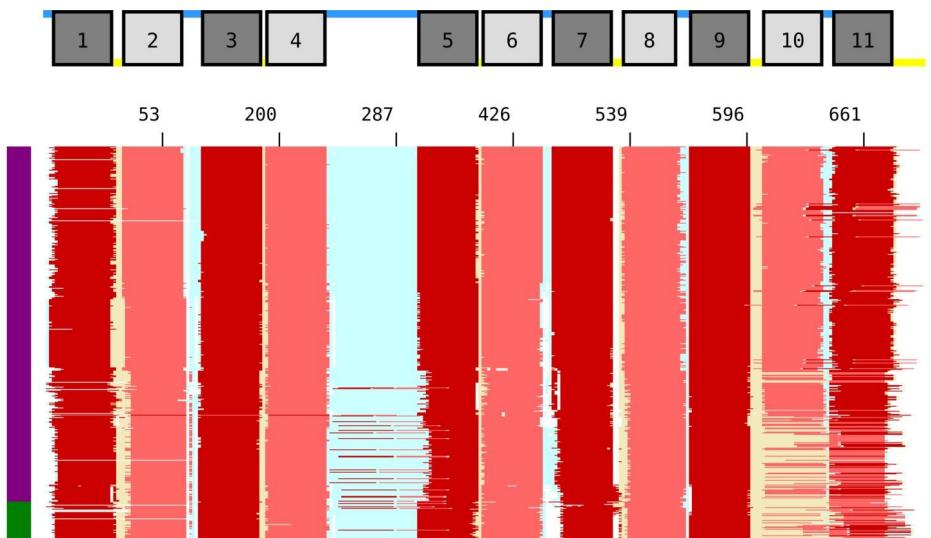


5A1S

Final topology γ

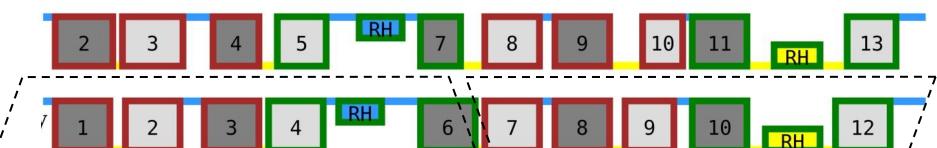


DUF819
Initial topology

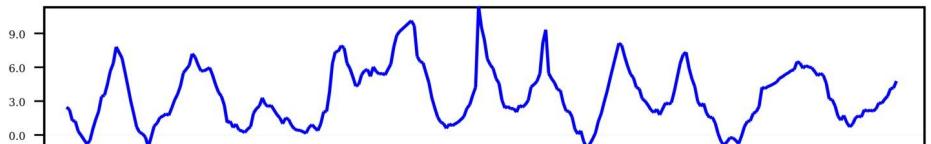


5A1S

Final topology

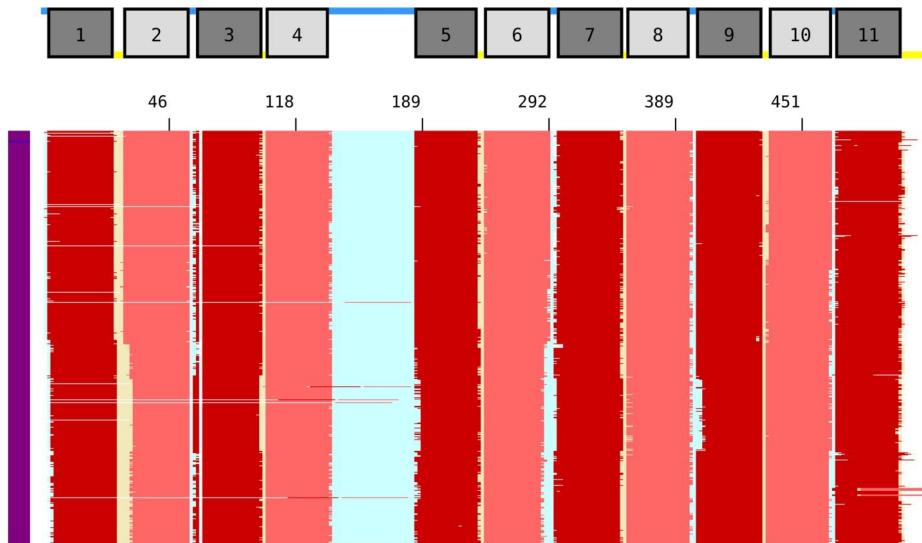


ΔG (kcal/mol)



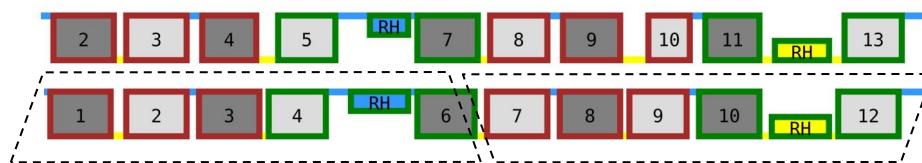
Glt_symporter

Initial topology

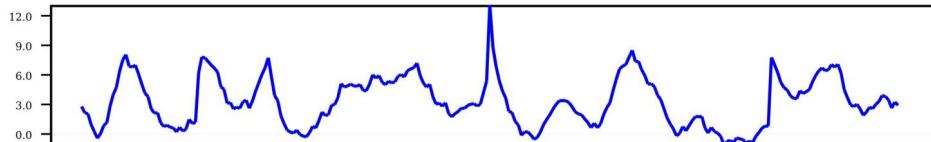


5A1S

Final topology

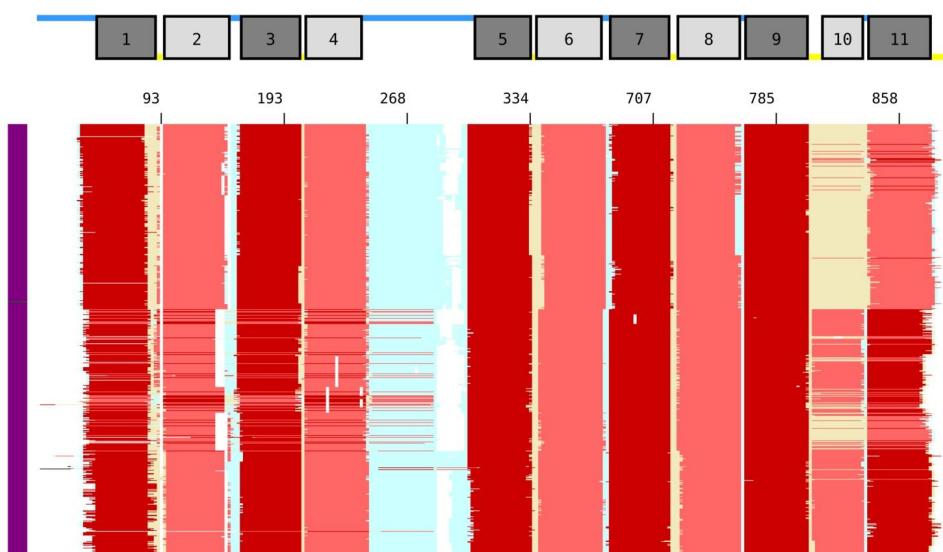


ΔG (kcal/mol)



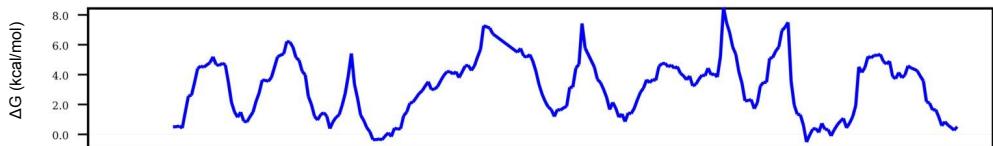
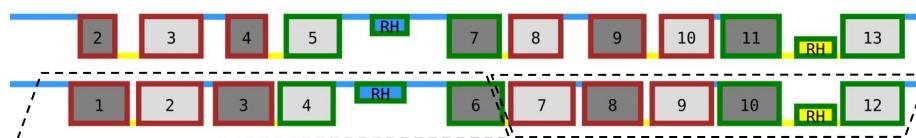
Asp_A1_Exchanger

Initial topology

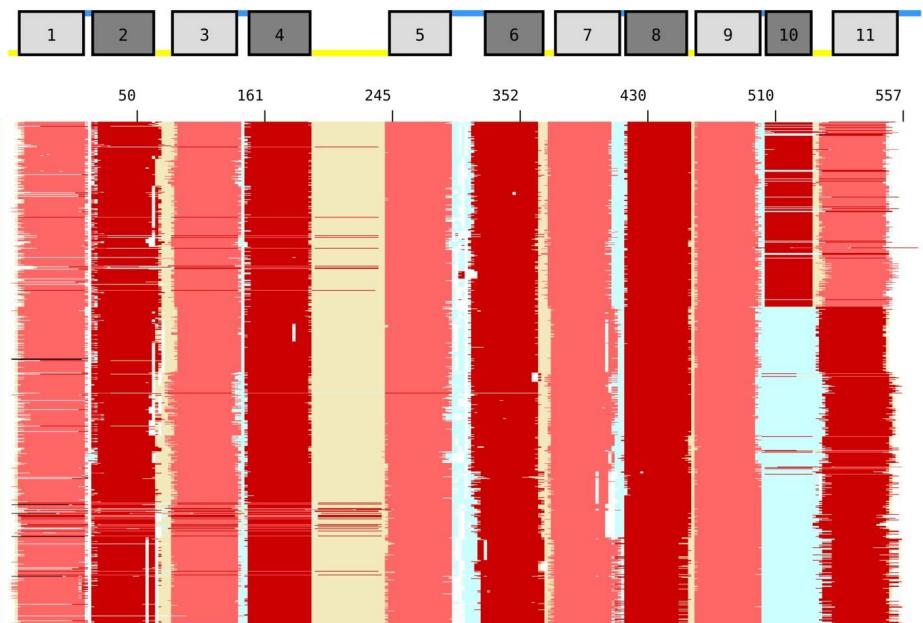


5A1S

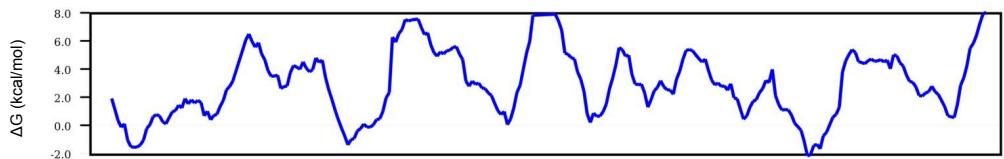
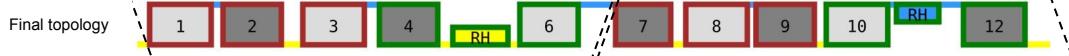
Final topology



AbrB



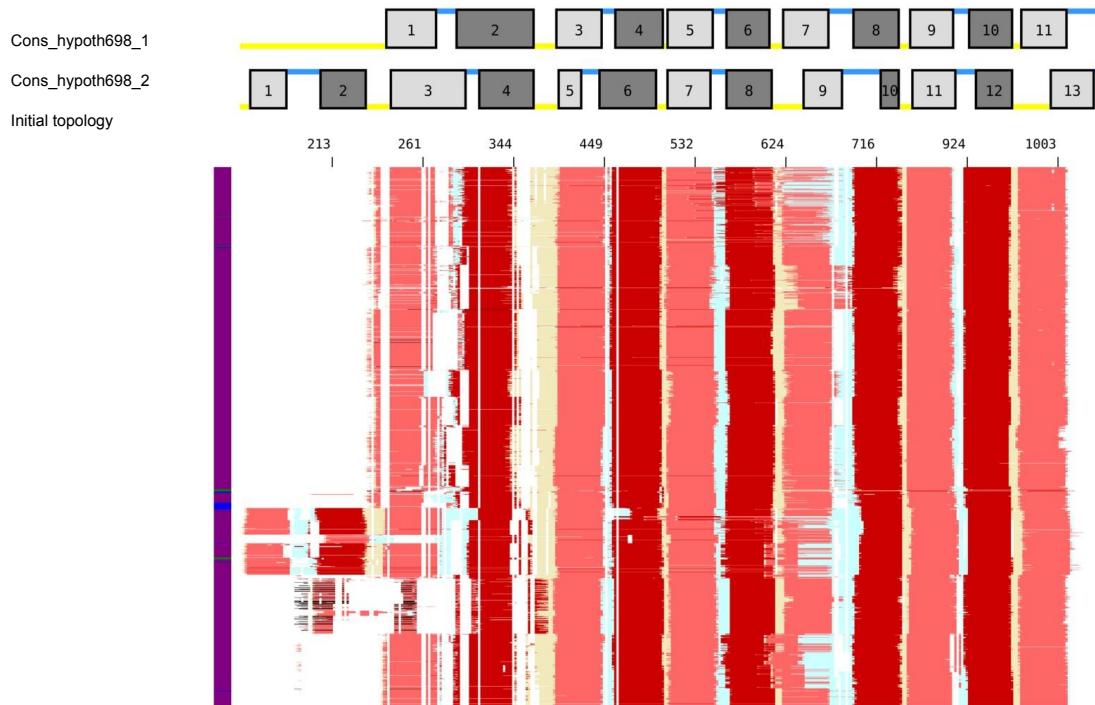
5A1S



Cons_hypothesis698_1

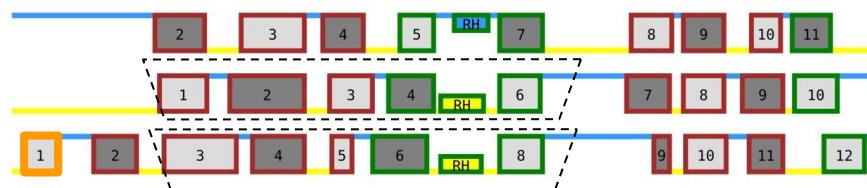
Cons_hypothesis698_2

Initial topology

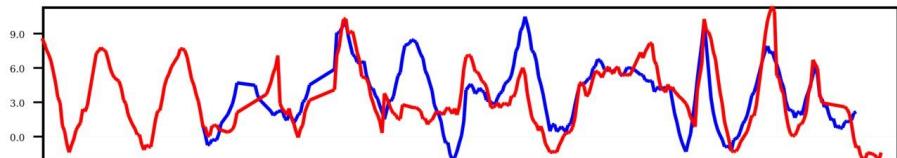


5A1S

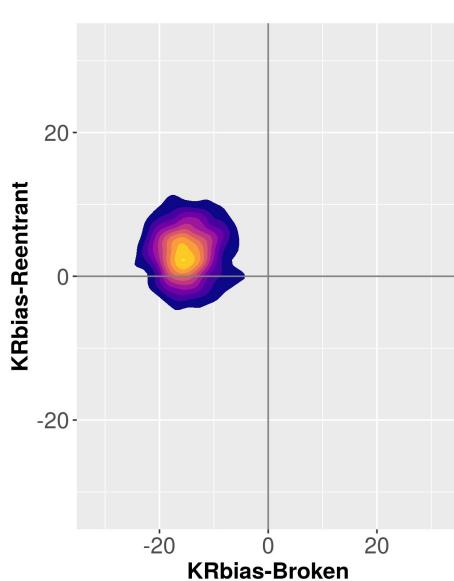
Final topology



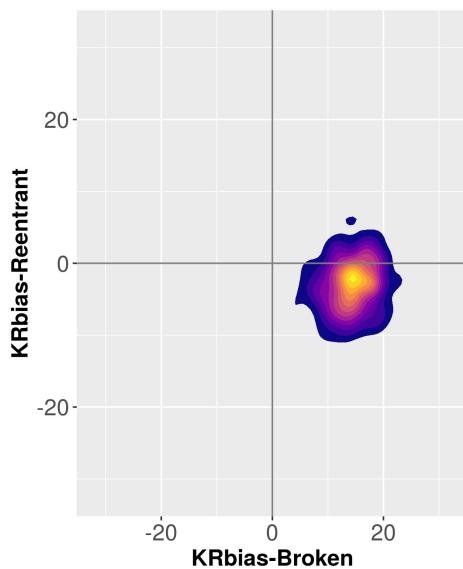
ΔG (kcal/mol)



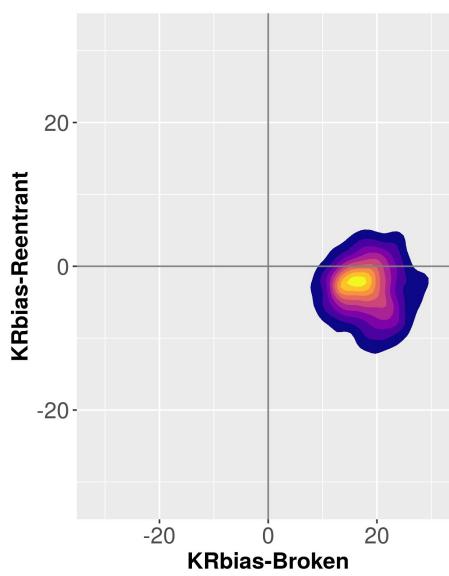
Na_H_Exchanger_1

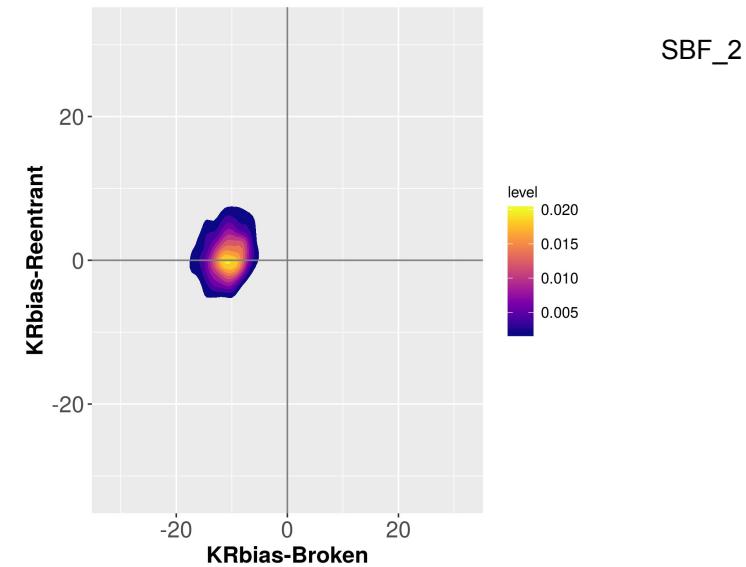
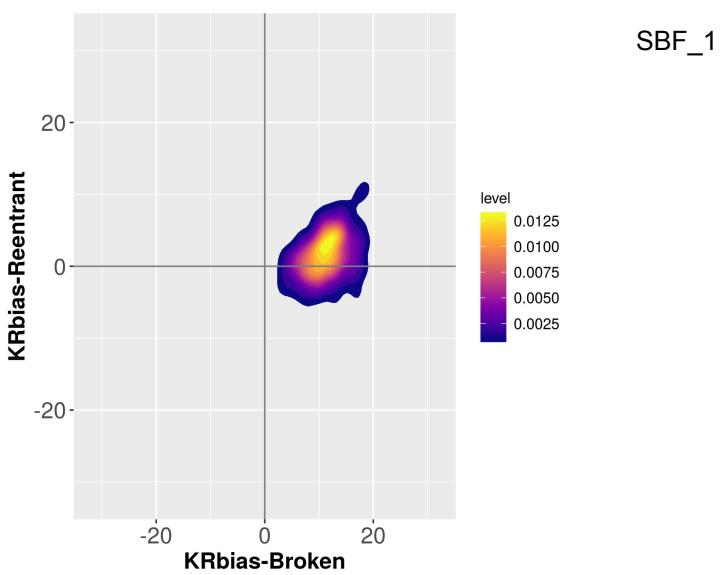


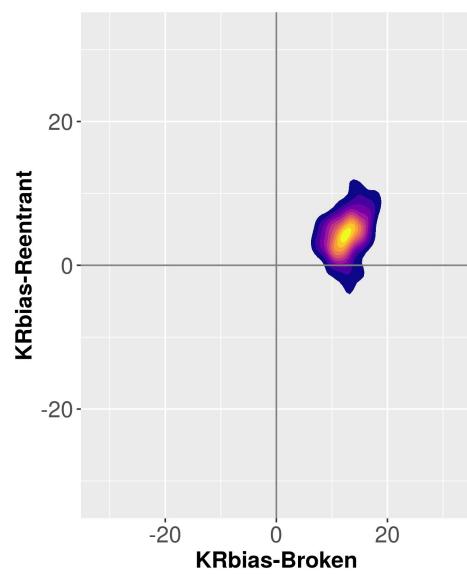
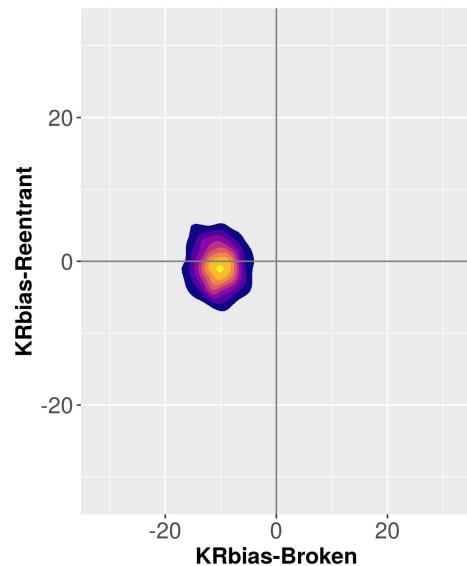
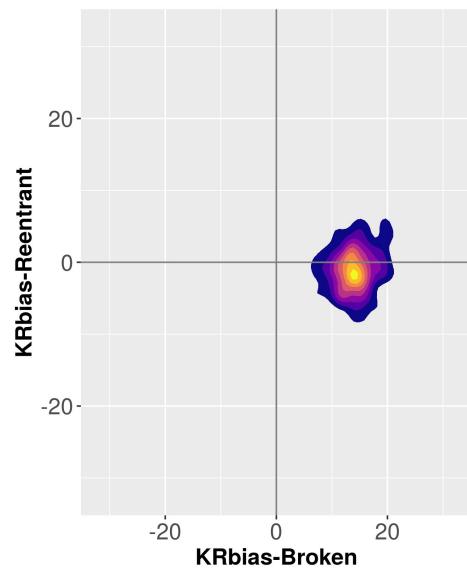
Na_H_Exchanger_2

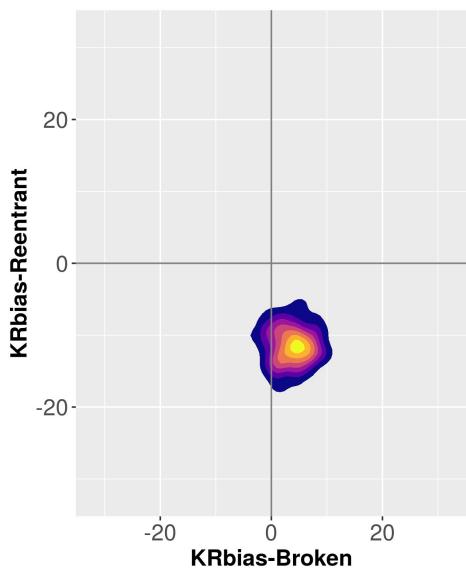


Na_H_antiport_1

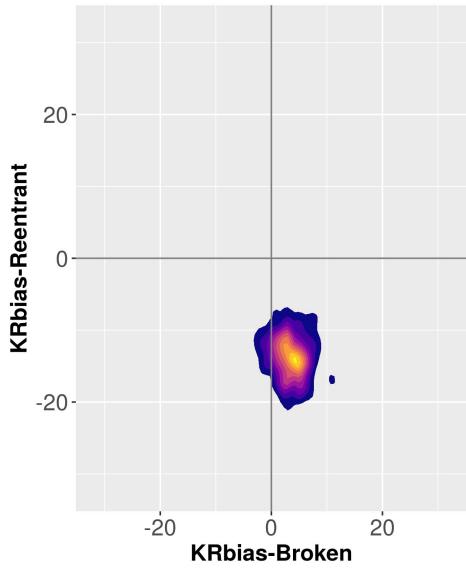




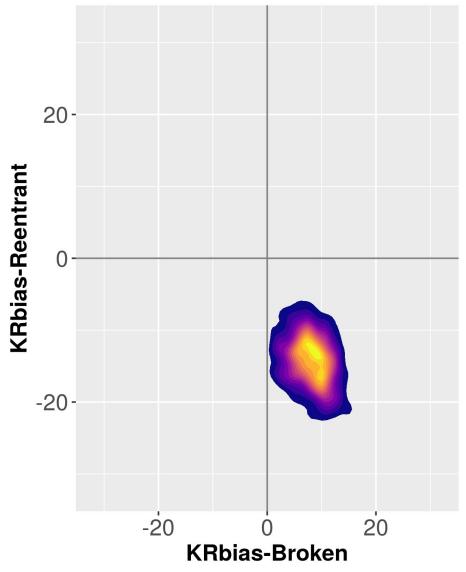




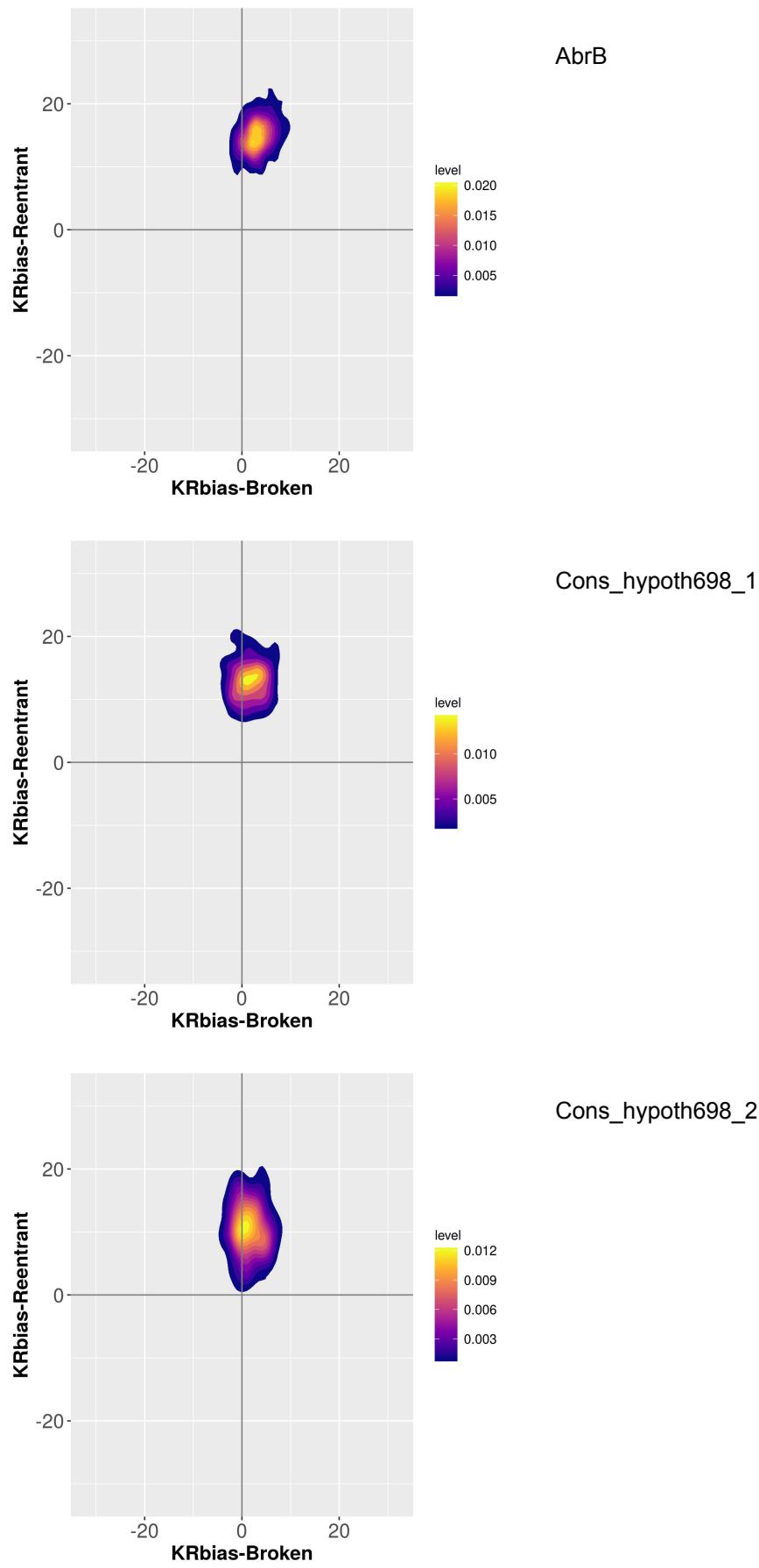
DUF819



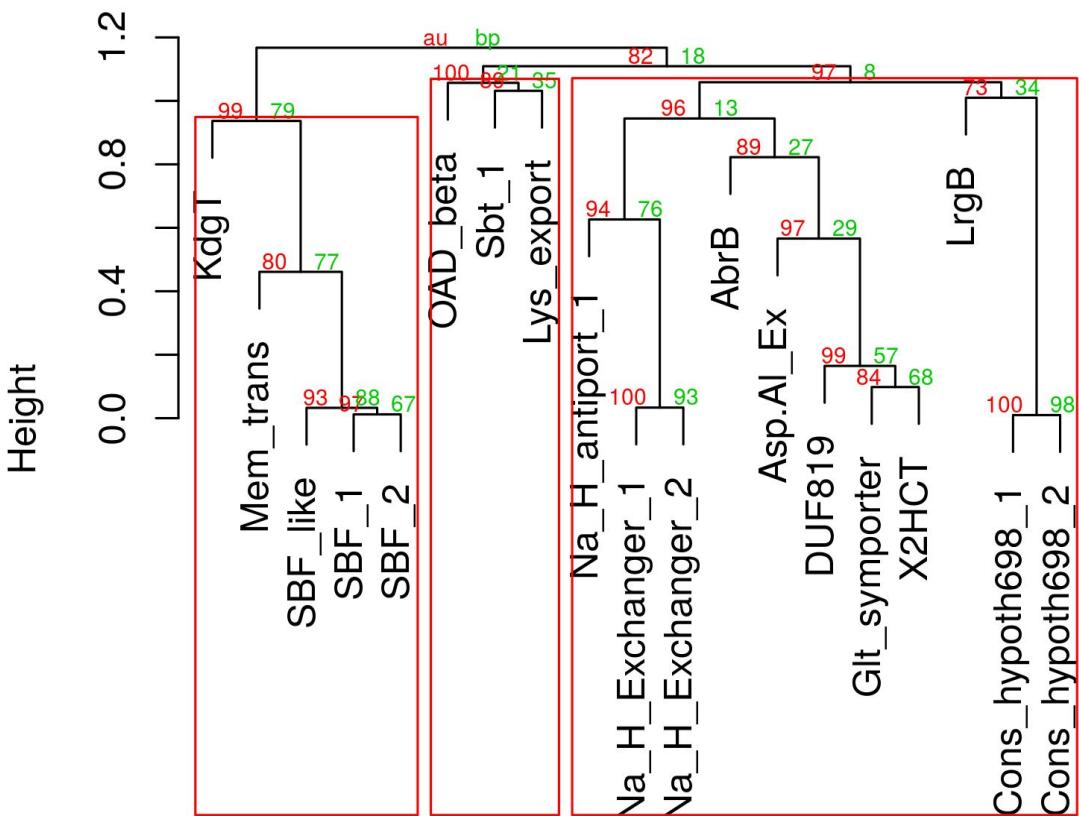
Glt_Symporter



Asp_Ai_exchanger



Cluster dendrogram with AU/BP values (%)



Distance: correlation
Cluster method: average

Supplemental figure legends

Figure S1-S14: Topology and subdomain annotation for all the families/subfamilies of CPA/AT transporters:

The topology alignment is reordered according to the phylogenetic tree to obtain a reordered topology alignment. The figure shows a reordered topology alignment. The TM helices (in-out) are coloured dark red or dark grey while TM helices (out-in) are coloured light red or light grey. Reentrant helices (in-in) are coloured yellow and (out-out) are coloured blue. The inside loops are coloured light yellow or yellow. The outside loops are coloured light blue or blue. The vertical bar is coloured based on the taxonomy of the sequences (Bacteria: Purple, Archaea: Dark blue Eukaryotes: Green). The signal peptide is coloured black. The TM helices are numbered. The initial topology is inferred from the reordered topology alignment (See Materials and methods section). The initial topology of the representative sequence of the family is shown. The representative sequence is aligned with family with known structure/topology (PDB id provided) with the lowest E-value. Based on the alignment between initial topology and known topology, the final topology is corrected for missing helices, errors in topology predictions and correction of orientation. The annotations of core and scaffold subdomain in a family with known topology are extrapolated to the aligned helices. Helices belonging to scaffold subdomains, broken core subdomains and reentrant core subdomains are shown as brown, magenta/purple (7 helical broken fold-type/5 helical broken fold-type) and green(6 helical reentrant fold-type) boxes. The additional helices are equivalent to the scaffold helices and are also shown as brown boxes. The additional helix which is not equivalent to the scaffold helix is coloured orange. N-repeat a C-repeat are shown as black trapezoids. ΔG values are obtained for the representative sequence and are plotted to the aligned residues in the representative sequence.

Figure S15-S19: KR bias calculations to validate the broken/reentrant type of transporters:

The final topology obtained for the family is used to make a broken and reentrant topology. The KR bias is calculated for both topologies. KR bias for broken transporter model and reentrant transporter model are plotted. The KR bias values are shown as 2D density scatterplot.

Figure S20: Hierarchical clustering of full length transporters with p-values:

Pvclust carries out hierarchical clustering by function hclust. Then, *p*-values for all clusters of original data is carried out. AU (Approximately Unbiased) *p*-value and BP (Bootstrap Probability) value are the two types of *p*-value provided. The clusters with *p*-value greater than or equal to $p=0.95$ are shown in red box.

Supplemental tables

Pfam Family	Number of clusters generated	Number of clusters with unique topology
1.Na_H_antiport_1: PF06965	1	1
2. Na_H_Exchanger: PF009999	57	2
3. SBF: PF01758	3	2
4. SBFlike: PF13593	1	1
5. KdgT: PF03812	1	1
6. Mem_trans: PF03547	10	1
7. 2HCT: PF03390	1	1
8. DUF819: PF05684	1	1
9. Glt_Symporter: PF03616	2	1
10. AbrB: PF05145	1	1
11. Asp_AI_Ex: PF06826	2	1
12. Cons_hypoth698: PF03601	1	2

Supplemental table 1: List of number of sequence clusters assessed to study the initial topology. Information about splitting Pfam families to subfamilies when the family showed more than one topology.

Alignment highlighted by TM regions

Alignment for AbrB-2HCT

AbrB/L0MCY2/5E-6	0	merfpa VLQWLILLLASLALGFLLAFlIPAALLGPMIVGVTI-GLLGAsvripkPLFIGA-----Q-----AVLGCMIAQSLSPS mlt	89
2HCT/5A1S_C/5E-6	0	--- TDLVGGFALMFVMGAIFGEIG krlpifnk YIGGAPVMIFLVAAYFVYAGI ftqkeidaisnvmdk SNFLNLFIAVLITGAILS VNRk	89
AbrB/L0MCY2/5E-6	90	pllad WPLILLVLLATLLASGISGWC lvrvfsdlppg TGAW-GASP---GGASAMVA-MAGD-----Fg	156
2HCT/5A1S_C/5E-6	90	lllksslgyip TILAGIVGASLFGIVIGLCFG ipvdriimly VLPIIMGGNGAGAVPLSEIYH svtg	156
AbrB/L0MCY2/5E-6	157	adv--rlvaf M--QYLRVLVFVATAAAVARIGL gdeagqgsat-----lnwfp	216
2HCT/5A1S_C/5E-6	157	rsreey YSTAIAILTIANIFAIFAAL ldmgkktytwlsgegelvrkasfkteddekagg	216
AbrB/L0MCY2/5E-6	217	pl DWRFLATLAVAAGAWLGPRL r-----ips GALLPMIIGAALHSSGAMALqVPEWLLALAY-----TLIGWSVGLRF trpill	306
2HCT/5A1S_C/5E-6	217	ith RETAGMVLSTTCFLLAYVVA kkilpsiggv SIHYFAWMVLIVAALNASGLC speikagakrlsd FFSKQLLWVLMVGVGVCYTDL q	306
AbrB/L0MCY2/5E-6	307	lalrtl-pq MLVSIAALMLFCGLLAWMLTC flpvdmmt AYLA-----TSPGGLDTVAIIAGSRv	371
2HCT/5A1S_C/5E-6	307	eiidalt FANVVIAAIIVVGAVVGAAIG gwligfypies <i>ITAGLCMANRGSGDLEVLSA</i> crrm	371
AbrB/L0MCY2/5E-6	372	dmsfv ALQTLRLFTILLTGPAlARFI snhatpassss	409
2HCT/5A1S_C/5E-6	372	n-----	409

Alignment highlighted by TM regions

Alignment for Cons_hypothesis698_1-2HCT

Cons_hypothesis698_1/N9X0P8/5.3E-13	0	mkk YTAGLLICLAlSIPAWFLGRLfPV---VG-GPVCAILIGMAIAPIK gkerfrpgi-	60
2HCT/5A1S_C/5.3E-13	0	p TDLVGGFALMFVMGAIFGEIG krlpifnk YIGGAPVMIFLVAAYFVYAGI ftqkeidais	60
Cons_hypothesis698_1/N9X0P8/5.3E-13	61	af----ts KKILQYAVVLLGFMNLSVVLe krgr QSLPIILATITTSILIAVLLF rlki	120
2HCT/5A1S_C/5.3E-13	61	nvmdk SNFLNLFIAVLITGAILS VNRkllksslgyip TILAGIVGASLFGIVIGLCFG i	120
Cons_hypothesis698_1/N9X0P8/5.3E-13	121	ptk SAILIGVGSSICGGSAIAAT--Ap v----iead-de EIAQSISVIFLFNIAAALIFP al	182
2HCT/5A1S_C/5.3E-13	121	pvdrimmyl VLPIIMGGNGAGAVPLSEIYH svtrsreey YSTAIAILTIANIFAIFAAL	182
Cons_hypothesis698_1/N9X0P8/5.3E-13	183	gtalglsnegfglfagtaindtssvtaaaaawdgiygsntleaa AIVKLTRTLAIIPITLFLAFY rtk	250
2HCT/5A1S_C/5.3E-13	183	dmvgkkytwlsg--egelvrk-----asfkteddekagqith RETAGMVLSTTCFLLAYVVA k	250
Cons_hypothesis698_1/N9X0P8/5.3E-13	251	keqsgsgntfqia KFPFFVLFLLASVLTVFHL patvtgplk DLSKFF---IIMAMAAIGTN-TNLV t	321
2HCT/5A1S_C/5.3E-13	251	kilp----siggv SIHYFAWMVLIVAALNASGLC speikagakrlsd FFSKQLLWVLMVGVGVCYTDL qe	321
Cons_hypothesis698_1/N9X0P8/5.3E-13	322	lvktgmkpi LLGLCCWIGISLVSLSMQSFL giw	354
2HCT/5A1S_C/5.3E-13	322	iidalt FANVVIAAIIVVGAVVGAAIGg-----	354

Alignment highlighted by TM regions

Alignment for Cons_hypothesis698_2-2HCT

Cons_Hypothesis698_2/Q251E9/8.6E-8	0	stntyarkkalqnedw WAALGLFIFALGLGPYFGAD llgwvtkasvwiepakafapvska	60
2HCT/5A1S_C/8.6E-8	0	-----	60
Cons_Hypothesis698_2/Q251E9/8.6E-8	61	tlng FTSLLVTFLVLAITTVAAKF vgsnlkky AIGFSIIFWVTMGCLMLG-NIA yiga	120
2HCT/5A1S_C/8.6E-8	61	----- LPLYAFALITLLSHF ynaip TDLVGGFALMFVMGAIFGEIG krlpif--	120
Cons_Hypothesis698_2/Q251E9/8.6E-8	121	tpdktasgig-wslgl GEMGYIIIAMVGLIIGNFFIK qadflkeaa-----kpe LEFIKIGIVVLGASIAIKTLDA f	200
2HCT/5A1S_C/8.6E-8	121	-----nk Y-IGGA-----PVMIFLVAAYFVYA-GI ftqkeidaisnvmdk SNFLNLFIAVLITGAILS VNRkllks	200
Cons_Hypothesis698_2/Q251E9/8.6E-8	201	glatti IIRGLCAVVEAYLIYWPVVYLiarkffkftp EWAAPLASGISICGVSAAIAT--gsa--	266

2HCT/5A1S_C/8.6E-8	201 llgyip TIL-----AGIVGASLFGIVIGL-CFG ipvdrimmly VLPIMGGNGAGAVPLSEIYH s	266
Cons_Hypoth698_2/Q251E9/8.6E-8	267 -irar-pvi PVI LSAVIIVFVALE LLLLPW laqaflfkdpmvagawmglavksdggaias	326
2HCT/5A1S_C/8.6E-8	267 vtgrsreey YSTAIAILTIANIFAIIFAAL ldmvgkk-ytwlsg--egelvrkasfk---	326
Cons_Hypoth698_2/Q251E9/8.6E-8	327 gaitdsrirgralrelginweegwilmvattkv FIDIFIGWAFILAIWSVFP idkna	386
2HCT/5A1S_C/8.6E-8	327 --tedde-----kaggith RETAVGMVLSTTCFLAYVVA kkilpsig	386
Cons_Hypoth698_2/Q251E9/8.6E-8	387 sanpgernkvsavdiwdrf PKFIIGFVLTFILFLVGVN pdgvkalstgvnegr AFRTIF---FGLCFFSIGLV-TNVR k	468
2HCT/5A1S_C/8.6E-8	387 -----gv SIHYFAWMVLIVAALN-ASGLC speika-----gakrlsd FFSKQLLWVLVMVGVGVCYTD qe	468
Cons_Hypoth698_2/Q251E9/8.6E-8	469 lwaegmgrivaiy GIALFGFILWFGLFISWLFYH	502
2HCT/5A1S_C/8.6E-8	469 iidal-t FANVVIAAIIVVGAVVGAAIG gwli--	502

Alignment highlighted by TM regions

Alignment for DUF819_2HCT

DUF819/A0A0B7I5I0/1.8E-30	0 mqlpi ANDAVVLGLLMVCLGFVFYTS sqktkfkwv- FYTIFPALLICYILPAILNSI giis	60
2HCT/5A1S_C/1.8E-30	0 --aip TDLVGGFALMFVMGAIFGEI-G krlpifnk YIGG---APVMIFLVAAYFVYAGI ft	60
DUF819/A0A0B7I5I0/1.8E-30	61 nk-tsny FYV-----ASRYLLPAALILMTLSID lravfnlgak ALIMFFAGTFIGIIIGGPLAIL ivst	128
2HCT/5A1S_C/1.8E-30	61 qkeidaisnvmdk SNFLNLFIAVLITGAILS vnrkllksllgyip TILAGIVGASLFGIVIGLCFG-	128
DUF819/A0A0B7I5I0/1.8E-30	129 fmpeavggvp DAWRGLSTVAGSWIGGGANQ aam--lei---ykyn-pekyg AMV---IVDIVVANIWMAFLLFGI g	207
2HCT/5A1S_C/1.8E-30	129 -----ipvdrimmly VLPIMGGNGAGAVPLSEIYH svtgrsreey YSTAIAILTIANIFAIIFAAL ldm---	207
DUF819/A0A0B7I5I0/1.8E-30	208 ksdkidrwlkadnssiedlnrvvisfsekttkkqptl VDYKVMLALAFGGVGLSHFGA dii	267
2HCT/5A1S_C/1.8E-30	208 ---vgkkytwlsgegelvrkasfkteddekagqith RETAVGMVLSTTCFLAYVVA kkii	267
DUF819/A0A0B7I5I0/1.8E-30	268 tdfksnfesirnaqsatsff GDTFFWLVTATLIGILLSFT karnyega GASKLGSVF---IYVLVATIGMK-M nlt	346
2HCT/5A1S_C/1.8E-30	268 lpsig-----gv SIHYFAWMVLIVAALN-ASGLC speika--gakrlsd FFSKQLLWVLVMVGVGVCYTD q	346
DUF819/A0A0B7I5I0/1.8E-30	347 qvfdn-- PGLLLVLGLIWIHVLMFLV akiirapyf FLAVG---SKANVGAASAPVVA sa	408
2HCT/5A1S_C/1.8E-30	347 eiidal-t FANVVIAAIIVVGAVVGAAIG gwligfypies <i>ITAGLCMANRGSGDLEVLSA</i> c	408
DUF819/A0A0B7I5I0/1.8E-30	409 fhpslat VGVLLAVLGYVV-GTYGAMLSA ylmeiasqmq	447
2HCT/5A1S_C/1.8E-30	409 nrmnlisyaqi SSRLGGGIVLVIASIVFSMMV-----	447

Alignment highlighted by TM regions

Alignment for Glt_symporter-2HCT

Glt_symporter/A0A0Q1HN67/6.9E-28	0 ki QLDMYQTAAAVLVLLGNYL rkkinflek FCIPAPVIGGLFAIFTC-ICY ttgiief	60
2HCT/5A1S_C/6.9E-28	0 aip TDLVGGFALMFVMGAIFGEI-G krlpifnk YIGG---APVMIFLVAAYFVYAGI ftq	60
Glt_symporter/A0A0Q1HN67/6.9E-28	61 sfddt L-----REVCVMFFTSVGFQANLKVL ksgr SLIVFLGLVITLFSQNLLAI gskllnl	130
2HCT/5A1S_C/6.9E-28	61 keidaisnvmdk SNFLNLFIAVLITGAILS vnrkllksllgyip TIL---AGIVGASLFGIVIGLCFG i	130
Glt_symporter/A0A0Q1HN67/6.9E-28	131 npl IGMCTGSIP-MVGGHGTAGA-FG pvled-fnihg-- ATTICTAAATGLITGSVLGG pi	192
2HCT/5A1S_C/6.9E-28	131 pvdrimmly VLPIMGGNGAGAVPLSEIYH svtgrsreey YSTAIAILTIANIFAIIFAAL i	192
Glt_symporter/A0A0Q1HN67/6.9E-28	193 gkrliekrklmdnvpteddsllvedeekhqrhtnm YAAAVFQLILAIGLGTFSYF ltkt	252
2HCT/5A1S_C/6.9E-28	193 dmvgkkytwlsgegel-vrkasfkteddekagqith RETAVGMVL-STTCFLAYVVA kk	252
Glt_symporter/A0A0Q1HN67/6.9E-28	253 g----- LTFPPIYIGAMLAALMRNITE ysgkgtihm <i>EINDLGG-----ICLSLFLGMAMITL</i> klw	319
2HCT/5A1S_C/6.9E-28	253 ilpsiggv SIHYFAWMVLIVAALN-ASGLC spe--ikagakrlsd FFSKQLLWVLVMVGVGVCYTD q	319

Glt_symporter/A0A0Q1HN67/6.9E-28	320	elatl A LPLVILLA Q TLLICVF T YFvifnvmgrdydaa V LSAGTCFG M GATPNAMANM q aic	383
2HCT/5A1S_C/6.9E-28	320	eiidalt F ANVVIAAI V GA V GA I Ggwligfypies <i>s</i> T AGLCMANRG G S D LEVL-S <i>c</i>	383
Glt_symporter/A0A0Q1HN67/6.9E-28	384	dryvpsvka Y LI I PLIGSL F AD F INS L VITffini	418
2HCT/5A1S_C/6.9E-28	384	nrmnlisyaqi S S- R LG G GIV L VI A SIV F SMM---	418

Alignment highlighted by TM regions

Alignment for KdgT-SBF_1

KdgT/A0A072XF91/4.9E-13	0	mkilksvkvp G GLM V IP L LL G A S INT F PTA	lsiggftt A LF K K S AT A LI A LF V LC N GA Q idvk	64
SBF_1/3ZUY_A/4.9E-13	0	mnilkiss F IG K TF S LWA A LF A AA A FF A P	dt-----fkwa G PY I P W LL G I M FG M GL T K <i>p</i>	64
KdgT/A0A072XF91/4.9E-13	65	qagkplykgi V L T --- V K F ILGAF I GW I V G K T <i>f</i>	g NAGV G L T PL A LV A ALTN S NGglya	124
SBF_1/3ZUY_A/4.9E-13	65	dfdilfkhp K V V I G V I A Q F A IMP A T A WL S skllnl P AE I AV G V I L V G C CP G GT A N <i>vmt</i>	124	
KdgT/A0A072XF91/4.9E-13	125	alaggqgdstdvgais I LS L ND G P F FT M LA F GI S GL A <i>n</i> I PF I A----- F IA V I I P I L V G F IL G <i>m</i>	191	
SBF_1/3ZUY_A/4.9E-13	125	ylar--gnva L SV A V T SV S TL I SP L LT P AI F <i>l</i> mlagemleiq A AG M LM S I V K M V L PI V GL <i>vhk</i>	191	
KdgT/A0A072XF91/4.9E-13	192	deelrkfl A Q--- G QT L IP F FA P FL G A AL N F <i>k</i> tiikag L PG L LL G FM V V L IT G FG G Y <i>f</i>	252	
SBF_1/3ZUY_A/4.9E-13	192	lgsktekld A L P LV S V A A V I L I G AV V G A S <i>k</i> gkimes G LL I F V V L H N G I G Y LL G <i>ff</i> <i>aa</i>	252	
KdgT/A0A072XF91/4.9E-13	253	rlf-skqkrav G AA I GT T AG N S V AT P AA L AL A <i>d</i> sslkpyvas A TA Q L A A V I V T A IL C PLL V <i>s</i> <i>yldkk</i>	320	
SBF_1/3ZUY_A/4.9E-13	253	kwtglpydaqktltievgmq N SG L AA A AA A HF A --- A P V V A <i>v</i> G AL F SV W H N I S GS L AT Y W A <i>ak</i>	320	
KdgT/A0A072XF91/4.9E-13	321	dkv 323		
SBF_1/3ZUY_A/4.9E-13	321	ag- 323		

Alignment highlighted by TM regions

Alignment for Mem_trans-SBF_1

Mem_trans/D4J5G2/3.8E-10/0.17	0	msnfm F SLNA-TLPVFLVIVLGWFL M Qkkmfnenfv <i>d</i> I INK F V K V S LP V LL F K D <i>AT</i> t pi	60
SBF_1/4N7W_A/3.8E-10/0.17	0	--dv V GML K SIL Q I V IP I TAG L <i>v</i> V htftktvkrip Y LP A MS M V C I L I A I S AV V AG <i>s</i>	60
Mem_trans/D4J5G2/3.8E-10/0.17	61	rda <i>f</i> -dp K VF I FC M VG T TI M FG I W A LT s ifmkdksmvgaf T Q A S R G S AA V LG I AF V Q N I Y <i>gns</i> M T P LM I V S A V P L Y N I Y S II L <i>t</i>	148
SBF_1/4N7W_A/3.8E-10/0.17	61	hias V GF V V I IA V I L H N G I G L <i>sg</i> F DE S TC R TL A I E VG M Q N <i>s</i> - G <i>la</i> t lgkiy f S PL A LP G AL F SV W h-- N LS G <i>sl</i>	148
Mem_trans/D4J5G2/3.8E-10/0.17	149	fcannqdhsdksatikrafkn I LT N PI I LG I AG V P F SL N <i>i</i> e lpplvl <i>k</i> T TV N V A QT A TP M ALL A VG G <i>fegr</i>	222
SBF_1/4N7W_A/3.8E-10/0.17	149	ywsgkpvkkdqe-----lvki TR LF P V W ALL S V A Y F R P <i>tt</i> f --- t gi G PY V G P LL M IM F AM G V T <i>RL</i> <i>d</i>	222
Mem_trans/D4J5G2/3.8E-10/0.17	223	kaikk---lkptmi A TF I K L VA P I Y F P FA I AM G <i>fres</i> A LV A IL I M V G S PT T V T C I M <i>ak</i>	283
SBF_1/4N7W_A/3.8E-10/0.17	223	dfkrvlsrp A P V AA T FL H Y L IM P LT A WI L <i>a</i> m lfrmp P D L S A GM V L G S V AS G T A N <i>viy</i>	283
Mem_trans/D4J5G2/3.8E-10/0.17	284	nmgnndgv <i>l</i> s <i>s</i> S I I V M AT L SS V T L T W I F L <i>ksmgl</i>	319
SBF_1/4N7W_A/3.8E-10/0.17	284	lakgdva L SV T IS A V S T L V G V F AT P LL <i>rly</i> ----	319

Alignment highlighted by TM regions

Alignment for Na_H_Exchanger_2-Na_H_Exchanger_1

Na_H_Exchanger_2/M3YCW9/8.4E-34	0	ayqeiqueetvmtskatdakeptegsnllnshekkllqlptesnnlqlrqtfcpphg F LDR G IT N VT M V V LL W AV V WS <i>i</i>	79
Na_H_Exchanger_1/4CZB_C/8.4E-34	0	-----	79
Na_H_Exchanger_2/M3YCW9/8.4E-34	80	tgseclpgg N L F GI I I F Y C AT G K L <i>gl</i> I klptl P PL P RL L G M <i>ll</i> AG F LL R N I P <i>vn</i>	140
Na_H_Exchanger_1/4CZB_C/8.4E-34	80	----- A IG Y GL A L V GL S LV A K I aeklk I P----- D IP L LL L GL I I G P - L Q I I <i>p</i>	140

Na_H_Exchanger_2/M3YCW9/8.4E-34 141 iqikhk**WSSALRSIALSIIILVRAGLGL**dskalkklkgv**CVRLSMGPCCLVEACTSALLAH**flm 202
 Na_H_Exchanger_1/4CZB_C/8.4E-34 141 sdsame**IFEYAGPIGLIFILLGGAFTM**risllkrviktvv**RLDTITFLITLLISGFIFNMV**l 202

 Na_H_Exchanger_2/M3YCW9/8.4E-34 203 glpw--**QWGFIILGFVLGAVSPAVVPS**mlllqeggygvekgiptllmaa**GSFDDILAITGFNTCLGMAFS**tg 274
 Na_H_Exchanger_1/4CZB_C/8.4E-34 203 nlpystsp**VGYLFGAITAATDPATLI**--**PVFsrvr**--tnpevaitleaes**IFNDPLGIVSTSVILGLFGLFs** 274

 Na_H_Exchanger_2/M3YCW9/8.4E-34 275 kllfas**LIREMIETILGEDFNTTLKFF**pqiyyiclkdk**LWVKRAFLVLGLSVLAVFSSyF**----**GFPGSGGLCTLVMSFLAGLR**was 363
 Na_H_Exchanger_1/4CZB_C/8.4E-34 275 s--snpl**IDLITLAGGAIIVVGLLLAKI**--Yekiiihcdfh**EYVAPLVGGAMLLLYVGDDL**lpsicg**YGFSGYMAVAIMGLYLGDAF**r 363

 Na_H_Exchanger_2/M3YCW9/8.4E-34 364 ek---aeveki**IAGAWYIFQPLLFGGLIGAEVS**iaslrpetv**GLCVAILGIAVLIRILTTFLM**v 427
 Na_H_Exchanger_1/4CZB_C/8.4E-34 364 addidykyivsfc**DDLSLLARVFIFVFLGACIKL**smleny**FIPGLLVALGSIFLARPLGVF**lgl 427

 Na_H_Exchanger_2/M3YCW9/8.4E-34 428 cfagfnikeki**FISFAWLPKATVQAAGSVAL**dtarshgekq-----leeygmd**VLTVAFLSILITAPIGSLLIG**l 507
 Na_H_Exchanger_1/4CZB_C/8.4E-34 428 igskhsfkekly**FALE-GPRGVVPAALAVTVGIE**ilknakipasitkyitptdiag**TIIIGTFMTILLSVILEASWA**gm 507

 Na_H_Exchanger_2/M3YCW9/8.4E-34 508 lgprllrkaehqnkgeevqeetsiq 532
 Na_H_Exchanger_1/4CZB_C/8.4E-34 508 lalkllgeykpkyleeeshh----- 532

Alignment highlighted by TM regions

Alignment for SBF_1-SBF_2

SBF_2/H2Y8C2/3.3E-31 0 kveqnrnint**AISVLVVVVLAFLVMVSLGCTM**tlskimeharkp**KGVIALVAQFLIMPASAFLG**lq 65
 SBF_1/4N7W_A/3.3E-31 0 **AYFRPTT**f-tgi**GPyVGPLLMLIMFAMGVTLRL**ddfkrvlsrpap**VAAATFLHYLIMPLTAWILA**m 65

 SBF_2/H2Y8C2/3.3E-31 66 a**FQLDTYAAIAVLICGCCPGGN**nsnmlayslsgdmdlsls**LMTTCSSVIGLGMMPPLSIYLY**s 126
 SBF_1/4N7W_A/3.3E-31 66 lfrmp**PDLASAGMVLVGSVASGTASN**miylakgdval**LSVTISAVSTLGVFATPLLT**rlyv 126

 SBF_2/H2Y8C2/3.3E-31 127 qlitplsasmv**PFDKIVINILL-TVLPGAGII**irhyrpqwtrnimrlmrtpplaesvrtq**RIFGGLMLLLCSISVAVLAGI**mlgd 211
 SBF_1/4N7W_A/3.3E-31 127 da-----tisvdv**VGMLKSILQIVVIPITAGLVI**hhtftktvkriep**YLP**-----**AMSMVCILA**--**IISAVVAG**--Sq 211

 SBF_2/H2Y8C2/3.3E-31 212 affrrfdas**SVIACCAILPMMSGYLGLYF**allfrenpkrr**TICVETGCQNVLCSTVLKLA**f 273
 SBF_1/4N7W_A/3.3E-31 212 shias**VGFVIIIAVILHNGIGLLSGY**wggklfg**FDESTCRTLAIEVGMQNSGLA**atlgkiyf 273

 SBF_2/H2Y8C2/3.3E-31 274 dpiivgvlf**LPLVYMAFQVAEAFLIIFVFR**vy 306
 SBF_1/4N7W_A/3.3E-31 274 **SPLA**---**ALPGALFSVWHNLSGS**lagywsgk 306

Alignment highlighted by TM regions

Alignment for Sbflike-SBF_1

Sbflike/A0A077PBM8/2.4E-36 0 mswwqkler**IDPFLVTLLITVVIATLFPCE**geskk**WFQYLTTAAIALLFFMHGAKL**srgail 60
 SBF_1/4N7W_A/2.4E-36 0 ---mlvki**TRLFPVWALLSVAAYFRPTT**f---tgi**GPyVGPLLMLIMFAMGVTLRL**ddfk 60

 Sbflike/A0A077PBM8/2.4E-36 61 agighwr**LHLVIFLSTFLFPILGMLY**fivpewlsp**VYMGFLYLCALPATVQSIAFT**t 120
 SBF_1/4N7W_A/2.4E-36 61 rvlsrpap**VAAATFLHYLIMPLTAWILA**mlfr--mp**PDLASAGMVLVGSVASGTASN**-mi 120

 Sbflike/A0A077PBM8/2.4E-36 121 svakgnva**AAICASASSLLGVFISPLLV**glliqtndgggytdt**KAIKDILQLMVPFIAGHLSR**p 187
 SBF_1/4N7W_A/2.4E-36 121 ylakgdval**LSVTISAVSTLGVFATPLLT**rlyvdat---isvdv**VGMLKSILQIVVIPITAGLVI**hh 187

 Sbflike/A0A077PBM8/2.4E-36 188 liaswvehkklvnttd**RSSILLLVVVAFSEAVVEGIW**hkida**YSLMMIGVCCVLLAIVLMIN**vy 253
 SBF_1/4N7W_A/2.4E-36 188 tftktvkriep**YLPAMSMVCILAIIISAVVA**---**GS**qshias-**VGFVIIIAVILHNGIGLLSGY**w 253

 Sbflike/A0A077PBM8/2.4E-36 254 ssrlfgfskededitivfcgskkslang**VPMANVLFPASMVGVMLLPLM**i**FHQIQQLMVCAVLAQRYARRPK** 324
 SBF_1/4N7W_A/2.4E-36 254 ggklfg**FDESTCRTLAIEVGMQNSGLA**atlgkiyf**SP**---**LAALPGALFSVWHNLSGS**lagywsgkpvk 324

 Sbflike/A0A077PBM8/2.4E-36 325 ad 326
 SBF_1/4N7W_A/2.4E-36 325 kd 326

Alignment highlighted by TM regions

Alignment for Cons_hypoth698_1-Cons_hypoth698_2

Cons_hypoth698_2/Q251E9/3.7e-54	0	WAAWLGLFIFALGLGPYFGADllgwvtkasvwiepakafapvskatglnqFTSLLVTFLVLAITTVAAKFv	71
Cons_hypoth698_1/Y1621/3.7e-54	0	-----	71
Cons_hypoth698_2/Q251E9/3.7e-54	72	gsnlkkyAIGFSIIFWVTMGCMLGNIAyigatpdktasygigwslglGEMGYIIAMVGLIIGNFFIKqa	142
Cons_hypoth698_1/Y1621/3.7e-54	72	-----QMLLLLLLCAAAAYIINLA-----dPALEP-----LFLALVFGIVAGN-L-QRd	142
Cons_hypoth698_2/Q251E9/3.7e-54	143	dflkeak--peLFIKIGIVVLGASIAIKTLDAfglattiIIRGLCAVVEAYLIYWVVYlia	205
Cons_hypoth698_1/Y1621/3.7e-54	143	eekkrvverYVPFLLPIGITLYGVNINIPYlgefhPEIVAATL-----ISTSLIFLTFWLs	205
Cons_hypoth698_2/Q251E9/3.7e-54	206	rkffkftpEWAAPLASGISICGVSAAIAtgsairarpviPVILSAVIIVFVALELLLLPwl	266
Cons_hypoth698_1/Y1621/3.7e-54	206	s-rlklksrqmSILLACGSGICGVSAIAIISPlikprkeeFSAAIMIITAVGLTGAILYPSi	266
Cons_hypoth698_2/Q251E9/3.7e-54	267	aqaflfkdpvgawmglavksdggaiasgaitdsrirgralrelginweegwilmvatttkvFIDIFIGVWAFILAIWSVFPi	351
Cons_hypoth698_1/Y1621/3.7e-54	267	ahyasi-spdefavlagatlhtqtgivkissqlfgve-----eeALAIKG--IRIAMIALVVLILS--Iyses	351
Cons_hypoth698_2/Q251E9/3.7e-54	352	dknasanpgernkvsavdiwdrfPKFIIGFVLTFLILFLVGVNpdgvkalstgvnegrAFRTIFFGLCFFSIGLVTNVRk	432
Cons_hypoth698_1/Y1621/3.7e-54	352	-----rFYVPWYIVSFGLVALFSSTYLpg-evv-----qaLRPLATVMFATTAAICYTVNvgr	432
Cons_hypoth698_2/Q251E9/3.7e-54	433	lwaegmgrivaiyGIALFGFILWFGLFISWLFYHgi	468
Cons_hypoth698_1/Y1621/3.7e-54	433	vqrvgvkpl-----	468

Alignment highlighted by TM regions

Alignment for Cons_hypoth698_1-DUF819

Cons_hypoth698_1/N9X0P8/3E-16	0	mkkYTAGLLICLAISIPAWFLGRLf----PVVGGPVCAILIGMAIAPIFKgk--erfrpgiaftsKKILQYAVVLLFGFMNLSSVLE	86
DUF819/Q9K8K1/3E-16	0	-----ILIGMTALIVWAeykiggkfFKYVPAIVLIVLGAAFMNTFGlfgdseslsntSYGVRNALLPAMILLMLLQCDlrkiik	86
Cons_hypoth698_1/N9X0P8/3E-16	87	kgrQSLPIILATITTSI---LIAVLLFrlld-kiptkSAILIGVGSSICGGSAAATApvi	146
DUF819/Q9K8K1/3E-16	87	lgpklLITYFVAAFSIVLGFITLTYLmqssfflddtwrafsalagswtggsanvalqdil	146
Cons_hypoth698_1/N9X0P8/3E-16	147	eaddeEIAQSISVIFLFNIAAALIFPaltalglsnegfglfagtaindtssvtaaaaaw	206
DUF819/Q9K8K1/3E-16	147	avpetifgyYALIMDTINYSFWMVMFWLVpf---ermfnrwtkadtsklesmsqeiaa-	206
Cons_hypoth698_1/N9X0P8/3E-16	207	dgiysntleaaAI-VKLTRTLAIIPITLFLAFYrtkkeqsgsgntfqiaiKFPFFVLLFLASVLTTFHLP	279
DUF819/Q9K8K1/3E-16	207	---tvtdekrepttFVHMIGLLGFSLFIAAALATVIgenlpq---igtgINAMTWILIVSIVGLLLALTpfa	279
Cons_hypoth698_1/N9X0P8/3E-16	280	atvtgplkDL SKFFIIMAMAAGTNTNLvtlvktgmkipLLGLCCWIGISLVSLSMQSFLg	340
DUF819/Q9K8K1/3E-16	280	si---pgsMDIGRVMLYTIVAIIASGADFssige-iPVYIIAGFMVLLFHGLLFGFaklkf	340
Cons_hypoth698_1/N9X0P8/3E-16	341	iw 342	
DUF819/Q9K8K1/3E-16	341	-- 342	

Alignment highlighted by TM regions

Alignment for Glt_symporter-AbrB

Glt_symporter/A0A0Q1HN67/3.7E-12	0	VIGGLLFAIFTCICYttg---ieefsfdttLREVCMVFFFTSVGQANLKvlksgrSLIVFLGLVITLIFSQNLLAIg	79
AbrB/F2IZI7/3.7E-12	0	LIGAQVSCL---LALSQRQLfgappswprsSRQIFLPIGLMISNAFTSEIlrqipdWWSSLLLLSVFLVLAHAVFL	79
Glt_symporter/A0A0Q1HN67/3.7E-12	80	lskllnlplIGMCTGSIPMVGGHTAGAFGpvledfnihgATTICTAAATFGLITGSLVGGpigkrl	148
AbrB/F2IZI7/3.7E-12	80	flkgrydlptaffa---sfpggfveatllgt---erggnq--rlilIQHFLRISLIVLIPLVFWWFg	148
Glt_symporter/A0A0Q1HN67/3.7E-12	149	ekrklmdnvpteddsslvedeekhqrhnmYAAAVFQLILAIGLGTIFSYflktgtLTFPIYIGAMLAAALMRNITE	226

AbrB/F2IZI7/3.7E-12

149 gqvvgsmvqsd-----lvprt **PLSVDVIVLAGAGIGGTLFA**rrlr--**LPAADISGAILFGAIVHLVGWt** 226Glt_symporter/A0A0Q1HN67/3.7E-12 227 sgkgtihmg**EINDLGGICLSLFLGMAMITL**klwelatl**ALPLVILLAAQTLLLICVFTYF**vif 288AbrB/F2IZI7/3.7E-12 227 dgt---pp**AVLIAVTQLVVGTSLGVGFGV**iaardlvqal**GLALAFAFLM-MTMAVLAAGL**h 288Glt_symporter/A0A0Q1HN67/3.7E-12 289 nvmgrdydaa**VLSAGTCGFMGATPNAMANM**qaicdryvpsvka**YLIPIPLIGSLFADFINSLVIT**f 354AbrB/F2IZI7/3.7E-12 289 gllgmrfeal**LL-----AFAPGGLAEMSIALS**LHLS**VPFVTLHHLYRIFFAVAVLPQA**yrf 354

Glt_symporter/A0A0Q1HN67/3.7E-12 355 fini 358

AbrB/F2IZI7/3.7E-12 355 v--- 358

Alignment highlighted by TM regions

Alignment for Glt_symporter-2HCT

Glt_symporter/A0A0Q1HN67/1.5E-30 0 ki**QLDMYQTAAAVLVLLLGNYL**rkkinflek**FCIPAPVIGGLLFAIFTCICY**ttgiiefs 602HCT/Q65FJ0/1.5E-30 0 elp**NMDLGGFAVIMILGIFLGDVG**qripilk**D--IGGPAILS**LFVPSF---LVFFKvlnpa 60Glt_symporter/A0A0Q1HN67/1.5E-30 61 -----fddt**LREVCMVFFFSTVGFQANLKV**lksggr**SLIVFLGLVITLIFSQNLLAI**glsklllnl 1302HCT/Q65FJ0/1.5E-30 61 smeavttlmkts**NFLFYTIACLVAGSILGMHRT**vliqqfmrmpfvpll---AGTIAAVAAGILVGLLFGYs 130Glt_symporter/A0A0Q1HN67/1.5E-30 131 pl**IGMCTSIPMV-GGHGTAGA-FG**pvled-fnihg**A--TTICTAAATFGGLITGSLVGG**pi 1912HCT/Q65FJ0/1.5E-30 131 pyeafffiivpiaaggigegilplslaysqlqstdvf**VSQLIPAAIIGNVVAISAGL**m 191Glt_symporter/A0A0Q1HN67/1.5E-30 192 gkrlikerklmdnvpteddsllvedeek-hqrhtnm**YAAAVFQLILAIGLGTIFS**Yflkttg**LTFPIYIGAMLAALMRNITE** 2752HCT/Q65FJ0/1.5E-30 192 kklgekrpelngnrlvkskkddeifnqkeepkid**LKLMGAGVLIA-ACSFFIFGGLVs**KF-IAIPGAILMIIAAAAV-KYAkl 275Glt_symporter/A0A0Q1HN67/1.5E-30 276 sgkgtihmg**EIND-----LGGICLSLFLGMAMITL**klwelatl**ALPLVILLAAQTLLLICVFTYF**vi 3412HCT/Q65FJ0/1.5E-30 276 lpasm---ekgahqly**KFMSSSFTWPLMVGLGILYIP**lddvasvi**SLRFIAVCASVVIAMVTSGYF**v 341Glt_symporter/A0A0Q1HN67/1.5E-30 342 fnvmgr-dydaa**VLSAGTCGFMGATPNAMANM**qaicdryvpsvka**YLIPIPLIGSLFADFINSLVIT**f 4092HCT/Q65FJ0/1.5E-30 342 gklmnmpvesaitg---chsglggtgdvai-l-sasgrmglmpfaq**ISTRLEGASTVIMAT**----- 409

Glt_symporter/A0A0Q1HN67/1.5E-30 410 fini 413

2HCT/Q65FJ0/1.5E-30 410 ---- 413

Alignment highlighted by TM regions

Alignment for KdgT-Na_H_Exchanger_1

KdgT/A0A072XF91/0.014 0 ilksvkvp**GGLMVIPLLLGASINTFFPTA**lsig---gftt**ALFKKSATALIALFVLCNGAQ**i 62Na_H_Exchanger_1/NAH/0.014 0 frkkll-**VGE--AVLGSITGLIFGPHAALK**vdpfswgdhgd**YLTVEICRIVLDVRVFASAI**el 62KdgT/A0A072XF91/0.014 63 dvkqagkplykgi**VLTTVKFILGAFI-GWIVGKTF**gNAGVLGLTPLALVAALTNSNGglyaala-- 128Na_H_Exchanger_1/NAH/0.014 63 pgayfqhnfrs**IIVMLLPVMAYGWLVTAGFAY**al---fpqinflg**SLLIAGCITSTDPVLSALIVG**e 128KdgT/A0A072XF91/0.014 129 --gqygdstdvga**ISLSNDGPFTMLAFGI-----SGLAn**IPFIIFIAVIPILVGFILGNmdeel 199Na_H_Exchanger_1/NAH/0.014 129 gplakktperirsll**IAESGCNDGMAVPFFYFAIKL**ltvkpsrnagrdw**VLLVVLYECAF**GIFFGCVIGYl 199KdgT/A0A072XF91/0.014 200 rkfl**AQGQ-----**TLLIPFFAFPLGAALNFkti- 292Na_H_Exchanger_1/NAH/0.014 200 lsfilkhaqkyrlida**ISYYSLPLAIPLLCSIGTII**gVDDLLMSFFAGILFNWNDLFSknisacsvpa**FIDQTFSLFFTYGTIIP--WN**n 292KdgT/A0A072XF91/0.014 293 -----ikag**LPGLLLGFMVVLITGFGGYF**strlfskqkrav**GAAIGT-TAGN-SVATPAALALAd** 359Na_H_Exchanger_1/NAH/0.014 293 fnwsvegl**PVWRLLIVFSILTVCRRLPVV**fsvkplvpdiktwe**ALFVGHF**PIGVCAVYMAFLAkl 359KdgT/A0A072XF91/0.014 360 ssl-----kpyva-----s**A-TAQLAAAVIVTAILCPLLVS**yldkdkv 412Na_H_Exchanger_1/NAH/0.014 360 llspdeiekxiyesttvfstlnei**IWPPIISFVILSSIIVHGFSIH**vlviw--- 412

Alignment highlighted by TM regions

Alignment for Na_H_Exchanger_1-DUF819

Na_H_Exchanger_1/Q9UZ55/1.3E-14	0	mi ELSLAEALFLILFTGVISMLI srrtg IS-----YVPIFILTGLVIGPLLKLI prdla HEIFDFVRVFGLVIIILFTEGH nls	84
DUF819/Q9K8K1/1.3E-14	0	----- I LIGMTALIVWA eykiggkf KYVPAIVLIYGAAMNTFG lfgdseslsnt SYGVRNALLPAMILLMLLQCDL	84
Na_H_Exchanger_1/Q9UZ55/1.3E-14	85	rllknmp TIVTLDTIGLILTALIAGFIF kvVFNSSF--LLGFLFGAIIGATDPatlipl	144
DUF819/Q9K8K1/1.3E-14	85	rkiiklgpk LITYFVAAFSIV--LGFTLTLYV mqssflldtwrafalsalagswtggsam	144
Na_H_Exchanger_1/Q9UZ55/1.3E-14	145	frqyr-vkqdietvivtes IFNDPLGIVLTLIAISMVLVPG ygggifstlseklgiyaggv	204
DUF819/Q9K8K1/1.3E-14	145	valqdilavpet-ifg YALIMDTINYSFWVMVMFWLV pfermfnrwtk-----	204
Na_H_Exchanger_1/Q9UZ55/1.3E-14	205	IYFLYNVSVSISLGI FGLGILGykfikrtg IFDFPEI-----EAFSLSLAFLGFFI ger L-----D-----ASGYLVATVTGIVLGNYKL	293
DUF819/Q9K8K1/1.3E-14	205	-----adtsklesmsqeiaatvdekreptt FVHMIGLGFSLFIAALATVI genlpqigtg INAMTWTLIVSIVGLLLALT pfa	293
Na_H_Exchanger_1/Q9UZ55/1.3E-14	294	kpreniirkrlqraiekevhfn DTLAALATIFVLLGAEMNL leviwsn LGKGLLVALGVMI LARPLATLpll	367
DUF819/Q9K8K1/1.3E-14	294	si-----pgs MDIGRVMLYTIVAIIASGADF ssige--i PVYIIAGFMVLLFHGLLIFGF a	367
Na_H_Exchanger_1/Q9UZ55/1.3E-14	368	k--wwnfrey FIALEGPRGVVPSALSLPLS alkyksplltvhwg EIIMATVVITVLTSVIVETLW i	436
DUF819/Q9K8K1/1.3E-14	368	klfkldlf TLGVASLANIGGMVSAPLAG afnra-----l IPVGVIMALIGGFMTWFGVL ta	436
Na_H_Exchanger_1/Q9UZ55/1.3E-14	437	pilkdkldvgetikerieekekerrkvrg	467
DUF819/Q9K8K1/1.3E-14	437	eilsr-----	467

Alignment highlighted by TM regions

Alignment for Na_H_Exchanger_1-Na_H_antipor_t_1

Na_H_Exchanger_1/Q9UZ55/3.5e-7	0	mi ELSLAEALFLILFTGVISMLI srrtg ISYVPIFILTGLVGPL-LKLI prdla HEIFDFVRVFGLVIIILFTEGH nls	78
Na_H_antipor_t_1/NHAA1/3.5e-7	0	----- SFLLFATI IALWWA nsdyaqsyqalih---tqlgffigdfelkas LKHIINDGLMVFFFFLLGLEIK	78
Na_H_Exchanger_1/Q9UZ55/3.5e-7	79	wrl-----kknmp TIVTLDTIGLILTALIAGFIF kvVFNSSFLLGFLFGAIIGATDPatliplfrqyr-	149
Na_H_antipor_t_1/NHAA1/3.5e-7	79	reviagelaqaknr RMLIICAMGGMVCPALI-----YSGF nwslds-qi GWGIPMATDTAFLALGVLTMVR k	149
Na_H_Exchanger_1/Q9UZ55/3.5e-7	150	-vkqdietvivtes IFNDPLGIVLTLIAISMVLVPG yggifstlseklgiyaggv IYFLYNVSVSISLGI FGLGILGykfikr	231
Na_H_antipor_t_1/NHAA1/3.5e-7	150	hipsslva FIVGLAIVDDVGAILVIAIFY tq EIS-----LMHLLSACALIGFLGVAN y	231
Na_H_Exchanger_1/Q9UZ55/3.5e-7	232	tg IFDFPEIEAFSLSLAFLGFFI ger LDASGYLVATVTGIVLGNYKL lkpreniirkrl	291
Na_H_antipor_t_1/NHAA1/3.5e-7	232	a G-----VRQPLFYFIIGVAAWWAMLK sGVHPTVAGVTIALTIPAQPKL asgkwleaksi	291
Na_H_Exchanger_1/Q9UZ55/3.5e-7	292	qrai-----ekevhfn DTLAAL-ATIFI-FULLGAEMNL e	359
Na_H_antipor_t_1/NHAA1/3.5e-7	292	isaiqnksknmdvlgngkhheqvlkvrdfaerastplrrwedal DLPVVLFILPLFALANAGVV nl	359
Na_H_Exchanger_1/Q9UZ55/3.5e-7	360	viws-n LGKGLLVALGVMI LARPLATLpll-----wwnfrey FIALE-GPRGVVPSALSLPLS l	433
Na_H_antipor_t_1/NHAA1/3.5e-7	360	sfiesvqhp VGLGIISGLI LKG LIGISGAC walkfnigclpdkvdln HVIGASLIAGIGFTMSTFIAT lgfd	433
Na_H_Exchanger_1/Q9UZ55/3.5e-7	434	alkyksplltvhwg EIIMATVVITVLTSVIVETLW ipilkdkldvgetikerieekek	493
Na_H_antipor_t_1/NHAA1/3.5e-7	434	q-----dtalhv AKTSILLASVLTAILGLLYL -----	493
Na_H_Exchanger_1/Q9UZ55/3.5e-7	494	errkvrg 500	
Na_H_antipor_t_1/NHAA1/3.5e-7	494	----- 500	

Alignment highlighted by TM regions

Alignment for Na_H_Exchanger_1-Na_H_Exchanger_2

Na_H_Exchanger_2/M3YCW9/3e-32	0	mgdedkviehdlepssgmdhtasayqeiqueetvmtskatdakeptegsnllnshekklok	60
Na_H_Exchanger_1/NAH/3e-32	0	-----	60
Na_H_Exchanger_2/M3YCW9/3e-32	61	lptesnnlqrlrqtfscpph FLDRGITNVTMVLLWAVVWS itgseclpgg NLFGIIILFYCAITGGKLLGL i	134
Na_H_Exchanger_1/NAH/3e-32	61	----- IVAGGFITFFCYFSEV frkkl	134
Na_H_Exchanger_2/M3YCW9/3e-32	135	klptl PPLPRLLGMLLAGFLLRNIPV isdninq----ikhk WSSALRSIALSIIILVRAGLGL d	196
Na_H_Exchanger_1/NAH/3e-32	135	l VG-----EAVLGSITGLIFGPHAAKL vdpfswgdhg YLTVEICRIVLDVRFASAI lp	196
Na_H_Exchanger_2/M3YCW9/3e-32	197	skalkklkgv CVRLSMGPCCLVEACTSALLAH f-lmglpw QWGFI LGFVLGA VSPAVVPS ml	259
Na_H_Exchanger_1/NAH/3e-32	197	gayfqhnfrs IIVMLLPVMAYGWLVTAGFAY alfpqinflg SLLIAGCITSTD PVLSALIV Ge	259
Na_H_Exchanger_2/M3YCW9/3e-32	260	lqeggygvekgipitllmaa GSFDDILAITGFNTCLGMA---FS tgkllfas LIREMIETILGEDFNTTLKFP p	332
Na_H_Exchanger_1/NAH/3e-32	260	-gplakktperirsll IAESGCNDGMAVPFFYFAIKL ltvkpsrnagrdw VLLVVLYECAGFIFGCIVIGY ll	332
Na_H_Exchanger_2/M3YCW9/3e-32	333	qiyclk---kdk LVWKRAFLVLGLSVLA VFSSV yFGFPGSGGLCTLVMSFLAG-LR wase	393
Na_H_Exchanger_1/NAH/3e-32	333	sfilkhqaqkyrlida ISYYSLPLAIPLLCSGIGTII --g VDDLLMSFFAGILFNWNDLFS k	393
Na_H_Exchanger_2/M3YCW9/3e-32	394	kaeveki IAGAWYIFQPLLFLIGAEVS iaslr-----petv GLCVAILGIAVLIRILTTFLM v	459
Na_H_Exchanger_1/NAH/3e-32	394	nisacsvpa FIDQTFSLLFTYYGTIIP--WN nfnwsvegl PVWRLIVFSILTLVCRRLPVV fsvk	459
Na_H_Exchanger_2/M3YCW9/3e-32	460	cfa--gfnikeki FIS-FAWLPKATVQAAIGSVAL dt-----arshgekqleeygmd VLTVAFLSILITAPIGSLLIG l	539
Na_H_Exchanger_1/NAH/3e-32	460	plvpdiktwk ALFVGHFGPIGVCAVYMAFLA kllspdeieksiesttvfstln <i>eiIWPIISFVI</i> SSIIIVHGFSIH v	539
Na_H_Exchanger_2/M3YCW9/3e-32	540	lgprllrkaehqnkgeevqeetsiqv	565
Na_H_Exchanger_1/NAH/3e-32	540	lviv-----	565

Alignment highlighted by TM regions

Alignment for SBF_1-SBF_2

SBF_2/H2Y8C2/1.7E-31	0	fkveqnrnint AISVLVVVVLA FVMVSLGCTMtlskimeharkp KGVI IALVAQFLIMPASA GL tq	66
SBF_1/C4ST46/1.7E-31	0	-AYFRPTT f-tgi GPYVGPLLMLIMFAMGVT RLddfkrvlrsra PVAATFLHYLIMPL TAWILA m	66
SBF_2/H2Y8C2/1.7E-31	67	a FQLDTYAAIAV LICGCCPGGN lsnmlayslsgdm dsi LMTCSSVIGLGMMP LSIYLY s	127
SBF_1/C4ST46/1.7E-31	67	lfrmp PDLSAGMV LVG SVA G TASNV miylakgdva LSVT ISA V STLV G FATPL L trlyv	127
SBF_2/H2Y8C2/1.7E-31	128	qlitplsasmv PFDKIVINILL-TVLPVGAGII irhyrpqwtrnimrlmrtpplaesvrtq RIFGGLM LLLCSIS VAVLAGI mlgd	212
SBF_1/C4ST46/1.7E-31	128	da-----tisvdv VGMLKSILQIVV IPIAGL VI hhtftktvkriep YLP -----AMSMVCILA--IISAVVAG---S q	212
SBF_2/H2Y8C2/1.7E-31	213	affrrffda SVIACCAILPMG SYLLGY FALL frencpkrr TICVETGC QNVQLC STVLKLA f	274
SBF_1/C4ST46/1.7E-31	213	shias VGFVIIIAVILHNGIGLLSGY wggkifg FDESCRTLAIEVGMQNSGLA atlgkiyf	274
SBF_2/H2Y8C2/1.7E-31	275	dpiivgvlf LPLVYMAFQVAEAFLIIFV FRvy	307
SBF_1/C4ST46/1.7E-31	275	SPLA ---ALPGALFSVWHNL SGSL lagywsgk	307

Alignment highlighted by TM regions

Alignment for Sbflike_DUF819

Sbflike/A0A077PBM8/0.0091	0	swwqkldr IDP-----FLVTLITV VIATLFPC E --geskk WFQYLTTAAIALLFFMHGAKL sr	64
DUF819/Q9K8K1/0.0091	0	VWA eykiggkf FKYVPAIVLIYLGA AFMNTFG lfgdseslsnt SYGVRNALLPAMILLMLQCD l	64
Sbflike/A0A077PBM8/0.0091	65	gailagighwr LHLVIFLSTFVL FP LGMGLY fivpewl--spt VYMGFLYLCALPATVQSIA FT	130
DUF819/Q9K8K1/0.0091	65	rkiik---lgpk LITYFVA FSIV-LGFT LYLV mqsfldtwrafalsalagswtggsanvalq	130
Sbflike/A0A077PBM8/0.0091	131	svagnva AAICSA SASSLLGV FISPL LLV glli -----q	190
DUF819/Q9K8K1/0.0091	131	dilavpetifg YALIMDTINYSFWVM MF WL v pfermf nrwtkadtsklesmsq eia tv	190

Sbflike/A0A077PBM8/0.0091	191	tndgggytdtw KAIKDIILQLM-----VPFIAGHLSR pliaswe	252
DUF819/Q9K8K1/0.0091	191	FVHMIGLLGFSLFIAALATVI genlpqigtg INAMTWTLIVSIVGLLLALT p	252
Sbflike/A0A077PBM8/0.0091	253	khkklvnttd RSSILLVVYVAFSEAVVEGIW hkida YSLMMIGVVCCVLLAIVLMIN vyss	313
DUF819/Q9K8K1/0.0091	253	fasi--pgs MDIGRVMLYTIVAIIASGADF ssige---i PVYIIAGFMVLLFHGLILFGF a	313
Sbflike/A0A077PBM8/0.0091	314	rlfgfskededitivfcgskkslang VPMANVLFPASMVGVMLLPLM i FHQIQLMVCVLAQRYARRPK k	382
DUF819/Q9K8K1/0.0091	314	TLGVAS-LANIGGMVSAPVLAG afn-ral IPVGVIMALIGGFMTWFGVL taeilsr----	382
Sbflike/A0A077PBM8/0.0091	383	ad	384
DUF819/Q9K8K1/0.0091	383	--	384

Alignment highlighted by TM regions

Alignment for Sbflike-Mem_trans

Sbflike/A0A077PBM8/9.8E-11/0.016	0	swwqklr IDPFLVTLITVVIATL-----FPCE geskk WFQYLTAAIALLFFMHGAKL sr	60
Mem_trans/PINI/9.8E-11/0.016	0	mvwrklin PNSYSSLFGITWSLISFKWNI empaliaks ISILSDAGLMAMFSLGLFMA l	60
Sbflike/A0A077PBM8/9.8E-11/0.016	61	gailagighwr LHLVIFLSTFVLFPILGMGLY fivpewlsp <i>t</i> VYMGFLYLCALPATVQSIAFT t	124
Mem_trans/PINI/9.8E-11/0.016	61	npriia-cgnrraa FAAAAMRFVVGPAVMLVASYAV g--lrg VLLHVAIQALPQGIVPFV-F a	124
Sbflike/A0A077PBM8/9.8E-11/0.016	125	svakgnva AAICSAASSLLGVFISPPLL vlliqtndgggytdtw KAIKDIILQLMVPFIAGHLSR p	191
Mem_trans/PINI/9.8E-11/0.016	125	keynvhpdi LSTAVIFGMLIALPITLYY-----V MTAMVPLYVAMILAYGSvk	191
Sbflike/A0A077PBM8/9.8E-11/0.016	192	l-iaswvekhkkvnttd RSSILLVVYVAFSEAVVEGIW hkida YSLMMIGVVCCVLLAIVLMIN vyss	260
Mem_trans/PINI/9.8E-11/0.016	192	wwkiftpdqcs GINRFVALFAVPLLSFHIA-----Annpymamlrf LAADSLQKVIVLSLLFLWCKLs	260
Sbflike/A0A077PBM8/9.8E-11/0.016	261	rlfgfskededitivfcgskkslan-g VPMANVLFPASMVGVMLLPLM i FHQIQLMVCVLAQRYARRPK k	330
Mem_trans/PINI/9.8E-11/0.016	261	r--ngs LDWTITLFSLSTLPNTLVMG pllkmgmygnfsgd LMVQIVVLOCIIWTLMLFLF eyrgaklli	330
Sbflike/A0A077PBM8/9.8E-11/0.016	331	ad	332
Mem_trans/PINI/9.8E-11/0.016	331	se	332

Supplemental data:

MSA-MSA alignments between families/subfamilies and best structural template in PDB/Pfam. Details such as uniprot ids, PDB ids and E-value of the relationship are provided. The TM helical regions are highlighted in red colour.