



wwPDB EM Validation Summary Report ⓘ

Jul 20, 2023 – 10:36 am BST

PDB ID : 6TGC
EMDB ID : EMD-10498
Title : CryoEM structure of the ternary DOCK2-ELMO1-RAC1 complex.
Authors : Chang, L.; Yang, J.; Chang, J.H.; Zhang, Z.; Boland, A.; McLaughlin, S.H.;
Abu-Thuraia, A.; Killoran, R.C.; Smith, M.J.; Cote, J.F.; Barford, D.
Deposited on : 2019-11-15
Resolution : 4.10 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev50
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.34

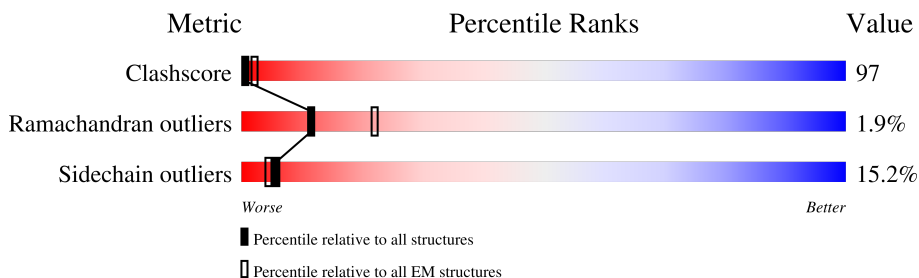
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 4.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1830	
1	D	1830	
2	B	727	
2	E	727	
3	C	192	
3	F	192	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 33282 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Deducator of cytokinesis protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	1450	10203	6463	1792	1894	54	0	0
1	D	1450	10203	6463	1792	1894	54	0	0

There are 1048 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	207A	UNK	ASP	conflict	UNP Q92608
A	207B	UNK	TYR	conflict	UNP Q92608
A	207C	UNK	ALA	conflict	UNP Q92608
A	207D	UNK	MET	conflict	UNP Q92608
A	207E	UNK	TYR	conflict	UNP Q92608
A	207F	UNK	SER	conflict	UNP Q92608
A	207G	UNK	ARG	conflict	UNP Q92608
A	207H	UNK	ILE	conflict	UNP Q92608
A	207I	UNK	SER	conflict	UNP Q92608
A	207J	UNK	SER	conflict	UNP Q92608
A	207K	UNK	SER	conflict	UNP Q92608
A	207L	UNK	PRO	conflict	UNP Q92608
A	207M	UNK	THR	conflict	UNP Q92608
A	207N	UNK	HIS	conflict	UNP Q92608
A	207O	UNK	SER	conflict	UNP Q92608
A	207P	UNK	LEU	conflict	UNP Q92608
A	207Q	UNK	TYR	conflict	UNP Q92608
A	207R	UNK	VAL	conflict	UNP Q92608
A	207S	UNK	PHE	conflict	UNP Q92608
A	207T	UNK	VAL	conflict	UNP Q92608
A	207U	UNK	ARG	conflict	UNP Q92608
A	207V	UNK	ASN	conflict	UNP Q92608
A	207W	UNK	PHE	conflict	UNP Q92608
A	207X	UNK	VAL	conflict	UNP Q92608
A	207Y	UNK	CYS	conflict	UNP Q92608
A	207Z	UNK	ARG	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	208A	UNK	ILE	conflict	UNP Q92608
A	208B	UNK	GLY	conflict	UNP Q92608
A	208C	UNK	GLU	conflict	UNP Q92608
A	208D	UNK	ASP	conflict	UNP Q92608
A	208E	UNK	ALA	conflict	UNP Q92608
A	208F	UNK	GLU	conflict	UNP Q92608
A	208G	UNK	LEU	conflict	UNP Q92608
A	208H	UNK	PHE	conflict	UNP Q92608
A	208I	UNK	MET	conflict	UNP Q92608
A	208J	UNK	SER	conflict	UNP Q92608
A	208K	UNK	LEU	conflict	UNP Q92608
A	208L	UNK	TYR	conflict	UNP Q92608
A	208M	UNK	ASP	conflict	UNP Q92608
A	208N	UNK	PRO	conflict	UNP Q92608
A	208O	UNK	ASN	conflict	UNP Q92608
A	208P	UNK	LYS	conflict	UNP Q92608
A	208Q	UNK	GLN	conflict	UNP Q92608
A	208R	UNK	THR	conflict	UNP Q92608
A	208S	UNK	VAL	conflict	UNP Q92608
A	208T	UNK	ILE	conflict	UNP Q92608
A	208U	UNK	SER	conflict	UNP Q92608
A	208V	UNK	GLU	conflict	UNP Q92608
A	208W	UNK	ASN	conflict	UNP Q92608
A	208X	UNK	TYR	conflict	UNP Q92608
A	208Y	UNK	LEU	conflict	UNP Q92608
A	208Z	UNK	VAL	conflict	UNP Q92608
A	209A	UNK	ARG	conflict	UNP Q92608
A	209B	UNK	TRP	conflict	UNP Q92608
A	209C	UNK	GLY	conflict	UNP Q92608
A	209D	UNK	SER	conflict	UNP Q92608
A	209E	UNK	ARG	conflict	UNP Q92608
A	209F	UNK	GLY	conflict	UNP Q92608
A	209G	UNK	PHE	conflict	UNP Q92608
A	209H	UNK	PRO	conflict	UNP Q92608
A	209I	UNK	LYS	conflict	UNP Q92608
A	209J	UNK	GLU	conflict	UNP Q92608
A	209K	UNK	ILE	conflict	UNP Q92608
A	209L	UNK	GLU	conflict	UNP Q92608
A	209M	UNK	MET	conflict	UNP Q92608
A	209N	UNK	LEU	conflict	UNP Q92608
A	209O	UNK	ASN	conflict	UNP Q92608
A	209P	UNK	ASN	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	209Q	UNK	LEU	conflict	UNP Q92608
A	209R	UNK	LYS	conflict	UNP Q92608
A	209S	UNK	VAL	conflict	UNP Q92608
A	219	UNK	VAL	conflict	UNP Q92608
A	220	UNK	PHE	conflict	UNP Q92608
A	221	UNK	THR	conflict	UNP Q92608
A	222	UNK	ASP	conflict	UNP Q92608
A	223	UNK	LEU	conflict	UNP Q92608
A	224	UNK	GLY	conflict	UNP Q92608
A	225	UNK	ASN	conflict	UNP Q92608
A	226	UNK	LYS	conflict	UNP Q92608
A	227	UNK	ASP	conflict	UNP Q92608
A	228	UNK	LEU	conflict	UNP Q92608
A	229	UNK	ASN	conflict	UNP Q92608
A	230	UNK	ARG	conflict	UNP Q92608
A	231	UNK	ASP	conflict	UNP Q92608
A	232	UNK	LYS	conflict	UNP Q92608
A	233	UNK	ILE	conflict	UNP Q92608
A	234	UNK	TYR	conflict	UNP Q92608
A	235	UNK	LEU	conflict	UNP Q92608
A	236	UNK	ILE	conflict	UNP Q92608
A	237	UNK	CYS	conflict	UNP Q92608
A	238	UNK	GLN	conflict	UNP Q92608
A	239	UNK	ILE	conflict	UNP Q92608
A	240	UNK	VAL	conflict	UNP Q92608
A	241	UNK	ARG	conflict	UNP Q92608
A	242	UNK	VAL	conflict	UNP Q92608
A	243	UNK	GLY	conflict	UNP Q92608
A	244	UNK	LYS	conflict	UNP Q92608
A	245	UNK	MET	conflict	UNP Q92608
A	246	UNK	ASP	conflict	UNP Q92608
A	247	UNK	LEU	conflict	UNP Q92608
A	248	UNK	LYS	conflict	UNP Q92608
A	249	UNK	ASP	conflict	UNP Q92608
A	250	UNK	THR	conflict	UNP Q92608
A	251	UNK	GLY	conflict	UNP Q92608
A	252	UNK	ALA	conflict	UNP Q92608
A	253	UNK	LYS	conflict	UNP Q92608
A	254	UNK	LYS	conflict	UNP Q92608
A	255	UNK	CYS	conflict	UNP Q92608
A	256	UNK	THR	conflict	UNP Q92608
A	257	UNK	GLN	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	258	UNK	GLY	conflict	UNP Q92608
A	259	UNK	LEU	conflict	UNP Q92608
A	260	UNK	ARG	conflict	UNP Q92608
A	261	UNK	ARG	conflict	UNP Q92608
A	262	UNK	PRO	conflict	UNP Q92608
A	263	UNK	PHE	conflict	UNP Q92608
A	264	UNK	GLY	conflict	UNP Q92608
A	265	UNK	VAL	conflict	UNP Q92608
A	266	UNK	ALA	conflict	UNP Q92608
A	267	UNK	VAL	conflict	UNP Q92608
A	268	UNK	MET	conflict	UNP Q92608
A	269	UNK	ASP	conflict	UNP Q92608
A	270	UNK	ILE	conflict	UNP Q92608
A	271	UNK	THR	conflict	UNP Q92608
A	272	UNK	ASP	conflict	UNP Q92608
A	273	UNK	ILE	conflict	UNP Q92608
A	274	UNK	ILE	conflict	UNP Q92608
A	275	UNK	LYS	conflict	UNP Q92608
A	276	UNK	GLY	conflict	UNP Q92608
A	277	UNK	LYS	conflict	UNP Q92608
A	278	UNK	ALA	conflict	UNP Q92608
A	279	UNK	GLU	conflict	UNP Q92608
A	280	UNK	SER	conflict	UNP Q92608
A	281	UNK	ASP	conflict	UNP Q92608
A	282	UNK	GLU	conflict	UNP Q92608
A	283	UNK	GLU	conflict	UNP Q92608
A	284	UNK	LYS	conflict	UNP Q92608
A	285	UNK	GLN	conflict	UNP Q92608
A	286	UNK	HIS	conflict	UNP Q92608
A	287	UNK	PHE	conflict	UNP Q92608
A	288	UNK	ILE	conflict	UNP Q92608
A	289	UNK	PRO	conflict	UNP Q92608
A	290	UNK	PHE	conflict	UNP Q92608
A	291	UNK	HIS	conflict	UNP Q92608
A	292	UNK	PRO	conflict	UNP Q92608
A	293	UNK	VAL	conflict	UNP Q92608
A	294	UNK	THR	conflict	UNP Q92608
A	295	UNK	ALA	conflict	UNP Q92608
A	296	UNK	GLU	conflict	UNP Q92608
A	297	UNK	ASN	conflict	UNP Q92608
A	298	UNK	ASP	conflict	UNP Q92608
A	299	UNK	PHE	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	300	UNK	LEU	conflict	UNP Q92608
A	301	UNK	HIS	conflict	UNP Q92608
A	302	UNK	SER	conflict	UNP Q92608
A	303	UNK	LEU	conflict	UNP Q92608
A	304	UNK	LEU	conflict	UNP Q92608
A	318	UNK	GLY	conflict	UNP Q92608
A	319	UNK	LYS	conflict	UNP Q92608
A	320	UNK	VAL	conflict	UNP Q92608
A	321	UNK	ILE	conflict	UNP Q92608
A	322	UNK	ALA	conflict	UNP Q92608
A	323	UNK	SER	conflict	UNP Q92608
A	324	UNK	LYS	conflict	UNP Q92608
A	325	UNK	GLY	conflict	UNP Q92608
A	326	UNK	ASP	conflict	UNP Q92608
A	327	UNK	SER	conflict	UNP Q92608
A	328	UNK	GLY	conflict	UNP Q92608
A	329	UNK	GLY	conflict	UNP Q92608
A	330	UNK	GLN	conflict	UNP Q92608
A	331	UNK	GLY	conflict	UNP Q92608
A	332	UNK	LEU	conflict	UNP Q92608
A	333	UNK	TRP	conflict	UNP Q92608
A	334	UNK	VAL	conflict	UNP Q92608
A	335	UNK	THR	conflict	UNP Q92608
A	336	UNK	MET	conflict	UNP Q92608
A	337	UNK	LYS	conflict	UNP Q92608
A	338	UNK	MET	conflict	UNP Q92608
A	339	UNK	LEU	conflict	UNP Q92608
A	340	UNK	VAL	conflict	UNP Q92608
A	341	UNK	GLY	conflict	UNP Q92608
A	342	UNK	ASP	conflict	UNP Q92608
A	343	UNK	ILE	conflict	UNP Q92608
A	344	UNK	ILE	conflict	UNP Q92608
A	345	UNK	GLN	conflict	UNP Q92608
A	346	UNK	ILE	conflict	UNP Q92608
A	347	UNK	ARG	conflict	UNP Q92608
A	348	UNK	LYS	conflict	UNP Q92608
A	349	UNK	ASP	conflict	UNP Q92608
A	350	UNK	TYR	conflict	UNP Q92608
A	351	UNK	PRO	conflict	UNP Q92608
A	377	UNK	HIS	conflict	UNP Q92608
A	378	UNK	LEU	conflict	UNP Q92608
A	379	UNK	VAL	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	380	UNK	ASP	conflict	UNP Q92608
A	381	UNK	ARG	conflict	UNP Q92608
A	382	UNK	THR	conflict	UNP Q92608
A	383	UNK	THR	conflict	UNP Q92608
A	384	UNK	VAL	conflict	UNP Q92608
A	385	UNK	VAL	conflict	UNP Q92608
A	386	UNK	ALA	conflict	UNP Q92608
A	387	UNK	ARG	conflict	UNP Q92608
A	388	UNK	LYS	conflict	UNP Q92608
A	389	UNK	LEU	conflict	UNP Q92608
A	609A	UNK	LYS	conflict	UNP Q92608
A	609B	UNK	LEU	conflict	UNP Q92608
A	609C	UNK	THR	conflict	UNP Q92608
A	609D	UNK	GLN	conflict	UNP Q92608
A	609E	UNK	ASN	conflict	UNP Q92608
A	609F	UNK	VAL	conflict	UNP Q92608
A	609G	UNK	GLY	conflict	UNP Q92608
A	609H	UNK	LEU	conflict	UNP Q92608
A	609I	UNK	LEU	conflict	UNP Q92608
A	609J	UNK	GLY	conflict	UNP Q92608
A	609K	UNK	LEU	conflict	UNP Q92608
A	609L	UNK	LEU	conflict	UNP Q92608
A	609M	UNK	LYS	conflict	UNP Q92608
A	609N	UNK	TRP	conflict	UNP Q92608
A	609O	UNK	ARG	conflict	UNP Q92608
A	609P	UNK	MET	conflict	UNP Q92608
A	609Q	UNK	LYS	conflict	UNP Q92608
A	609R	UNK	PRO	conflict	UNP Q92608
A	609S	UNK	GLN	conflict	UNP Q92608
A	609T	UNK	LEU	conflict	UNP Q92608
A	609U	UNK	LEU	conflict	UNP Q92608
A	609V	UNK	GLN	conflict	UNP Q92608
A	609W	UNK	GLU	conflict	UNP Q92608
A	609X	UNK	ASN	conflict	UNP Q92608
A	609Y	UNK	LEU	conflict	UNP Q92608
A	609Z	UNK	GLU	conflict	UNP Q92608
A	610A	UNK	LYS	conflict	UNP Q92608
A	610B	UNK	LEU	conflict	UNP Q92608
A	610C	UNK	LYS	conflict	UNP Q92608
A	610D	UNK	ILE	conflict	UNP Q92608
A	610E	UNK	VAL	conflict	UNP Q92608
A	610F	UNK	ASP	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	626	UNK	GLY	conflict	UNP Q92608
A	627	UNK	GLU	conflict	UNP Q92608
A	628	UNK	GLU	conflict	UNP Q92608
A	629	UNK	VAL	conflict	UNP Q92608
A	630	UNK	VAL	conflict	UNP Q92608
A	631	UNK	LYS	conflict	UNP Q92608
A	632	UNK	PHE	conflict	UNP Q92608
A	633	UNK	LEU	conflict	UNP Q92608
A	634	UNK	GLN	conflict	UNP Q92608
A	635	UNK	ASP	conflict	UNP Q92608
A	636	UNK	THR	conflict	UNP Q92608
A	637	UNK	LEU	conflict	UNP Q92608
A	638	UNK	ASP	conflict	UNP Q92608
A	639	UNK	ALA	conflict	UNP Q92608
A	640	UNK	LEU	conflict	UNP Q92608
A	641	UNK	PHE	conflict	UNP Q92608
A	642	UNK	ASN	conflict	UNP Q92608
A	679A	UNK	HIS	conflict	UNP Q92608
A	679B	UNK	PHE	conflict	UNP Q92608
A	679C	UNK	ASN	conflict	UNP Q92608
A	679D	UNK	THR	conflict	UNP Q92608
A	679E	UNK	VAL	conflict	UNP Q92608
A	679F	UNK	LEU	conflict	UNP Q92608
A	679G	UNK	GLU	conflict	UNP Q92608
A	679H	UNK	ALA	conflict	UNP Q92608
A	679I	UNK	TYR	conflict	UNP Q92608
A	679J	UNK	ILE	conflict	UNP Q92608
A	679K	UNK	GLN	conflict	UNP Q92608
A	679L	UNK	GLN	conflict	UNP Q92608
A	679M	UNK	HIS	conflict	UNP Q92608
A	679N	UNK	PHE	conflict	UNP Q92608
A	679O	UNK	SER	conflict	UNP Q92608
A	679P	UNK	ALA	conflict	UNP Q92608
A	679Q	UNK	THR	conflict	UNP Q92608
A	688	UNK	LEU	conflict	UNP Q92608
A	689	UNK	ALA	conflict	UNP Q92608
A	690	UNK	TYR	conflict	UNP Q92608
A	691	UNK	LYS	conflict	UNP Q92608
A	692	UNK	LYS	conflict	UNP Q92608
A	693	UNK	LEU	conflict	UNP Q92608
A	694	UNK	MET	conflict	UNP Q92608
A	695	UNK	THR	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	696	UNK	VAL	conflict	UNP Q92608
A	697	UNK	LEU	conflict	UNP Q92608
A	698	UNK	LYS	conflict	UNP Q92608
A	699	UNK	THR	conflict	UNP Q92608
A	700	UNK	TYR	conflict	UNP Q92608
A	701	UNK	LEU	conflict	UNP Q92608
A	702	UNK	ASP	conflict	UNP Q92608
A	703	UNK	THR	conflict	UNP Q92608
A	704	UNK	SER	conflict	UNP Q92608
A	705	UNK	SER	conflict	UNP Q92608
A	706	UNK	ARG	conflict	UNP Q92608
A	707	UNK	GLY	conflict	UNP Q92608
A	708	UNK	GLU	conflict	UNP Q92608
A	709	UNK	GLN	conflict	UNP Q92608
A	710	UNK	CYS	conflict	UNP Q92608
A	711	UNK	GLU	conflict	UNP Q92608
A	712	UNK	PRO	conflict	UNP Q92608
A	713	UNK	ILE	conflict	UNP Q92608
A	714	UNK	LEU	conflict	UNP Q92608
A	715	UNK	ARG	conflict	UNP Q92608
A	716	UNK	THR	conflict	UNP Q92608
A	717	UNK	LEU	conflict	UNP Q92608
A	718	UNK	LYS	conflict	UNP Q92608
A	719	UNK	ALA	conflict	UNP Q92608
A	720	UNK	LEU	conflict	UNP Q92608
A	721	UNK	GLU	conflict	UNP Q92608
A	722	UNK	TYR	conflict	UNP Q92608
A	723	UNK	VAL	conflict	UNP Q92608
A	724	UNK	PHE	conflict	UNP Q92608
A	725	UNK	LYS	conflict	UNP Q92608
A	726	UNK	PHE	conflict	UNP Q92608
A	727	UNK	ILE	conflict	UNP Q92608
A	728	UNK	VAL	conflict	UNP Q92608
A	729	UNK	ARG	conflict	UNP Q92608
A	730	UNK	SER	conflict	UNP Q92608
A	731	UNK	ARG	conflict	UNP Q92608
A	732	UNK	THR	conflict	UNP Q92608
A	733	UNK	LEU	conflict	UNP Q92608
A	734	UNK	PHE	conflict	UNP Q92608
A	735	UNK	SER	conflict	UNP Q92608
A	736	UNK	GLN	conflict	UNP Q92608
A	742	UNK	LEU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	743	UNK	TYR	conflict	UNP Q92608
A	744	UNK	GLU	conflict	UNP Q92608
A	745	UNK	GLY	conflict	UNP Q92608
A	746	UNK	LYS	conflict	UNP Q92608
A	747	UNK	GLU	conflict	UNP Q92608
A	748	UNK	GLN	conflict	UNP Q92608
A	749	UNK	MET	conflict	UNP Q92608
A	750	UNK	GLU	conflict	UNP Q92608
A	751	UNK	PHE	conflict	UNP Q92608
A	752	UNK	GLU	conflict	UNP Q92608
A	753	UNK	GLU	conflict	UNP Q92608
A	754	UNK	SER	conflict	UNP Q92608
A	755	UNK	MET	conflict	UNP Q92608
A	756	UNK	ARG	conflict	UNP Q92608
A	757	UNK	ARG	conflict	UNP Q92608
A	758	UNK	LEU	conflict	UNP Q92608
A	759	UNK	PHE	conflict	UNP Q92608
A	760	UNK	GLU	conflict	UNP Q92608
A	761	UNK	SER	conflict	UNP Q92608
A	762	UNK	ILE	conflict	UNP Q92608
A	763	UNK	ASN	conflict	UNP Q92608
A	764	UNK	ASN	conflict	UNP Q92608
A	765	UNK	LEU	conflict	UNP Q92608
A	766	UNK	MET	conflict	UNP Q92608
A	767	UNK	LYS	conflict	UNP Q92608
A	768	UNK	SER	conflict	UNP Q92608
A	769	UNK	GLN	conflict	UNP Q92608
A	770	UNK	TYR	conflict	UNP Q92608
A	771	UNK	LYS	conflict	UNP Q92608
A	772	UNK	THR	conflict	UNP Q92608
A	773	UNK	THR	conflict	UNP Q92608
A	774	UNK	ILE	conflict	UNP Q92608
A	775	UNK	LEU	conflict	UNP Q92608
A	776	UNK	LEU	conflict	UNP Q92608
A	777	UNK	GLN	conflict	UNP Q92608
A	778	UNK	VAL	conflict	UNP Q92608
A	779	UNK	ALA	conflict	UNP Q92608
A	780	UNK	ALA	conflict	UNP Q92608
A	781	UNK	LEU	conflict	UNP Q92608
A	782	UNK	LYS	conflict	UNP Q92608
A	783	UNK	TYR	conflict	UNP Q92608
A	784	UNK	ILE	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	785	UNK	PRO	conflict	UNP Q92608
A	786	UNK	SER	conflict	UNP Q92608
A	787	UNK	VAL	conflict	UNP Q92608
A	788	UNK	LEU	conflict	UNP Q92608
A	789	UNK	HIS	conflict	UNP Q92608
A	790	UNK	ASP	conflict	UNP Q92608
A	791	UNK	VAL	conflict	UNP Q92608
A	792	UNK	GLU	conflict	UNP Q92608
A	793	UNK	MET	conflict	UNP Q92608
A	794	UNK	VAL	conflict	UNP Q92608
A	795	UNK	PHE	conflict	UNP Q92608
A	796	UNK	ASP	conflict	UNP Q92608
A	797	UNK	ALA	conflict	UNP Q92608
A	798	UNK	LYS	conflict	UNP Q92608
A	799	UNK	LEU	conflict	UNP Q92608
A	801	UNK	LEU	conflict	UNP Q92608
A	802	UNK	SER	conflict	UNP Q92608
A	803	UNK	GLN	conflict	UNP Q92608
A	804	UNK	LEU	conflict	UNP Q92608
A	805	UNK	LEU	conflict	UNP Q92608
A	806	UNK	TYR	conflict	UNP Q92608
A	807	UNK	GLU	conflict	UNP Q92608
A	808	UNK	PHE	conflict	UNP Q92608
A	809	UNK	TYR	conflict	UNP Q92608
A	810	UNK	THR	conflict	UNP Q92608
A	811	UNK	CYS	conflict	UNP Q92608
A	812	UNK	ILE	conflict	UNP Q92608
A	813	UNK	PRO	conflict	UNP Q92608
A	814	UNK	PRO	conflict	UNP Q92608
A	815	UNK	VAL	conflict	UNP Q92608
A	816	UNK	LYS	conflict	UNP Q92608
A	817	UNK	LEU	conflict	UNP Q92608
A	818	UNK	GLN	conflict	UNP Q92608
A	819	UNK	LYS	conflict	UNP Q92608
A	820	UNK	GLN	conflict	UNP Q92608
A	821	UNK	LYS	conflict	UNP Q92608
A	822	UNK	VAL	conflict	UNP Q92608
A	823	UNK	GLN	conflict	UNP Q92608
A	824	UNK	SER	conflict	UNP Q92608
A	825	UNK	MET	conflict	UNP Q92608
A	826	UNK	ASN	conflict	UNP Q92608
A	827	UNK	GLU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	828	UNK	ILE	conflict	UNP Q92608
A	829	UNK	VAL	conflict	UNP Q92608
A	830	UNK	GLN	conflict	UNP Q92608
A	831	UNK	SER	conflict	UNP Q92608
A	832	UNK	ASN	conflict	UNP Q92608
A	833	UNK	LEU	conflict	UNP Q92608
A	834	UNK	PHE	conflict	UNP Q92608
A	835	UNK	LYS	conflict	UNP Q92608
A	836	UNK	LYS	conflict	UNP Q92608
A	837	UNK	GLN	conflict	UNP Q92608
A	838	UNK	GLU	conflict	UNP Q92608
A	839	UNK	CYS	conflict	UNP Q92608
A	840	UNK	ARG	conflict	UNP Q92608
A	841	UNK	ASP	conflict	UNP Q92608
A	842	UNK	ILE	conflict	UNP Q92608
A	843	UNK	LEU	conflict	UNP Q92608
A	844	UNK	LEU	conflict	UNP Q92608
A	845	UNK	PRO	conflict	UNP Q92608
A	846	UNK	VAL	conflict	UNP Q92608
A	847	UNK	ILE	conflict	UNP Q92608
A	848	UNK	THR	conflict	UNP Q92608
A	849	UNK	LYS	conflict	UNP Q92608
A	850	UNK	GLU	conflict	UNP Q92608
A	851	UNK	LEU	conflict	UNP Q92608
A	852	UNK	LYS	conflict	UNP Q92608
A	853	UNK	GLU	conflict	UNP Q92608
A	854	UNK	LEU	conflict	UNP Q92608
A	855	UNK	LEU	conflict	UNP Q92608
A	856	UNK	GLU	conflict	UNP Q92608
A	857	UNK	GLN	conflict	UNP Q92608
A	858	UNK	LYS	conflict	UNP Q92608
A	859	UNK	ASP	conflict	UNP Q92608
A	860	UNK	ASP	conflict	UNP Q92608
A	861	UNK	MET	conflict	UNP Q92608
A	862	UNK	GLN	conflict	UNP Q92608
A	863	UNK	HIS	conflict	UNP Q92608
A	864	UNK	GLN	conflict	UNP Q92608
A	865	UNK	VAL	conflict	UNP Q92608
A	866	UNK	LEU	conflict	UNP Q92608
A	867	UNK	GLU	conflict	UNP Q92608
A	868	UNK	ARG	conflict	UNP Q92608
A	869	UNK	LYS	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	870	UNK	TYR	conflict	UNP Q92608
A	871	UNK	CYS	conflict	UNP Q92608
A	872	UNK	VAL	conflict	UNP Q92608
A	873	UNK	GLU	conflict	UNP Q92608
A	874	UNK	LEU	conflict	UNP Q92608
A	875	UNK	LEU	conflict	UNP Q92608
A	876	UNK	ASN	conflict	UNP Q92608
A	877	UNK	SER	conflict	UNP Q92608
A	878	UNK	ILE	conflict	UNP Q92608
A	879	UNK	LEU	conflict	UNP Q92608
A	880	UNK	GLU	conflict	UNP Q92608
A	881	UNK	VAL	conflict	UNP Q92608
A	882	UNK	LEU	conflict	UNP Q92608
A	883	UNK	SER	conflict	UNP Q92608
A	884	UNK	TYR	conflict	UNP Q92608
A	885	UNK	GLN	conflict	UNP Q92608
A	886	UNK	ASP	conflict	UNP Q92608
A	887	UNK	ALA	conflict	UNP Q92608
A	888	UNK	ALA	conflict	UNP Q92608
A	889	UNK	PHE	conflict	UNP Q92608
A	890	UNK	THR	conflict	UNP Q92608
A	891	UNK	TYR	conflict	UNP Q92608
A	892	UNK	HIS	conflict	UNP Q92608
A	896	UNK	HIS	conflict	UNP Q92608
A	897	UNK	ILE	conflict	UNP Q92608
A	898	UNK	GLN	conflict	UNP Q92608
A	899	UNK	GLU	conflict	UNP Q92608
A	900	UNK	ILE	conflict	UNP Q92608
A	901	UNK	MET	conflict	UNP Q92608
A	902	UNK	VAL	conflict	UNP Q92608
A	903	UNK	GLN	conflict	UNP Q92608
A	904	UNK	LEU	conflict	UNP Q92608
A	905	UNK	LEU	conflict	UNP Q92608
A	906	UNK	ARG	conflict	UNP Q92608
A	907	UNK	THR	conflict	UNP Q92608
A	908	UNK	VAL	conflict	UNP Q92608
A	909	UNK	ASN	conflict	UNP Q92608
A	910	UNK	ARG	conflict	UNP Q92608
A	911	UNK	THR	conflict	UNP Q92608
A	912	UNK	VAL	conflict	UNP Q92608
A	913	UNK	ILE	conflict	UNP Q92608
A	914	UNK	THR	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
A	915	UNK	MET	conflict	UNP Q92608
A	916	UNK	GLY	conflict	UNP Q92608
A	917	UNK	ARG	conflict	UNP Q92608
A	918	UNK	ASP	conflict	UNP Q92608
A	919	UNK	HIS	conflict	UNP Q92608
A	920	UNK	ILE	conflict	UNP Q92608
A	921	UNK	LEU	conflict	UNP Q92608
A	922	UNK	ILE	conflict	UNP Q92608
A	923	UNK	SER	conflict	UNP Q92608
A	934	UNK	HIS	conflict	UNP Q92608
A	935	UNK	PHE	conflict	UNP Q92608
A	936	UNK	VAL	conflict	UNP Q92608
A	937	UNK	ALA	conflict	UNP Q92608
A	938	UNK	CYS	conflict	UNP Q92608
A	939	UNK	MET	conflict	UNP Q92608
A	940	UNK	THR	conflict	UNP Q92608
A	941	UNK	ALA	conflict	UNP Q92608
A	942	UNK	ILE	conflict	UNP Q92608
A	943	UNK	LEU	conflict	UNP Q92608
A	944	UNK	ASN	conflict	UNP Q92608
A	945	UNK	GLN	conflict	UNP Q92608
A	946	UNK	MET	conflict	UNP Q92608
A	947	UNK	GLY	conflict	UNP Q92608
A	948	UNK	ASP	conflict	UNP Q92608
A	949	UNK	GLN	conflict	UNP Q92608
A	950	UNK	HIS	conflict	UNP Q92608
A	951	UNK	TYR	conflict	UNP Q92608
A	952	UNK	SER	conflict	UNP Q92608
A	953	UNK	PHE	conflict	UNP Q92608
A	954	UNK	TYR	conflict	UNP Q92608
A	955	UNK	ILE	conflict	UNP Q92608
A	956	UNK	GLU	conflict	UNP Q92608
A	957	UNK	THR	conflict	UNP Q92608
A	958	UNK	PHE	conflict	UNP Q92608
A	959	UNK	GLN	conflict	UNP Q92608
A	960	UNK	THR	conflict	UNP Q92608
D	207A	UNK	ASP	conflict	UNP Q92608
D	207B	UNK	TYR	conflict	UNP Q92608
D	207C	UNK	ALA	conflict	UNP Q92608
D	207D	UNK	MET	conflict	UNP Q92608
D	207E	UNK	TYR	conflict	UNP Q92608
D	207F	UNK	SER	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	207G	UNK	ARG	conflict	UNP Q92608
D	207H	UNK	ILE	conflict	UNP Q92608
D	207I	UNK	SER	conflict	UNP Q92608
D	207J	UNK	SER	conflict	UNP Q92608
D	207K	UNK	SER	conflict	UNP Q92608
D	207L	UNK	PRO	conflict	UNP Q92608
D	207M	UNK	THR	conflict	UNP Q92608
D	207N	UNK	HIS	conflict	UNP Q92608
D	207O	UNK	SER	conflict	UNP Q92608
D	207P	UNK	LEU	conflict	UNP Q92608
D	207Q	UNK	TYR	conflict	UNP Q92608
D	207R	UNK	VAL	conflict	UNP Q92608
D	207S	UNK	PHE	conflict	UNP Q92608
D	207T	UNK	VAL	conflict	UNP Q92608
D	207U	UNK	ARG	conflict	UNP Q92608
D	207V	UNK	ASN	conflict	UNP Q92608
D	207W	UNK	PHE	conflict	UNP Q92608
D	207X	UNK	VAL	conflict	UNP Q92608
D	207Y	UNK	CYS	conflict	UNP Q92608
D	207Z	UNK	ARG	conflict	UNP Q92608
D	208A	UNK	ILE	conflict	UNP Q92608
D	208B	UNK	GLY	conflict	UNP Q92608
D	208C	UNK	GLU	conflict	UNP Q92608
D	208D	UNK	ASP	conflict	UNP Q92608
D	208E	UNK	ALA	conflict	UNP Q92608
D	208F	UNK	GLU	conflict	UNP Q92608
D	208G	UNK	LEU	conflict	UNP Q92608
D	208H	UNK	PHE	conflict	UNP Q92608
D	208I	UNK	MET	conflict	UNP Q92608
D	208J	UNK	SER	conflict	UNP Q92608
D	208K	UNK	LEU	conflict	UNP Q92608
D	208L	UNK	TYR	conflict	UNP Q92608
D	208M	UNK	ASP	conflict	UNP Q92608
D	208N	UNK	PRO	conflict	UNP Q92608
D	208O	UNK	ASN	conflict	UNP Q92608
D	208P	UNK	LYS	conflict	UNP Q92608
D	208Q	UNK	GLN	conflict	UNP Q92608
D	208R	UNK	THR	conflict	UNP Q92608
D	208S	UNK	VAL	conflict	UNP Q92608
D	208T	UNK	ILE	conflict	UNP Q92608
D	208U	UNK	SER	conflict	UNP Q92608
D	208V	UNK	GLU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	208W	UNK	ASN	conflict	UNP Q92608
D	208X	UNK	TYR	conflict	UNP Q92608
D	208Y	UNK	LEU	conflict	UNP Q92608
D	208Z	UNK	VAL	conflict	UNP Q92608
D	209A	UNK	ARG	conflict	UNP Q92608
D	209B	UNK	TRP	conflict	UNP Q92608
D	209C	UNK	GLY	conflict	UNP Q92608
D	209D	UNK	SER	conflict	UNP Q92608
D	209E	UNK	ARG	conflict	UNP Q92608
D	209F	UNK	GLY	conflict	UNP Q92608
D	209G	UNK	PHE	conflict	UNP Q92608
D	209H	UNK	PRO	conflict	UNP Q92608
D	209I	UNK	LYS	conflict	UNP Q92608
D	209J	UNK	GLU	conflict	UNP Q92608
D	209K	UNK	ILE	conflict	UNP Q92608
D	209L	UNK	GLU	conflict	UNP Q92608
D	209M	UNK	MET	conflict	UNP Q92608
D	209N	UNK	LEU	conflict	UNP Q92608
D	209O	UNK	ASN	conflict	UNP Q92608
D	209P	UNK	ASN	conflict	UNP Q92608
D	209Q	UNK	LEU	conflict	UNP Q92608
D	209R	UNK	LYS	conflict	UNP Q92608
D	209S	UNK	VAL	conflict	UNP Q92608
D	219	UNK	VAL	conflict	UNP Q92608
D	220	UNK	PHE	conflict	UNP Q92608
D	221	UNK	THR	conflict	UNP Q92608
D	222	UNK	ASP	conflict	UNP Q92608
D	223	UNK	LEU	conflict	UNP Q92608
D	224	UNK	GLY	conflict	UNP Q92608
D	225	UNK	ASN	conflict	UNP Q92608
D	226	UNK	LYS	conflict	UNP Q92608
D	227	UNK	ASP	conflict	UNP Q92608
D	228	UNK	LEU	conflict	UNP Q92608
D	229	UNK	ASN	conflict	UNP Q92608
D	230	UNK	ARG	conflict	UNP Q92608
D	231	UNK	ASP	conflict	UNP Q92608
D	232	UNK	LYS	conflict	UNP Q92608
D	233	UNK	ILE	conflict	UNP Q92608
D	234	UNK	TYR	conflict	UNP Q92608
D	235	UNK	LEU	conflict	UNP Q92608
D	236	UNK	ILE	conflict	UNP Q92608
D	237	UNK	CYS	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	238	UNK	GLN	conflict	UNP Q92608
D	239	UNK	ILE	conflict	UNP Q92608
D	240	UNK	VAL	conflict	UNP Q92608
D	241	UNK	ARG	conflict	UNP Q92608
D	242	UNK	VAL	conflict	UNP Q92608
D	243	UNK	GLY	conflict	UNP Q92608
D	244	UNK	LYS	conflict	UNP Q92608
D	245	UNK	MET	conflict	UNP Q92608
D	246	UNK	ASP	conflict	UNP Q92608
D	247	UNK	LEU	conflict	UNP Q92608
D	248	UNK	LYS	conflict	UNP Q92608
D	249	UNK	ASP	conflict	UNP Q92608
D	250	UNK	THR	conflict	UNP Q92608
D	251	UNK	GLY	conflict	UNP Q92608
D	252	UNK	ALA	conflict	UNP Q92608
D	253	UNK	LYS	conflict	UNP Q92608
D	254	UNK	LYS	conflict	UNP Q92608
D	255	UNK	CYS	conflict	UNP Q92608
D	256	UNK	THR	conflict	UNP Q92608
D	257	UNK	GLN	conflict	UNP Q92608
D	258	UNK	GLY	conflict	UNP Q92608
D	259	UNK	LEU	conflict	UNP Q92608
D	260	UNK	ARG	conflict	UNP Q92608
D	261	UNK	ARG	conflict	UNP Q92608
D	262	UNK	PRO	conflict	UNP Q92608
D	263	UNK	PHE	conflict	UNP Q92608
D	264	UNK	GLY	conflict	UNP Q92608
D	265	UNK	VAL	conflict	UNP Q92608
D	266	UNK	ALA	conflict	UNP Q92608
D	267	UNK	VAL	conflict	UNP Q92608
D	268	UNK	MET	conflict	UNP Q92608
D	269	UNK	ASP	conflict	UNP Q92608
D	270	UNK	ILE	conflict	UNP Q92608
D	271	UNK	THR	conflict	UNP Q92608
D	272	UNK	ASP	conflict	UNP Q92608
D	273	UNK	ILE	conflict	UNP Q92608
D	274	UNK	ILE	conflict	UNP Q92608
D	275	UNK	LYS	conflict	UNP Q92608
D	276	UNK	GLY	conflict	UNP Q92608
D	277	UNK	LYS	conflict	UNP Q92608
D	278	UNK	ALA	conflict	UNP Q92608
D	279	UNK	GLU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	280	UNK	SER	conflict	UNP Q92608
D	281	UNK	ASP	conflict	UNP Q92608
D	282	UNK	GLU	conflict	UNP Q92608
D	283	UNK	GLU	conflict	UNP Q92608
D	284	UNK	LYS	conflict	UNP Q92608
D	285	UNK	GLN	conflict	UNP Q92608
D	286	UNK	HIS	conflict	UNP Q92608
D	287	UNK	PHE	conflict	UNP Q92608
D	288	UNK	ILE	conflict	UNP Q92608
D	289	UNK	PRO	conflict	UNP Q92608
D	290	UNK	PHE	conflict	UNP Q92608
D	291	UNK	HIS	conflict	UNP Q92608
D	292	UNK	PRO	conflict	UNP Q92608
D	293	UNK	VAL	conflict	UNP Q92608
D	294	UNK	THR	conflict	UNP Q92608
D	295	UNK	ALA	conflict	UNP Q92608
D	296	UNK	GLU	conflict	UNP Q92608
D	297	UNK	ASN	conflict	UNP Q92608
D	298	UNK	ASP	conflict	UNP Q92608
D	299	UNK	PHE	conflict	UNP Q92608
D	300	UNK	LEU	conflict	UNP Q92608
D	301	UNK	HIS	conflict	UNP Q92608
D	302	UNK	SER	conflict	UNP Q92608
D	303	UNK	LEU	conflict	UNP Q92608
D	304	UNK	LEU	conflict	UNP Q92608
D	318	UNK	GLY	conflict	UNP Q92608
D	319	UNK	LYS	conflict	UNP Q92608
D	320	UNK	VAL	conflict	UNP Q92608
D	321	UNK	ILE	conflict	UNP Q92608
D	322	UNK	ALA	conflict	UNP Q92608
D	323	UNK	SER	conflict	UNP Q92608
D	324	UNK	LYS	conflict	UNP Q92608
D	325	UNK	GLY	conflict	UNP Q92608
D	326	UNK	ASP	conflict	UNP Q92608
D	327	UNK	SER	conflict	UNP Q92608
D	328	UNK	GLY	conflict	UNP Q92608
D	329	UNK	GLY	conflict	UNP Q92608
D	330	UNK	GLN	conflict	UNP Q92608
D	331	UNK	GLY	conflict	UNP Q92608
D	332	UNK	LEU	conflict	UNP Q92608
D	333	UNK	TRP	conflict	UNP Q92608
D	334	UNK	VAL	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	335	UNK	THR	conflict	UNP Q92608
D	336	UNK	MET	conflict	UNP Q92608
D	337	UNK	LYS	conflict	UNP Q92608
D	338	UNK	MET	conflict	UNP Q92608
D	339	UNK	LEU	conflict	UNP Q92608
D	340	UNK	VAL	conflict	UNP Q92608
D	341	UNK	GLY	conflict	UNP Q92608
D	342	UNK	ASP	conflict	UNP Q92608
D	343	UNK	ILE	conflict	UNP Q92608
D	344	UNK	ILE	conflict	UNP Q92608
D	345	UNK	GLN	conflict	UNP Q92608
D	346	UNK	ILE	conflict	UNP Q92608
D	347	UNK	ARG	conflict	UNP Q92608
D	348	UNK	LYS	conflict	UNP Q92608
D	349	UNK	ASP	conflict	UNP Q92608
D	350	UNK	TYR	conflict	UNP Q92608
D	351	UNK	PRO	conflict	UNP Q92608
D	377	UNK	HIS	conflict	UNP Q92608
D	378	UNK	LEU	conflict	UNP Q92608
D	379	UNK	VAL	conflict	UNP Q92608
D	380	UNK	ASP	conflict	UNP Q92608
D	381	UNK	ARG	conflict	UNP Q92608
D	382	UNK	THR	conflict	UNP Q92608
D	383	UNK	THR	conflict	UNP Q92608
D	384	UNK	VAL	conflict	UNP Q92608
D	385	UNK	VAL	conflict	UNP Q92608
D	386	UNK	ALA	conflict	UNP Q92608
D	387	UNK	ARG	conflict	UNP Q92608
D	388	UNK	LYS	conflict	UNP Q92608
D	389	UNK	LEU	conflict	UNP Q92608
D	609A	UNK	LYS	conflict	UNP Q92608
D	609B	UNK	LEU	conflict	UNP Q92608
D	609C	UNK	THR	conflict	UNP Q92608
D	609D	UNK	GLN	conflict	UNP Q92608
D	609E	UNK	ASN	conflict	UNP Q92608
D	609F	UNK	VAL	conflict	UNP Q92608
D	609G	UNK	GLY	conflict	UNP Q92608
D	609H	UNK	LEU	conflict	UNP Q92608
D	609I	UNK	LEU	conflict	UNP Q92608
D	609J	UNK	GLY	conflict	UNP Q92608
D	609K	UNK	LEU	conflict	UNP Q92608
D	609L	UNK	LEU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	609M	UNK	LYS	conflict	UNP Q92608
D	609N	UNK	TRP	conflict	UNP Q92608
D	609O	UNK	ARG	conflict	UNP Q92608
D	609P	UNK	MET	conflict	UNP Q92608
D	609Q	UNK	LYS	conflict	UNP Q92608
D	609R	UNK	PRO	conflict	UNP Q92608
D	609S	UNK	GLN	conflict	UNP Q92608
D	609T	UNK	LEU	conflict	UNP Q92608
D	609U	UNK	LEU	conflict	UNP Q92608
D	609V	UNK	GLN	conflict	UNP Q92608
D	609W	UNK	GLU	conflict	UNP Q92608
D	609X	UNK	ASN	conflict	UNP Q92608
D	609Y	UNK	LEU	conflict	UNP Q92608
D	609Z	UNK	GLU	conflict	UNP Q92608
D	610A	UNK	LYS	conflict	UNP Q92608
D	610B	UNK	LEU	conflict	UNP Q92608
D	610C	UNK	LYS	conflict	UNP Q92608
D	610D	UNK	ILE	conflict	UNP Q92608
D	610E	UNK	VAL	conflict	UNP Q92608
D	610F	UNK	ASP	conflict	UNP Q92608
D	626	UNK	GLY	conflict	UNP Q92608
D	627	UNK	GLU	conflict	UNP Q92608
D	628	UNK	GLU	conflict	UNP Q92608
D	629	UNK	VAL	conflict	UNP Q92608
D	630	UNK	VAL	conflict	UNP Q92608
D	631	UNK	LYS	conflict	UNP Q92608
D	632	UNK	PHE	conflict	UNP Q92608
D	633	UNK	LEU	conflict	UNP Q92608
D	634	UNK	GLN	conflict	UNP Q92608
D	635	UNK	ASP	conflict	UNP Q92608
D	636	UNK	THR	conflict	UNP Q92608
D	637	UNK	LEU	conflict	UNP Q92608
D	638	UNK	ASP	conflict	UNP Q92608
D	639	UNK	ALA	conflict	UNP Q92608
D	640	UNK	LEU	conflict	UNP Q92608
D	641	UNK	PHE	conflict	UNP Q92608
D	642	UNK	ASN	conflict	UNP Q92608
D	679A	UNK	HIS	conflict	UNP Q92608
D	679B	UNK	PHE	conflict	UNP Q92608
D	679C	UNK	ASN	conflict	UNP Q92608
D	679D	UNK	THR	conflict	UNP Q92608
D	679E	UNK	VAL	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	679F	UNK	LEU	conflict	UNP Q92608
D	679G	UNK	GLU	conflict	UNP Q92608
D	679H	UNK	ALA	conflict	UNP Q92608
D	679I	UNK	TYR	conflict	UNP Q92608
D	679J	UNK	ILE	conflict	UNP Q92608
D	679K	UNK	GLN	conflict	UNP Q92608
D	679L	UNK	GLN	conflict	UNP Q92608
D	679M	UNK	HIS	conflict	UNP Q92608
D	679N	UNK	PHE	conflict	UNP Q92608
D	679O	UNK	SER	conflict	UNP Q92608
D	679P	UNK	ALA	conflict	UNP Q92608
D	679Q	UNK	THR	conflict	UNP Q92608
D	688	UNK	LEU	conflict	UNP Q92608
D	689	UNK	ALA	conflict	UNP Q92608
D	690	UNK	TYR	conflict	UNP Q92608
D	691	UNK	LYS	conflict	UNP Q92608
D	692	UNK	LYS	conflict	UNP Q92608
D	693	UNK	LEU	conflict	UNP Q92608
D	694	UNK	MET	conflict	UNP Q92608
D	695	UNK	THR	conflict	UNP Q92608
D	696	UNK	VAL	conflict	UNP Q92608
D	697	UNK	LEU	conflict	UNP Q92608
D	698	UNK	LYS	conflict	UNP Q92608
D	699	UNK	THR	conflict	UNP Q92608
D	700	UNK	TYR	conflict	UNP Q92608
D	701	UNK	LEU	conflict	UNP Q92608
D	702	UNK	ASP	conflict	UNP Q92608
D	703	UNK	THR	conflict	UNP Q92608
D	704	UNK	SER	conflict	UNP Q92608
D	705	UNK	SER	conflict	UNP Q92608
D	706	UNK	ARG	conflict	UNP Q92608
D	707	UNK	GLY	conflict	UNP Q92608
D	708	UNK	GLU	conflict	UNP Q92608
D	709	UNK	GLN	conflict	UNP Q92608
D	710	UNK	CYS	conflict	UNP Q92608
D	711	UNK	GLU	conflict	UNP Q92608
D	712	UNK	PRO	conflict	UNP Q92608
D	713	UNK	ILE	conflict	UNP Q92608
D	714	UNK	LEU	conflict	UNP Q92608
D	715	UNK	ARG	conflict	UNP Q92608
D	716	UNK	THR	conflict	UNP Q92608
D	717	UNK	LEU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	718	UNK	LYS	conflict	UNP Q92608
D	719	UNK	ALA	conflict	UNP Q92608
D	720	UNK	LEU	conflict	UNP Q92608
D	721	UNK	GLU	conflict	UNP Q92608
D	722	UNK	TYR	conflict	UNP Q92608
D	723	UNK	VAL	conflict	UNP Q92608
D	724	UNK	PHE	conflict	UNP Q92608
D	725	UNK	LYS	conflict	UNP Q92608
D	726	UNK	PHE	conflict	UNP Q92608
D	727	UNK	ILE	conflict	UNP Q92608
D	728	UNK	VAL	conflict	UNP Q92608
D	729	UNK	ARG	conflict	UNP Q92608
D	730	UNK	SER	conflict	UNP Q92608
D	731	UNK	ARG	conflict	UNP Q92608
D	732	UNK	THR	conflict	UNP Q92608
D	733	UNK	LEU	conflict	UNP Q92608
D	734	UNK	PHE	conflict	UNP Q92608
D	735	UNK	SER	conflict	UNP Q92608
D	736	UNK	GLN	conflict	UNP Q92608
D	742	UNK	LEU	conflict	UNP Q92608
D	743	UNK	TYR	conflict	UNP Q92608
D	744	UNK	GLU	conflict	UNP Q92608
D	745	UNK	GLY	conflict	UNP Q92608
D	746	UNK	LYS	conflict	UNP Q92608
D	747	UNK	GLU	conflict	UNP Q92608
D	748	UNK	GLN	conflict	UNP Q92608
D	749	UNK	MET	conflict	UNP Q92608
D	750	UNK	GLU	conflict	UNP Q92608
D	751	UNK	PHE	conflict	UNP Q92608
D	752	UNK	GLU	conflict	UNP Q92608
D	753	UNK	GLU	conflict	UNP Q92608
D	754	UNK	SER	conflict	UNP Q92608
D	755	UNK	MET	conflict	UNP Q92608
D	756	UNK	ARG	conflict	UNP Q92608
D	757	UNK	ARG	conflict	UNP Q92608
D	758	UNK	LEU	conflict	UNP Q92608
D	759	UNK	PHE	conflict	UNP Q92608
D	760	UNK	GLU	conflict	UNP Q92608
D	761	UNK	SER	conflict	UNP Q92608
D	762	UNK	ILE	conflict	UNP Q92608
D	763	UNK	ASN	conflict	UNP Q92608
D	764	UNK	ASN	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	765	UNK	LEU	conflict	UNP Q92608
D	766	UNK	MET	conflict	UNP Q92608
D	767	UNK	LYS	conflict	UNP Q92608
D	768	UNK	SER	conflict	UNP Q92608
D	769	UNK	GLN	conflict	UNP Q92608
D	770	UNK	TYR	conflict	UNP Q92608
D	771	UNK	LYS	conflict	UNP Q92608
D	772	UNK	THR	conflict	UNP Q92608
D	773	UNK	THR	conflict	UNP Q92608
D	774	UNK	ILE	conflict	UNP Q92608
D	775	UNK	LEU	conflict	UNP Q92608
D	776	UNK	LEU	conflict	UNP Q92608
D	777	UNK	GLN	conflict	UNP Q92608
D	778	UNK	VAL	conflict	UNP Q92608
D	779	UNK	ALA	conflict	UNP Q92608
D	780	UNK	ALA	conflict	UNP Q92608
D	781	UNK	LEU	conflict	UNP Q92608
D	782	UNK	LYS	conflict	UNP Q92608
D	783	UNK	TYR	conflict	UNP Q92608
D	784	UNK	ILE	conflict	UNP Q92608
D	785	UNK	PRO	conflict	UNP Q92608
D	786	UNK	SER	conflict	UNP Q92608
D	787	UNK	VAL	conflict	UNP Q92608
D	788	UNK	LEU	conflict	UNP Q92608
D	789	UNK	HIS	conflict	UNP Q92608
D	790	UNK	ASP	conflict	UNP Q92608
D	791	UNK	VAL	conflict	UNP Q92608
D	792	UNK	GLU	conflict	UNP Q92608
D	793	UNK	MET	conflict	UNP Q92608
D	794	UNK	VAL	conflict	UNP Q92608
D	795	UNK	PHE	conflict	UNP Q92608
D	796	UNK	ASP	conflict	UNP Q92608
D	797	UNK	ALA	conflict	UNP Q92608
D	798	UNK	LYS	conflict	UNP Q92608
D	799	UNK	LEU	conflict	UNP Q92608
D	801	UNK	LEU	conflict	UNP Q92608
D	802	UNK	SER	conflict	UNP Q92608
D	803	UNK	GLN	conflict	UNP Q92608
D	804	UNK	LEU	conflict	UNP Q92608
D	805	UNK	LEU	conflict	UNP Q92608
D	806	UNK	TYR	conflict	UNP Q92608
D	807	UNK	GLU	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	808	UNK	PHE	conflict	UNP Q92608
D	809	UNK	TYR	conflict	UNP Q92608
D	810	UNK	THR	conflict	UNP Q92608
D	811	UNK	CYS	conflict	UNP Q92608
D	812	UNK	ILE	conflict	UNP Q92608
D	813	UNK	PRO	conflict	UNP Q92608
D	814	UNK	PRO	conflict	UNP Q92608
D	815	UNK	VAL	conflict	UNP Q92608
D	816	UNK	LYS	conflict	UNP Q92608
D	817	UNK	LEU	conflict	UNP Q92608
D	818	UNK	GLN	conflict	UNP Q92608
D	819	UNK	LYS	conflict	UNP Q92608
D	820	UNK	GLN	conflict	UNP Q92608
D	821	UNK	LYS	conflict	UNP Q92608
D	822	UNK	VAL	conflict	UNP Q92608
D	823	UNK	GLN	conflict	UNP Q92608
D	824	UNK	SER	conflict	UNP Q92608
D	825	UNK	MET	conflict	UNP Q92608
D	826	UNK	ASN	conflict	UNP Q92608
D	827	UNK	GLU	conflict	UNP Q92608
D	828	UNK	ILE	conflict	UNP Q92608
D	829	UNK	VAL	conflict	UNP Q92608
D	830	UNK	GLN	conflict	UNP Q92608
D	831	UNK	SER	conflict	UNP Q92608
D	832	UNK	ASN	conflict	UNP Q92608
D	833	UNK	LEU	conflict	UNP Q92608
D	834	UNK	PHE	conflict	UNP Q92608
D	835	UNK	LYS	conflict	UNP Q92608
D	836	UNK	LYS	conflict	UNP Q92608
D	837	UNK	GLN	conflict	UNP Q92608
D	838	UNK	GLU	conflict	UNP Q92608
D	839	UNK	CYS	conflict	UNP Q92608
D	840	UNK	ARG	conflict	UNP Q92608
D	841	UNK	ASP	conflict	UNP Q92608
D	842	UNK	ILE	conflict	UNP Q92608
D	843	UNK	LEU	conflict	UNP Q92608
D	844	UNK	LEU	conflict	UNP Q92608
D	845	UNK	PRO	conflict	UNP Q92608
D	846	UNK	VAL	conflict	UNP Q92608
D	847	UNK	ILE	conflict	UNP Q92608
D	848	UNK	THR	conflict	UNP Q92608
D	849	UNK	LYS	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	850	UNK	GLU	conflict	UNP Q92608
D	851	UNK	LEU	conflict	UNP Q92608
D	852	UNK	LYS	conflict	UNP Q92608
D	853	UNK	GLU	conflict	UNP Q92608
D	854	UNK	LEU	conflict	UNP Q92608
D	855	UNK	LEU	conflict	UNP Q92608
D	856	UNK	GLU	conflict	UNP Q92608
D	857	UNK	GLN	conflict	UNP Q92608
D	858	UNK	LYS	conflict	UNP Q92608
D	859	UNK	ASP	conflict	UNP Q92608
D	860	UNK	ASP	conflict	UNP Q92608
D	861	UNK	MET	conflict	UNP Q92608
D	862	UNK	GLN	conflict	UNP Q92608
D	863	UNK	HIS	conflict	UNP Q92608
D	864	UNK	GLN	conflict	UNP Q92608
D	865	UNK	VAL	conflict	UNP Q92608
D	866	UNK	LEU	conflict	UNP Q92608
D	867	UNK	GLU	conflict	UNP Q92608
D	868	UNK	ARG	conflict	UNP Q92608
D	869	UNK	LYS	conflict	UNP Q92608
D	870	UNK	TYR	conflict	UNP Q92608
D	871	UNK	CYS	conflict	UNP Q92608
D	872	UNK	VAL	conflict	UNP Q92608
D	873	UNK	GLU	conflict	UNP Q92608
D	874	UNK	LEU	conflict	UNP Q92608
D	875	UNK	LEU	conflict	UNP Q92608
D	876	UNK	ASN	conflict	UNP Q92608
D	877	UNK	SER	conflict	UNP Q92608
D	878	UNK	ILE	conflict	UNP Q92608
D	879	UNK	LEU	conflict	UNP Q92608
D	880	UNK	GLU	conflict	UNP Q92608
D	881	UNK	VAL	conflict	UNP Q92608
D	882	UNK	LEU	conflict	UNP Q92608
D	883	UNK	SER	conflict	UNP Q92608
D	884	UNK	TYR	conflict	UNP Q92608
D	885	UNK	GLN	conflict	UNP Q92608
D	886	UNK	ASP	conflict	UNP Q92608
D	887	UNK	ALA	conflict	UNP Q92608
D	888	UNK	ALA	conflict	UNP Q92608
D	889	UNK	PHE	conflict	UNP Q92608
D	890	UNK	THR	conflict	UNP Q92608
D	891	UNK	TYR	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	892	UNK	HIS	conflict	UNP Q92608
D	896	UNK	HIS	conflict	UNP Q92608
D	897	UNK	ILE	conflict	UNP Q92608
D	898	UNK	GLN	conflict	UNP Q92608
D	899	UNK	GLU	conflict	UNP Q92608
D	900	UNK	ILE	conflict	UNP Q92608
D	901	UNK	MET	conflict	UNP Q92608
D	902	UNK	VAL	conflict	UNP Q92608
D	903	UNK	GLN	conflict	UNP Q92608
D	904	UNK	LEU	conflict	UNP Q92608
D	905	UNK	LEU	conflict	UNP Q92608
D	906	UNK	ARG	conflict	UNP Q92608
D	907	UNK	THR	conflict	UNP Q92608
D	908	UNK	VAL	conflict	UNP Q92608
D	909	UNK	ASN	conflict	UNP Q92608
D	910	UNK	ARG	conflict	UNP Q92608
D	911	UNK	THR	conflict	UNP Q92608
D	912	UNK	VAL	conflict	UNP Q92608
D	913	UNK	ILE	conflict	UNP Q92608
D	914	UNK	THR	conflict	UNP Q92608
D	915	UNK	MET	conflict	UNP Q92608
D	916	UNK	GLY	conflict	UNP Q92608
D	917	UNK	ARG	conflict	UNP Q92608
D	918	UNK	ASP	conflict	UNP Q92608
D	919	UNK	HIS	conflict	UNP Q92608
D	920	UNK	ILE	conflict	UNP Q92608
D	921	UNK	LEU	conflict	UNP Q92608
D	922	UNK	ILE	conflict	UNP Q92608
D	923	UNK	SER	conflict	UNP Q92608
D	934	UNK	HIS	conflict	UNP Q92608
D	935	UNK	PHE	conflict	UNP Q92608
D	936	UNK	VAL	conflict	UNP Q92608
D	937	UNK	ALA	conflict	UNP Q92608
D	938	UNK	CYS	conflict	UNP Q92608
D	939	UNK	MET	conflict	UNP Q92608
D	940	UNK	THR	conflict	UNP Q92608
D	941	UNK	ALA	conflict	UNP Q92608
D	942	UNK	ILE	conflict	UNP Q92608
D	943	UNK	LEU	conflict	UNP Q92608
D	944	UNK	ASN	conflict	UNP Q92608
D	945	UNK	GLN	conflict	UNP Q92608
D	946	UNK	MET	conflict	UNP Q92608

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Chain	Residue	Modelled	Actual	Comment	Reference
D	947	UNK	GLY	conflict	UNP Q92608
D	948	UNK	ASP	conflict	UNP Q92608
D	949	UNK	GLN	conflict	UNP Q92608
D	950	UNK	HIS	conflict	UNP Q92608
D	951	UNK	TYR	conflict	UNP Q92608
D	952	UNK	SER	conflict	UNP Q92608
D	953	UNK	PHE	conflict	UNP Q92608
D	954	UNK	TYR	conflict	UNP Q92608
D	955	UNK	ILE	conflict	UNP Q92608
D	956	UNK	GLU	conflict	UNP Q92608
D	957	UNK	THR	conflict	UNP Q92608
D	958	UNK	PHE	conflict	UNP Q92608
D	959	UNK	GLN	conflict	UNP Q92608
D	960	UNK	THR	conflict	UNP Q92608

- Molecule 2 is a protein called Engulfment and cell motility protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	680	Total	C	N	O	S	0	0
			5054	3269	841	917	27		
2	E	680	Total	C	N	O	S	0	0
			5056	3270	840	917	29		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	139	LEU	ARG	conflict	UNP Q92556
E	139	LEU	ARG	conflict	UNP Q92556

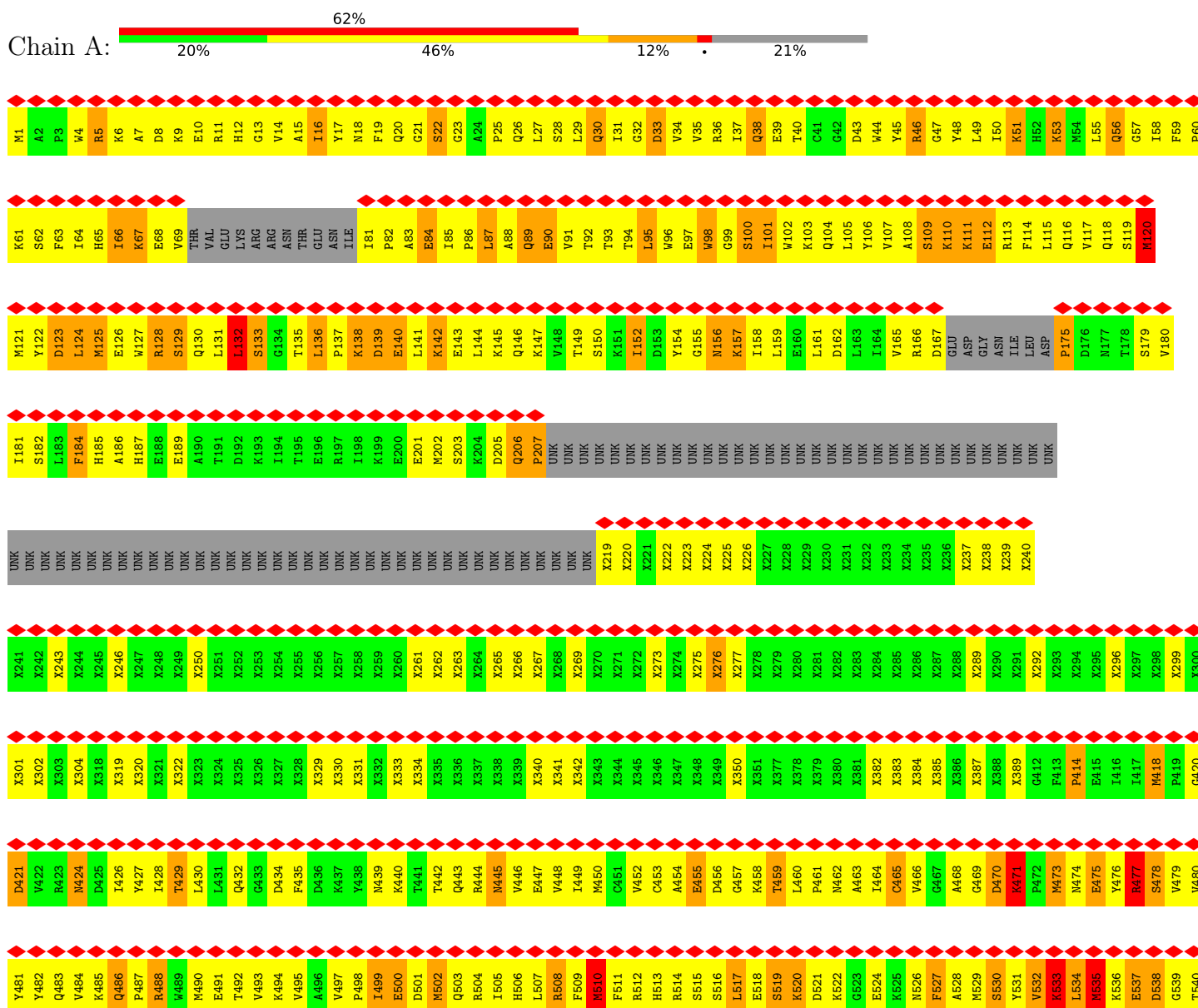
- Molecule 3 is a protein called Ras-related C3 botulinum toxin substrate 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	177	Total	C	N	O	S	0	0
			1383	889	228	258	8		
3	F	177	Total	C	N	O	S	0	0
			1383	889	228	258	8		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

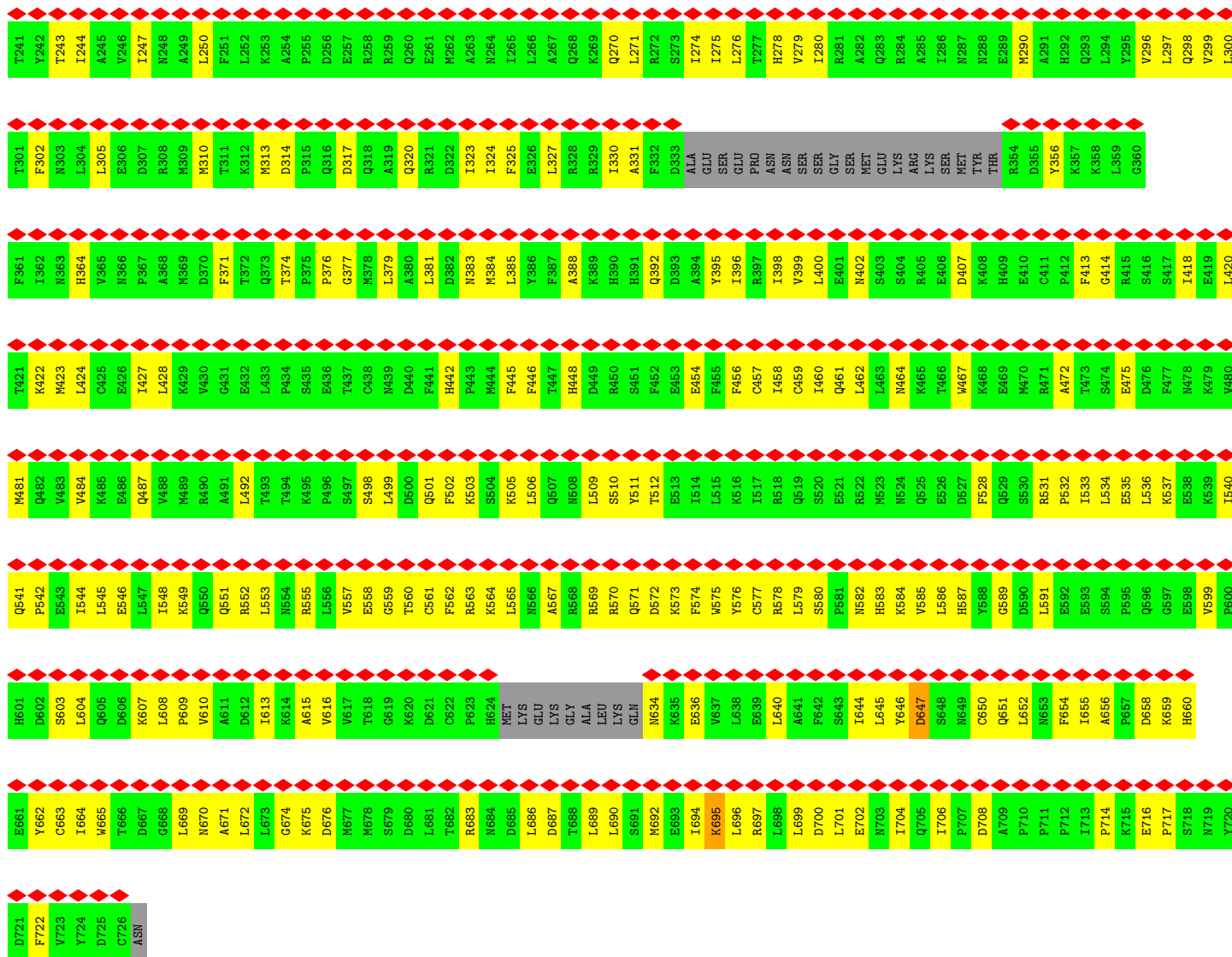
• Molecule 1: Dedicator of cytokinesis protein 2



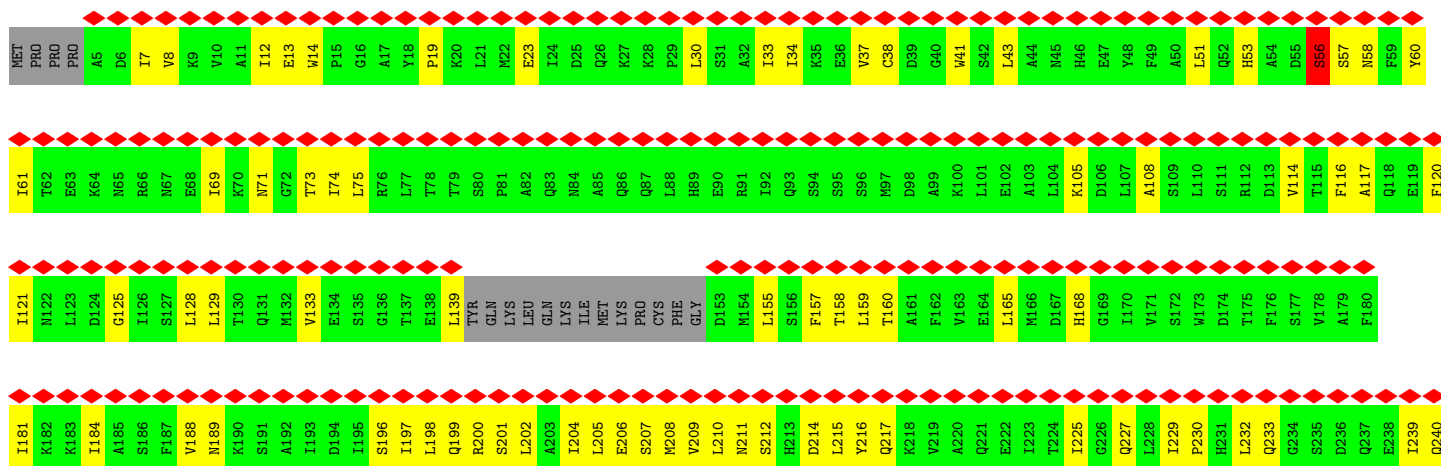
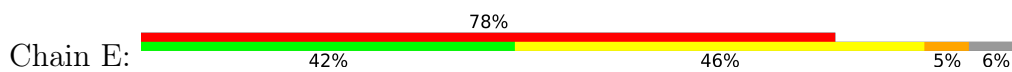
GLN	T541	T542	T543	T544	T545	T546	T547	T548	T549	T550	T551	T552	T553	T554	T555	T556	T557	T558	T559	T560	T561	T562	T563	T564	T565	T566	T567	T568	T569	T570	T571	T572	T573	T574	T575	T576	T577	T578	T579	T580	T581	T582	T583	T584	T585	T586	T587	T588	T589	T590	T591	T592	T593	T594	T595	T596	T597	T598	T599	T600																																																								
VAL	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	F600																																																									
MET	I602	I603	I604	I605	I606	I607	I608	I609	I610	I611	I612	I613	I614	I615	I616	I617	I618	I619	I620	I621	I622	I623	I624	I625	I626	I627	I628	I629	I630	I631	I632	I633	I634	I635	I636	I637	I638	I639	I640	I641	I642	I643	I644	I645	I646	I647	I648	I649	I650	I651	I652	I653	I654	I655	I656	I657	I658	I659	I660	I661	I662	I663	I664	I665	I666	I667	I668	I669	I670	I671	I672	I673	I674	I675	I676	I677	I678	I679	I680	I681	I682	I683	I684	I685	I686	I687	I688	I689	I690	I691	I692	I693	I694	I695	I696	I697	I698	I699	I700																	
THR	T601	T602	T603	T604	T605	T606	T607	T608	T609	T610	T611	T612	T613	T614	T615	T616	T617	T618	T619	T620	T621	T622	T623	T624	T625	T626	T627	T628	T629	T630	T631	T632	T633	T634	T635	T636	T637	T638	T639	T640	T641	T642	T643	T644	T645	T646	T647	T648	T649	T650	T651	T652	T653	T654	T655	T656	T657	T658	T659	T660	T661	T662	T663	T664	T665	T666	T667	T668	T669	T670	T671	T672	T673	T674	T675	T676	T677	T678	T679	T680	T681	T682	T683	T684	T685	T686	T687	T688	T689	T690	T691	T692	T693	T694	T695	T696	T697	T698	T699	T700																
GLY	L605	L606	L607	L608	L609	L610	L611	L612	L613	L614	L615	L616	L617	L618	L619	L620	L621	L622	L623	L624	L625	L626	L627	L628	L629	L630	L631	L632	L633	L634	L635	L636	L637	L638	L639	L640	L641	L642	L643	L644	L645	L646	L647	L648	L649	L650	L651	L652	L653	L654	L655	L656	L657	L658	L659	L660	L661	L662	L663	L664	L665	L666	L667	L668	L669	L670	L671	L672	L673	L674	L675	L676	L677	L678	L679	L680	L681	L682	L683	L684	L685	L686	L687	L688	L689	L690	L691	L692	L693	L694	L695	L696	L697	L698	L699	L700																				
GLN	M650	M651	M652	M653	M654	M655	M656	M657	M658	M659	M660	M661	M662	M663	M664	M665	M666	M667	M668	M669	M670	M671	M672	M673	M674	M675	M676	M677	M678	M679	M680	M681	M682	M683	M684	M685	M686	M687	M688	M689	M690	M691	M692	M693	M694	M695	M696	M697	M698	M699	M700	M701	M702	M703	M704	M705	M706	M707	M708	M709	M710	M711	M712	M713	M714	M715	M716	M717	M718	M719	M720	M721	M722	M723	M724	M725	M726	M727	M728	M729	M730	M731	M732	M733	M734	M735	M736	M737	M738	M739	M740	M741	M742	M743	M744	M745	M746	M747	M748	M749	M750	M751	M752	M753	M754	M755	M756	M757	M758	M759	M760	M761	M762	M763	M764	M765
GLN	X626	X627	X628	X629	X630	X631	X632	X633	X634	X635	X636	X637	X638	X639	X640	X641	X642	X643	X644	X645	X646	X647	X648	X649	X650	X651	X652	X653	X654	X655	X656	X657	X658	X659	X660	X661	X662	X663	X664	X665	X666	X667	X668	X669	X670	X671	X672	X673	X674	X675	X676	X677	X678	X679	X680	X681	X682	X683	X684	X685	X686	X687	X688	X689	X690	X691	X692	X693	X694	X695	X696	X697	X698	X699	X700																																									
GLN	X701	X702	X703	X704	X705	X706	X707	X708	X709	X710	X711	X712	X713	X714	X715	X716	X717	X718	X719	X720	X721	X722	X723	X724	X725	X726	X727	X728	X729	X730	X731	X732	X733	X734	X735	X736	X737	X738	X739	X740	X741	X742	X743	X744	X745	X746	X747	X748	X749	X750	X751	X752	X753	X754	X755	X756	X757	X758	X759	X760	X761	X762	X763	X764	X765																																																			
GLN	X766	X767	X768	X769	X770	X771	X772	X773	X774	X775	X776	X777	X778	X779	X780	X781	X782	X783	X784	X785	X786	X787	X788	X789	X790	X791	X792	X793	X794	X795	X796	X797	X798	X799	X800	X801	X802	X803	X804	X805	X806	X807	X808	X809	X810	X811	X812	X813	X814	X815	X816	X817	X818	X819	X820	X821	X822	X823	X824	X825	X826																																																							
GLN	X827	X828	X829	X830	X831	X832	X833	X834	X835	X836	X837	X838	X839	X840	X841	X842	X843	X844	X845	X846	X847	X848	X849	X850	X851	X852	X853	X854	X855	X856	X857	X858	X859	X860	X861	X862	X863	X864	X865	X866	X867	X868	X869	X870	X871	X872	X873	X874	X875	X876	X877	X878	X879	X880	X881	X882	X883	X884	X885	X886																																																								
GLN	X887	X888	X889	X890	X891	X892	X893	X894	X895	X896	X897	X898	X899	X900	X901	X902	X903	X904	X905	X906	X907	X908	X909	X910	X911	X912	X913	X914	X915	X916	X917	X918	X919	X920	X921	X922	X923	X924	X925	X926	X927	X928	X929	X930	X931	X932	X933	X934	X935	X936	X937	X938	X939	X940	X941	X942	X943	X944	X945	X946	X947	X948	X949	X950	X951	X952	X953	X954	X955	X956	X957	X958	X959																																											
GLN	X960	X961	X962	X963	X964	X965	X966	X967	X968	X969	X970	X971	X972	X973	X974	X975	X976	X977	X978	X979	X980	X981	X982	X983	X984	X985	X986	X987	X988	X989	X990	X991	X992	X993	X994	X995	X996	X997	X998	X999	F1000	L1001	L1002	L1003	L1004	L1005	L1006	L1007	L1008	L1009	L1010	L1011	L1012	L1013	L1014	L1015	L1016	L1017	L1018	L1019	L1020																																																							
GLN	F1021	F1022	F1023	F1024	L1025	L1026	M1027	N1028	Y1029	F1030	H1031	L1032	A1033	V1034	A1035	F1036	T1037	L1038	Q1039	D1040	S1041	L1042	Q1043	L1044	L1045	Q1046	F1047	S1048	H1049	A1050	K1051	Y1052	M1053	K1054	I1055	L1056	M1057	M1058	Y1059	G1060	D1061	M1062	R1063	L1064	M1065	L1066	G1067	F1068	S1069	L1070	R1071	D1072	M1073	W1074	Y1075	K1076	L1077	G1078	Q1079	N1080																																																								
GLN	K1081	I1082	C1083	F1084	I1085	P1086	G1087	M1088	V1089	G1090	P1091	L1092	L1093	E1094	M1095	T1096	L1097	I1098	P1099	E1100	A1101	E1102	L1103	R1104	K1105	L1106	T1107	I1108	P1109	I1110	F1111	F1112	D1113	M1114	M1115	L1116	C1117	TYR	GLN	ARG	GLY	D1124	F1125	K1126	K1127	F1128	E1129	M1130	E1131	I1132	I1133	L1134	K1135	L1136	D1137	H1138	E1139	V1140																																																										
GLN	E1141	G1142	G1143	R1144	G1145	D1146	E1147	Q1148	Y1149	M1150	Q1151	L1152	L1153	E1154	S1155	I1156	L1157	M1158	E1159	C1160	A1161	A1162	E1163	H1164	P1165	T1166	I1167	A1168	K1169	S1170	V1171	E1172	M1173	F1174	V1175	M1176	L1177	V1178	K1179	G1180	L1181	L1182	E1183	K1184	L1185	L1186	D1187	Y1188	R1189	G1190	V1191	M1192	T1193	L1194	E1195	S1196	K1197	D1198	M1199	R1200																																																								
GLN	M1201	S1202	C1203	V1205	N1206	L1207	L1208	N1209	F1210	Y1211	K1212	L1213	N1214	N1215	R1216	E1217	E1218	M1219	Y1220	I1221	L1222	Y1223	L1224	I1225	G1226	K1227	M1228	D1229	L1230	H1231	E1232	L1233	C1234	D1235	N1236	Y1237	E1238	E1239	A1240	A1241	Q1242	T1243	L1244	L1245	L1246	H1247	T1248	W1249	L1250	L1251	K1252	W1253	S1254	D1255	E1256	GLN	CYS	ALA	SER																																																									

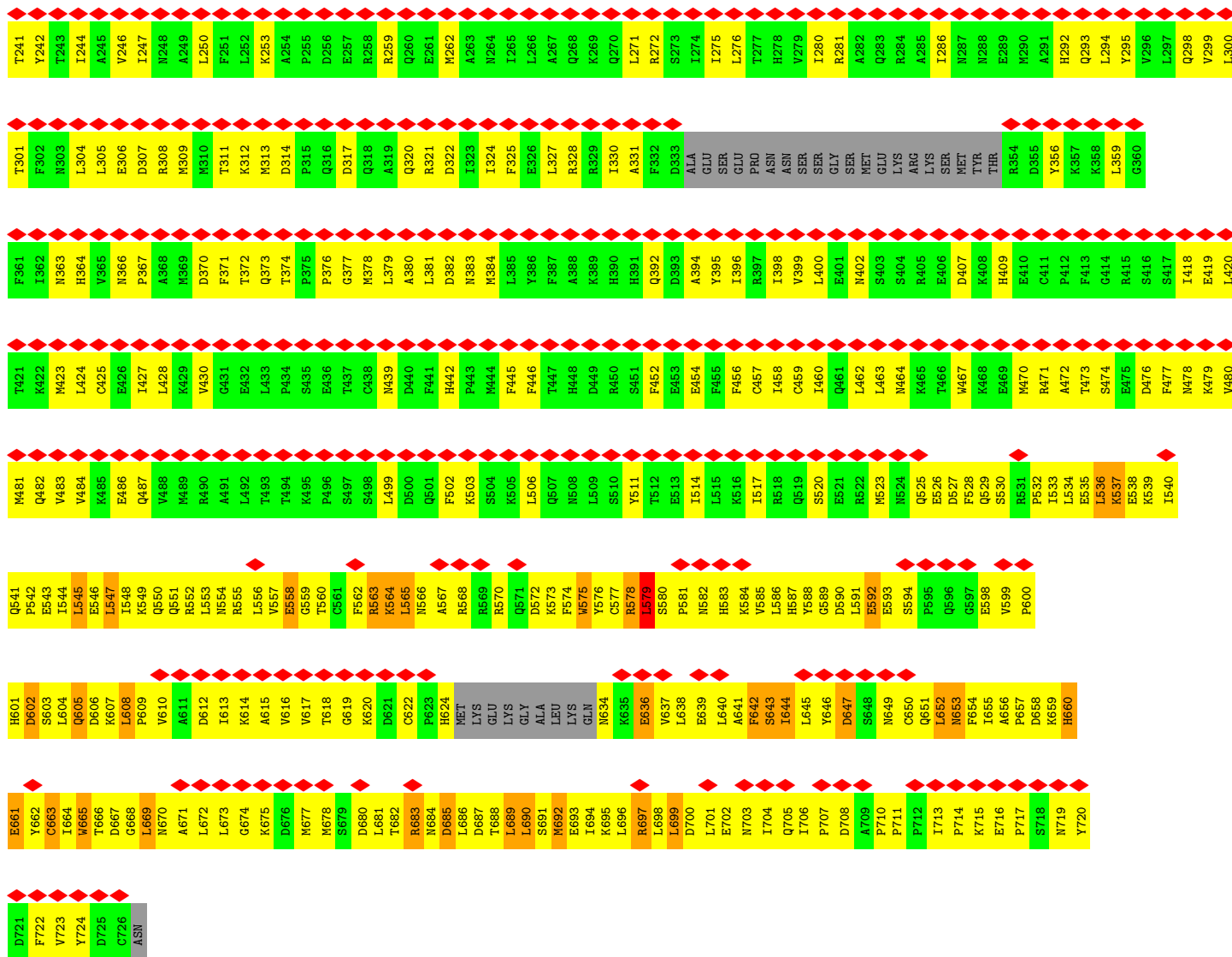


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I1156	L1157	M1158	E1159	C1160	A1161	A1162	E1163	H1164	P1165	T1166	L1167	A1168	K1169	S1170	V1171	A1172	M1173	F1174	V1175	M1176	L1177	L1178	K1179	G1180	L1181	L1182	L1183	L1184	L1185	L1186	D1187	Y1188	L1189	G1190	H1191	M1192	L1193	D1194	E1195	S1196	K1197	D1198	M1199	R1200	M1201	S1202	C1203	T1204	V1205	N1206	L1207	GLY	GLN	GLN	HIS	F1210	Y1211	K1212	T1213	H1214	L1215
I1092	L1093	E1094	M1095	L1096	I1097	I1098	P1099	E1100	E1101	E1102	L1103	K1104	K1105	A1106	T1107	I1108	P1109	I1110	F1111	L1112	GLU	TYR	GLN	ARG	SER	GLY	D1124	F1125	F1126	K1127	E1128	N1129	M1130	E1131	I1132	L1133	L1134	K1135	L1136	D1137	H1138	E1139	V1140	G1143	R1144	G1145	D1146	E1147	Q1148	Y1149	M1150	Q1151	L1152	L1153	E1154	S1155					
F988	L989	T972	M975	F976	K977	D978	L979	R980	G981	K982	N983	Y984	Y985	D986	M989	M990	A991	M992	S993	M994	V995	G996	N997	R998	V999	F1000	L1001	R1002	A1003	I1004	N1005	F1006	G1007	F1008	E1009	T1010	M1011	N1012	Q1013	K1014	F1015	L1016	E1017	H1018	T1019	N1020	F1021	E1022	F1023	Q1024	I1085	P1086	L1025	M1026	M1027	M1028	Y1029	F1030			
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X878	X881	X884	X885	X886	X887	X888	X889	X890	X891	X900	X901	X902	X903	X904	X905	X906	X908	X909	X912	X916	X934	X935	X936	X937	X938	X939	X940	X941	X942	X943	X944	X945	X946	X947	X948	X949	X950	X951	X952	X953	X954	X955	X956	X957	X958	X959	E964	L965	V966	D967											
X787	X788	X789	X793	X794	X795	X796	X797	X798	X799	X801	X802	X705	X709	X710	X711	X712	X713	X714	X715	X716	X717	X718	X719	X720	X721	X722	X730	X731	X732	X746	X750	X757	X761	X768	X769	X770	X771	X772	X773	X774	X775	X776	X777	X778	X779	X780	X781	X782	X783	X784											
UNK	X688	X691	X695	X696	X697	X698	X699	X700	X701	X702	X626	X627	X631	X634	X635	X636	X639	X640	E657	V658	D669	L661	D664	L667	L668	L669	L672	D675	Q679	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK					
L568	P569	F509	M510	F511	R512	R513	R514	R515	S516	L517	GLY	ALA	THR	LEU	SER	ARG	SER	SER	SER	VAL	G590	G591	L592	S593	V594	V595	S596	R597	L534	F537	S600	I602	S603	T604	L605	V606	C607	S608	T609	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK	UNK						
R508	F509	M510	F511	R512	R513	R514	R515	S516	L517	GLY	ALA	THR	LEU	SER	ARG	SER	SER	SER	VAL	G590	G591	L592	S593	V594	V595	S596	R597	L534	F537	S600	I602	S603	T604	L605	V606	C607	S608	T609	F546	H547	D548	L549	V550	V551	L552	K553	G554	D555	S556	K557	K558	M559	E560	D561	S562	A563	A564	V565	L566	T567	
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X331	X332	X333	X334	X339	X340	X341	X342	X345	X346	X347	X350	X351	X377	X380	X381	X382	X383	X384	X385	X386	X387	X388	X389	P414	M418	P419	G420	D421	M424	D425	I426	Y427	I428	T429	L430	L431	Q432	G433	D434	F435	D436	K437	V438	M439	T440	T441	T442	Q443	R444	R504	I505	H506	L507								
X257	X258	X259	X260	X261	X262	X263	X264	X265	X266	X267	X268	X269	X270	X271	X272	X273	X274	X275	X276	X277	X278	X279	X280	X281	X282	X283	X284	X285	X286	X287	X288	X289	X290	X291	X292	X293	X294	X295	X296	X297	X298	X299	X300	X301	X302	X303	X304	X308	X310	X319	X320	X321	X322	X323	X324	X325	X326	X329	X330		

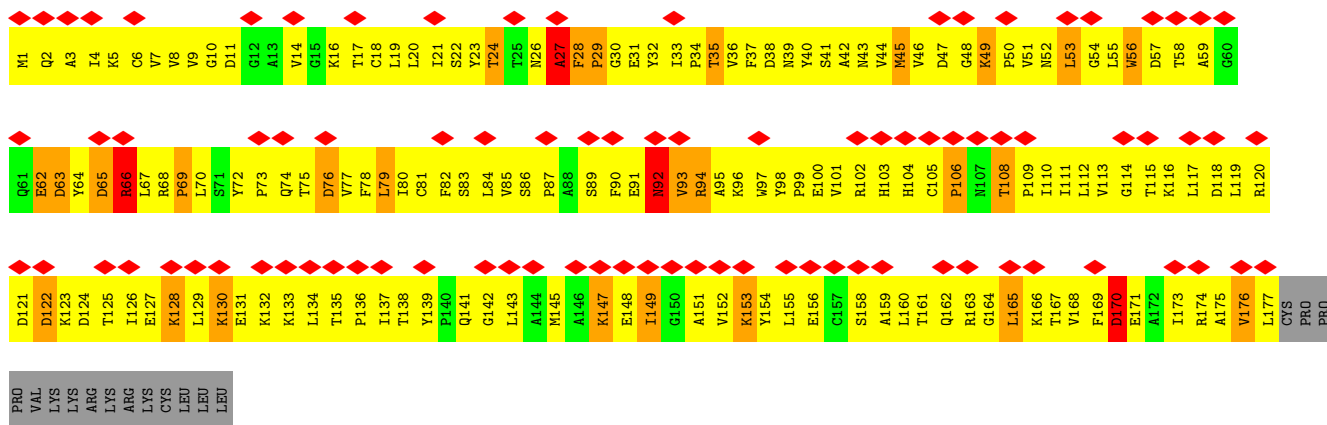
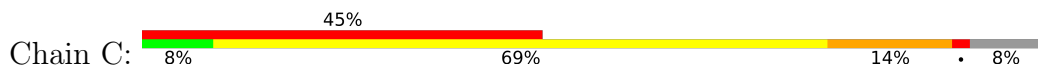


• Molecule 2: Engulfment and cell motility protein 1

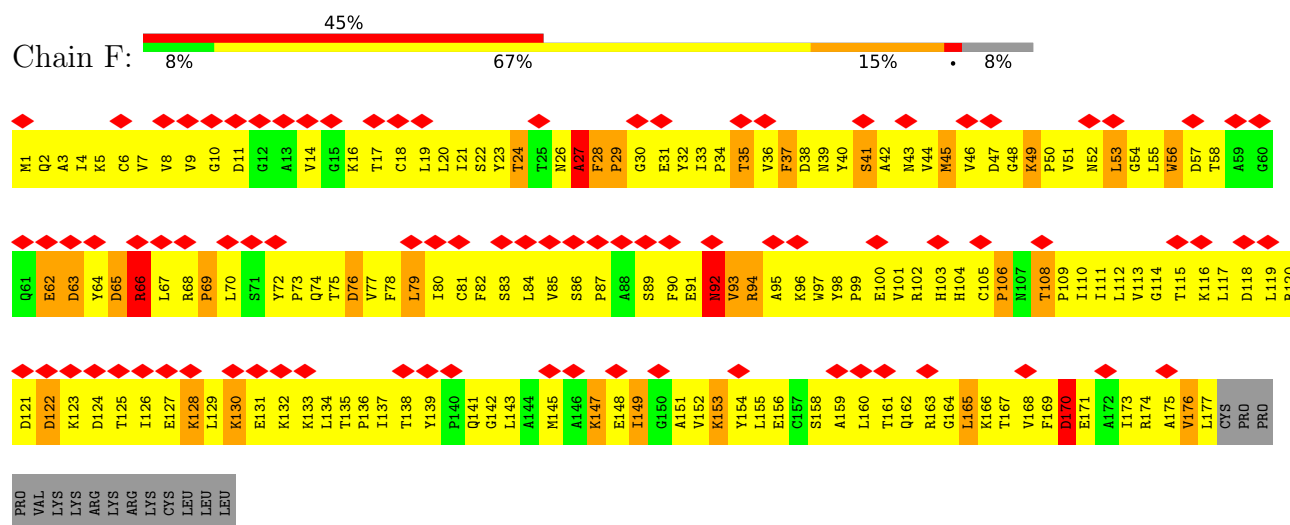




• Molecule 3: Ras-related C3 botulinum toxin substrate 1



• Molecule 3: Ras-related C3 botulinum toxin substrate 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	245763	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.174	Depositor
Minimum map value	-0.072	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.04	Depositor
Map size (Å)	403.25998, 403.25998, 403.25998	wwPDB
Map dimensions	282, 282, 282	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.43, 1.43, 1.43	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.97	28/8364 (0.3%)	1.08	52/11318 (0.5%)
1	D	0.97	27/8364 (0.3%)	1.08	52/11318 (0.5%)
2	B	0.27	0/5147	0.50	0/6959
2	E	0.56	6/5149 (0.1%)	0.76	15/6961 (0.2%)
3	C	0.80	2/1413 (0.1%)	1.12	9/1922 (0.5%)
3	F	0.80	2/1413 (0.1%)	1.12	9/1922 (0.5%)
All	All	0.81	65/29850 (0.2%)	0.95	137/40400 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	33
1	D	0	33
2	B	0	2
2	E	0	8
3	C	0	2
3	F	0	3
All	All	0	81

The worst 5 of 65 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1363	TYR	CD2-CE2	-10.37	1.23	1.39
1	D	1363	TYR	CD2-CE2	-10.32	1.23	1.39
1	A	1294	TRP	CB-CG	-10.23	1.31	1.50
1	D	1294	TRP	CB-CG	-10.18	1.31	1.50
2	E	661	GLU	CB-CG	-8.07	1.36	1.52

The worst 5 of 137 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1300	LEU	CA-CB-CG	-15.88	78.78	115.30
1	D	1300	LEU	CA-CB-CG	-15.88	78.78	115.30
1	D	1521	THR	C-N-CA	12.32	152.51	121.70
1	A	1521	THR	C-N-CA	12.32	152.49	121.70
2	E	699	LEU	CA-CB-CG	-11.82	88.12	115.30

There are no chirality outliers.

5 of 81 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	132	LEU	Peptide
1	A	276	UNK	Peptide
1	A	341	UNK	Peptide
1	A	418	MET	Peptide
1	A	66	ILE	Peptide

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	10203	0	8220	2225	0
1	D	10203	0	8220	2247	0
2	B	5054	0	4721	255	0
2	E	5056	0	4724	670	0
3	C	1383	0	1405	443	0
3	F	1383	0	1405	416	0
All	All	33282	0	28695	5998	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 97.

The worst 5 of 5998 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:1441:ARG:HA	1:D:1469:PHE:O	1.25	1.31
2:E:641:ALA:HA	2:E:654:PHE:O	1.33	1.25

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1441:ARG:HA	1:A:1469:PHE:O	1.25	1.24
1:D:1585:LYS:O	1:D:1588:GLU:HB3	1.36	1.20
1:D:1346:GLY:O	1:D:1406:ILE:HA	1.39	1.20

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1029/1830 (56%)	689 (67%)	312 (30%)	28 (3%)	5	33
1	D	1029/1830 (56%)	689 (67%)	312 (30%)	28 (3%)	5	33
2	B	672/727 (92%)	641 (95%)	29 (4%)	2 (0%)	41	75
2	E	672/727 (92%)	593 (88%)	75 (11%)	4 (1%)	25	63
3	C	175/192 (91%)	121 (69%)	49 (28%)	5 (3%)	4	32
3	F	175/192 (91%)	121 (69%)	49 (28%)	5 (3%)	4	32
All	All	3752/5498 (68%)	2854 (76%)	826 (22%)	72 (2%)	11	39

5 of 72 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	180	VAL
1	A	414	PRO
1	A	1196	SER
1	A	1238	THR
1	A	1428	ASP

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	829/1180 (70%)	635 (77%)	194 (23%)	1	5
1	D	829/1180 (70%)	635 (77%)	194 (23%)	1	5
2	B	497/662 (75%)	493 (99%)	4 (1%)	81	88
2	E	498/662 (75%)	486 (98%)	12 (2%)	49	69
3	C	153/168 (91%)	130 (85%)	23 (15%)	3	17
3	F	153/168 (91%)	130 (85%)	23 (15%)	3	17
All	All	2959/4020 (74%)	2509 (85%)	450 (15%)	6	16

5 of 450 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	56	GLN
3	F	122	ASP
1	D	508	ARG
3	F	86	SER
1	D	1466	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	1199	ASN
2	E	240	GLN
1	D	1275	GLN
1	D	1568	HIS
2	E	303	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	7
1	D	7

The worst 5 of 14 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	389:UNK	C	412:GLY	N	30.55
1	D	389:UNK	C	412:GLY	N	30.55
1	A	351:UNK	C	377:UNK	N	20.14
1	D	351:UNK	C	377:UNK	N	20.14
1	A	892:UNK	C	896:UNK	N	9.23

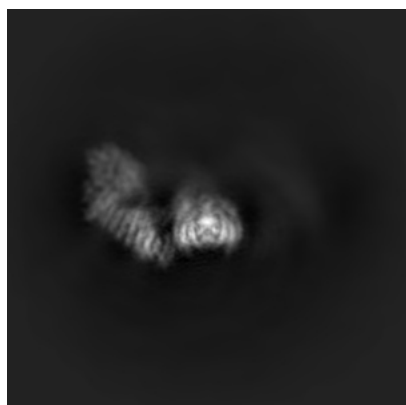
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10498. These allow visual inspection of the internal detail of the map and identification of artifacts.

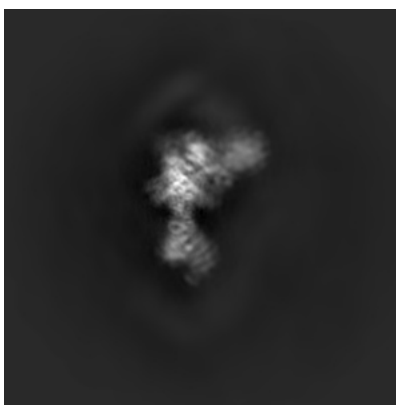
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

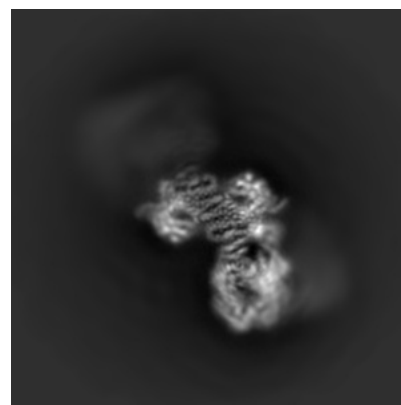
6.1.1 Primary map



X



Y

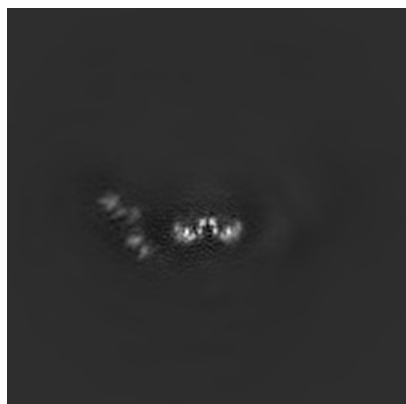


Z

The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

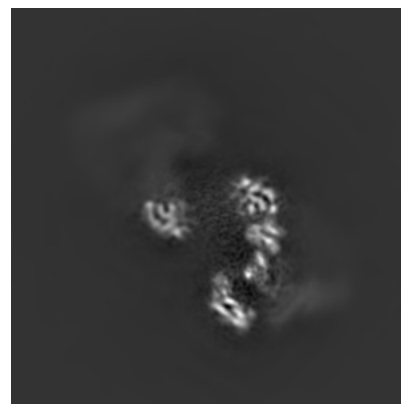
6.2.1 Primary map



X Index: 141



Y Index: 141



Z Index: 141

The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

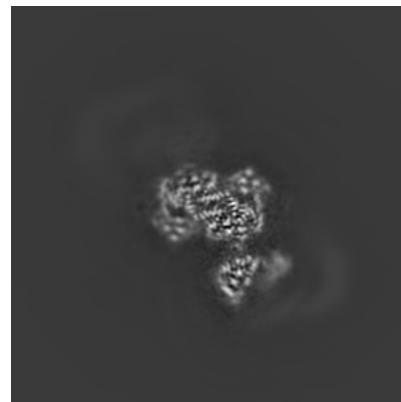
6.3.1 Primary map



X Index: 156



Y Index: 124



Z Index: 124

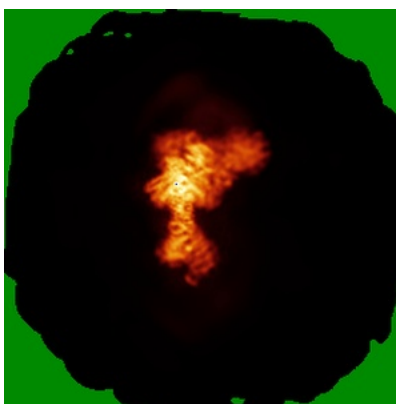
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

6.4.1 Primary map



X



Y

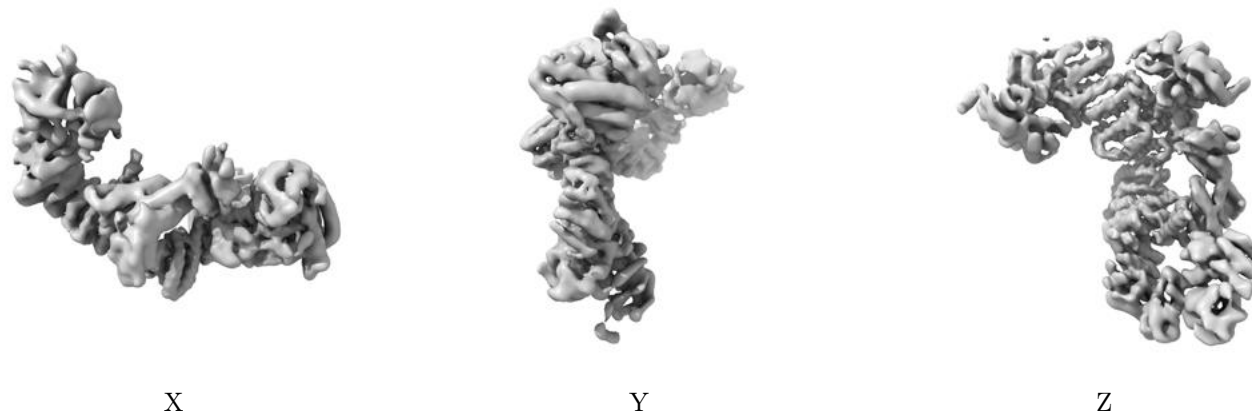


Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.04. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

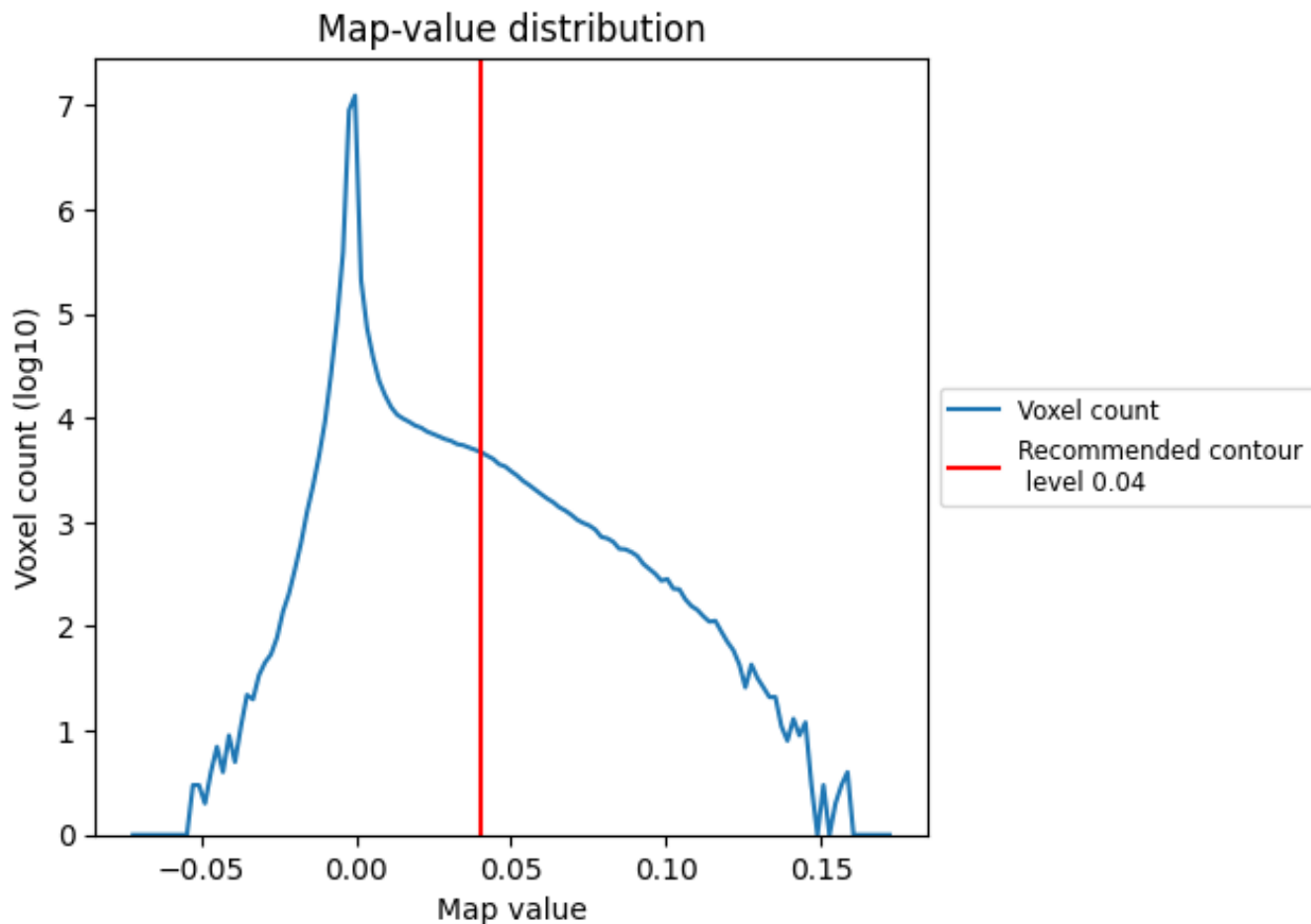
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

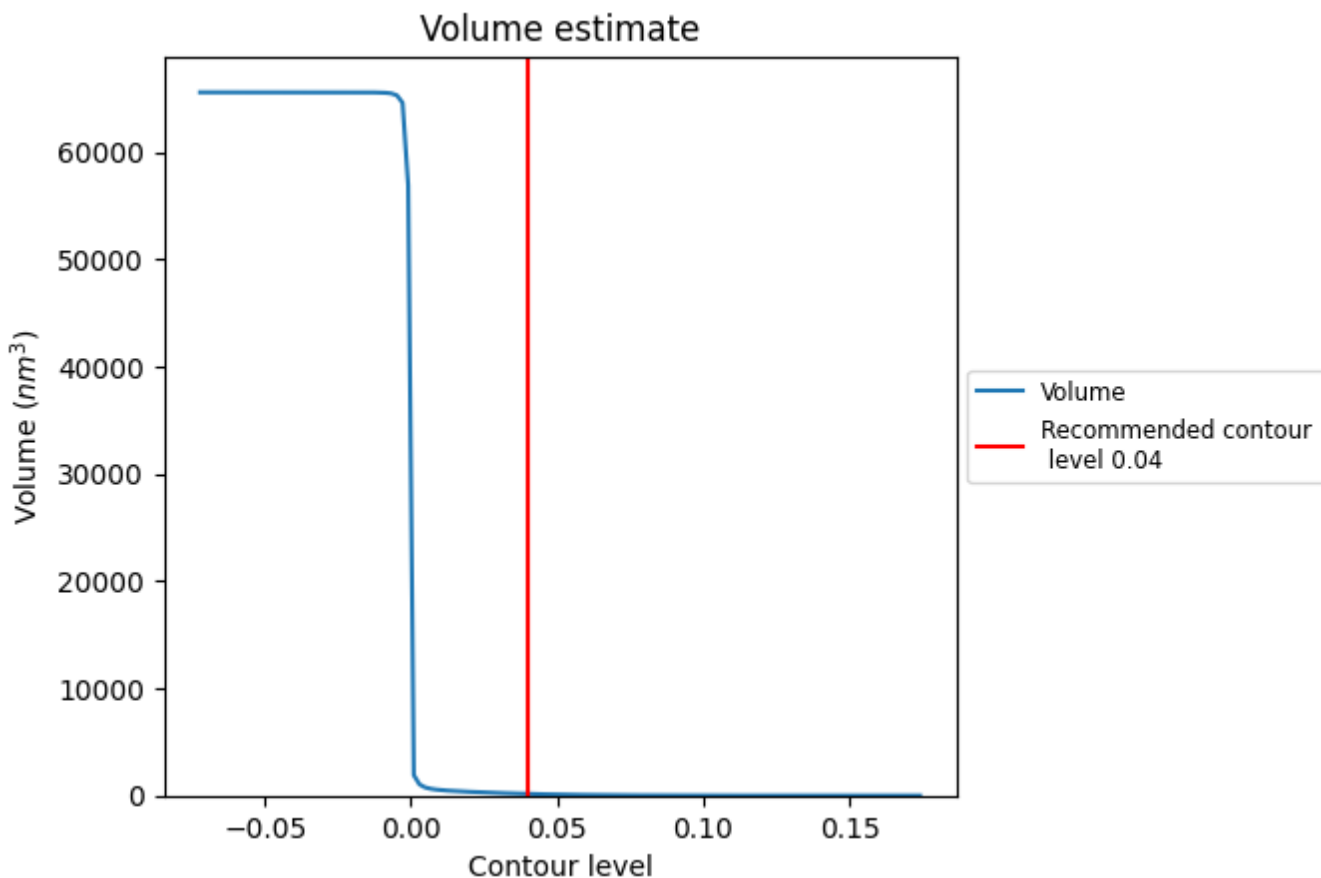
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

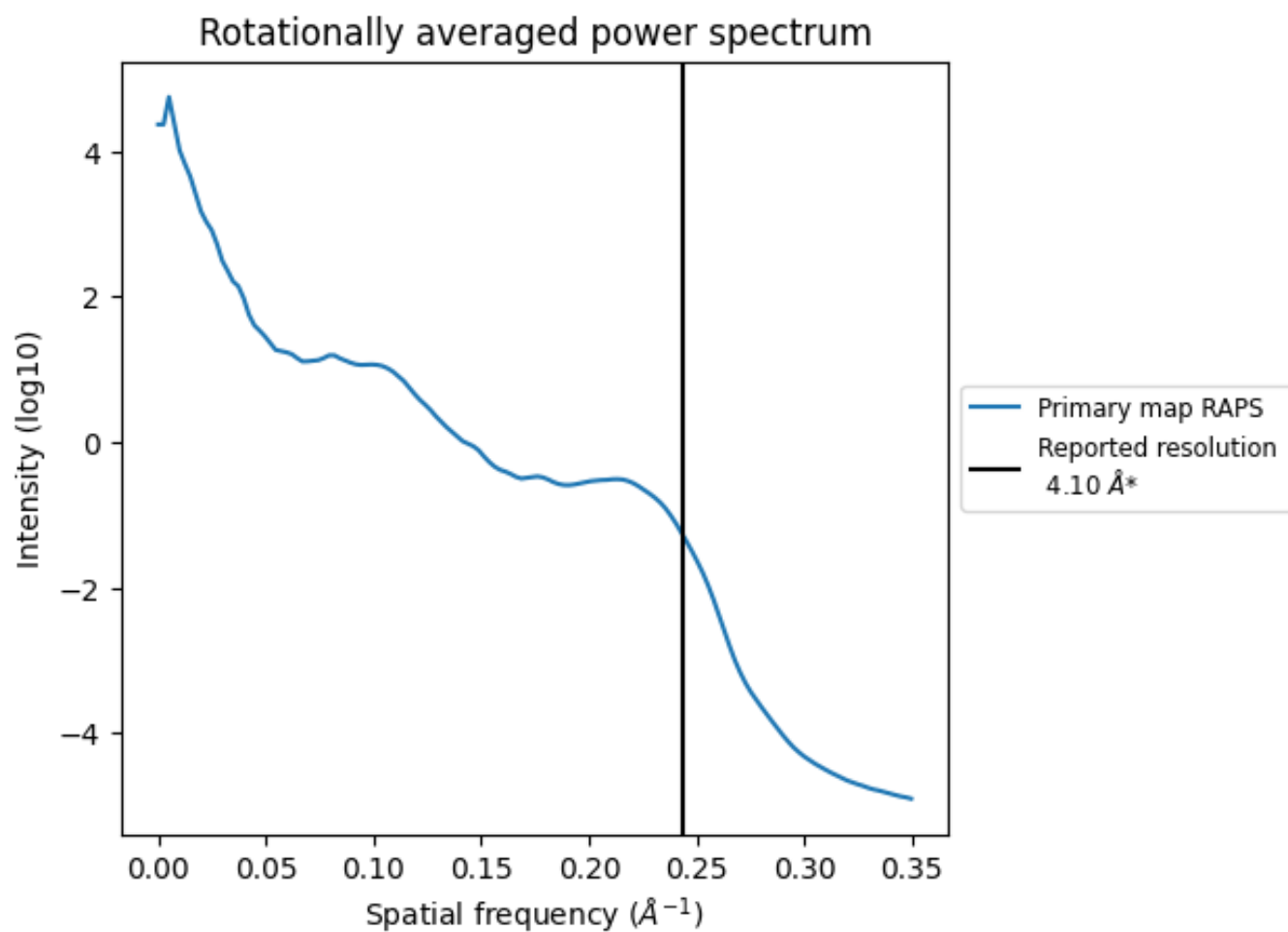
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 158 nm³; this corresponds to an approximate mass of 143 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.244\AA^{-1}

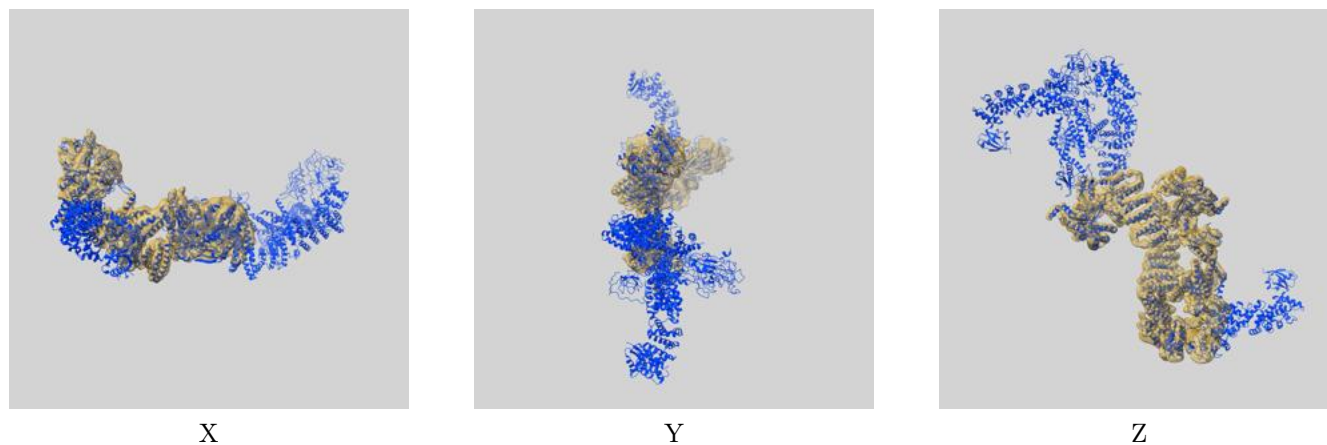
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

9 Map-model fit [i](#)

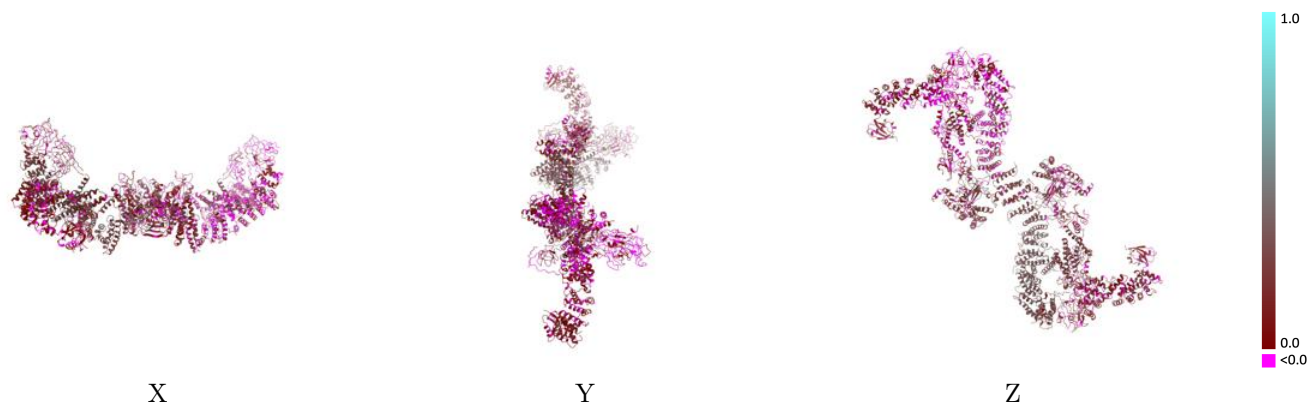
This section contains information regarding the fit between EMDB map EMD-10498 and PDB model 6TGC. Per-residue inclusion information can be found in section [3](#) on page [29](#).

9.1 Map-model overlay [i](#)



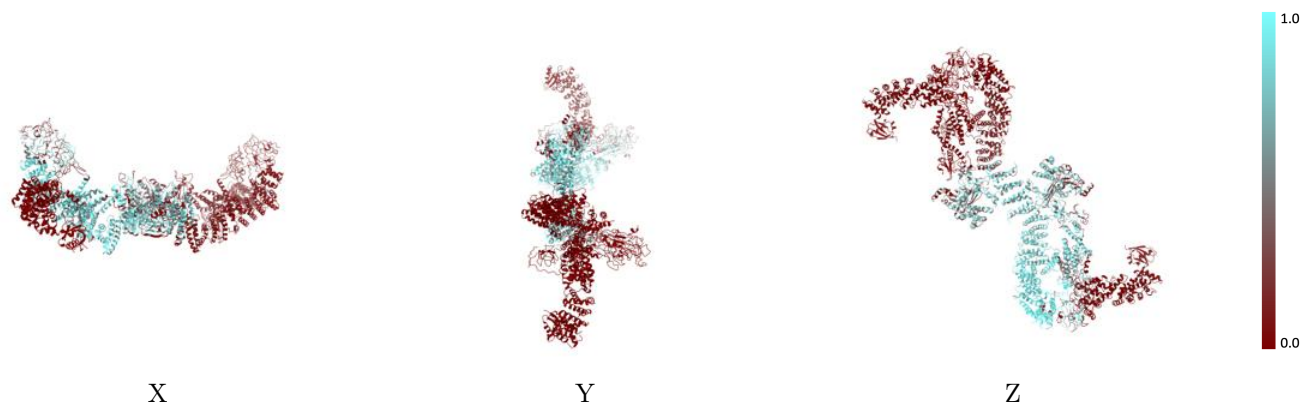
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [\(i\)](#)



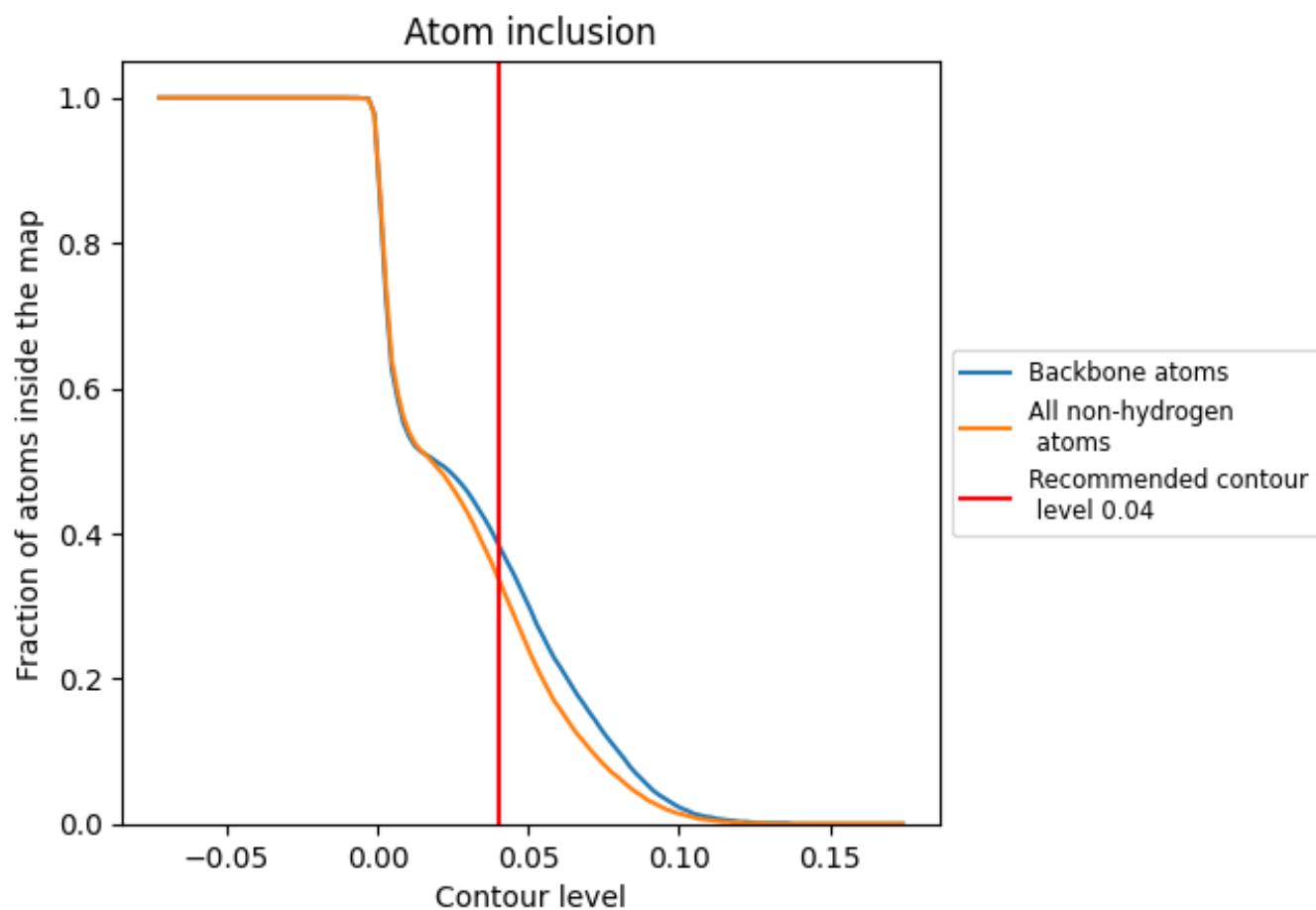
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [\(i\)](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.04).















9.4 Atom inclusion [i](#)



At the recommended contour level, 39% of all backbone atoms, 34% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3390	 0.1290
A	 0.2110	 0.0740
B	 0.0010	 0.0570
C	 0.4220	 0.1730
D	 0.6980	 0.2220
E	 0.1610	 0.1160
F	 0.4460	 0.1180

