



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 01:14 PM UTC

PDB ID : 8WUI / pdb_00008wui
EMDB ID : EMD-37855
Title : SKOR D312N L271P double mutation
Authors : Gao, X.; Sun, T.; Lu, Y.; Jia, Y.; Xu, X.; Zhang, Y.; Fu, P.; Yang, G.
Deposited on : 2023-10-20
Resolution : 3.40 Å(reported)

This is a Full wwPDB EM Validation 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

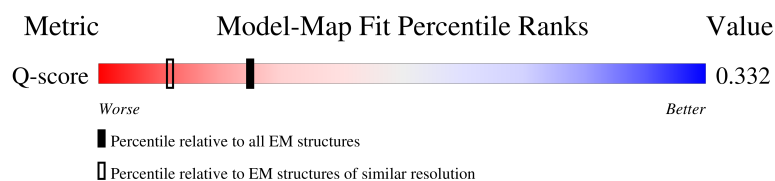
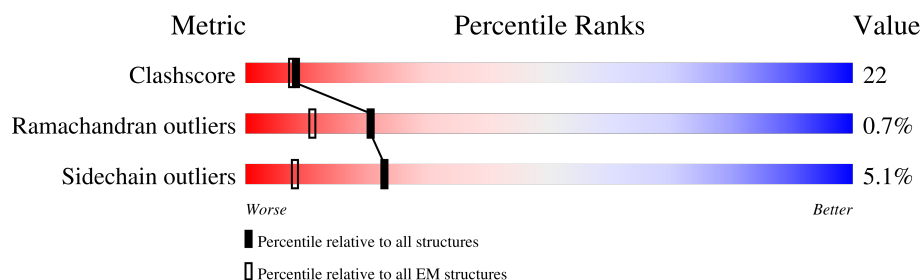
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14717 (2.90 - 3.90)

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	838	26% 34% 19% 45%
1	B	838	27% 34% 19% 46%
1	C	838	27% 34% 19% 45%
1	D	838	27% 33% 19% 46%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15340 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 Potassium channel SKOR.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	449	Total	C	N	O	S	0	0
			3706	2432	612	639	23		
1	A	464	Total	C	N	O	S	0	0
			3832	2510	637	662	23		
1	D	449	Total	C	N	O	S	0	0
			3706	2432	612	639	23		
1	C	464	Total	C	N	O	S	0	0
			3832	2510	637	662	23		

There are 48 discrepancies between the modelled and reference sequences:

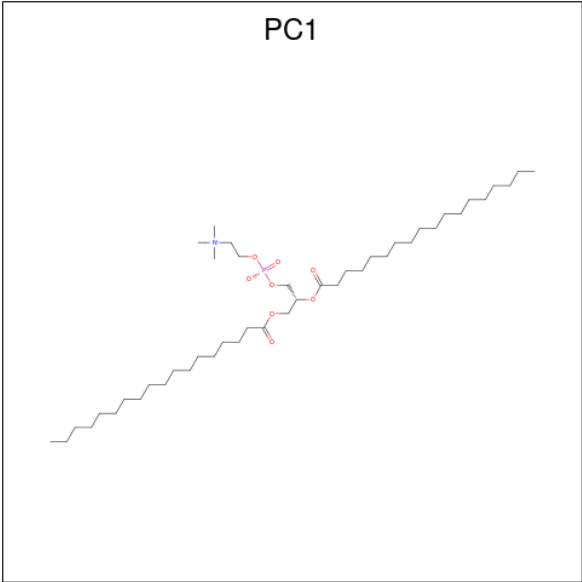
Chain	Residue	Modelled	Actual	Comment	Reference
B	-9	MET	-	initiating methionine	UNP Q9M8S6
B	-8	ASP	-	expression tag	UNP Q9M8S6
B	-7	TYR	-	expression tag	UNP Q9M8S6
B	-6	LYS	-	expression tag	UNP Q9M8S6
B	-5	ASP	-	expression tag	UNP Q9M8S6
B	-4	ASP	-	expression tag	UNP Q9M8S6
B	-3	ASP	-	expression tag	UNP Q9M8S6
B	-2	ASP	-	expression tag	UNP Q9M8S6
B	-1	LYS	-	expression tag	UNP Q9M8S6
B	0	HIS	-	expression tag	UNP Q9M8S6
B	271	PRO	LEU	engineered mutation	UNP Q9M8S6
B	312	ASN	ASP	engineered mutation	UNP Q9M8S6
A	-9	MET	-	initiating methionine	UNP Q9M8S6
A	-8	ASP	-	expression tag	UNP Q9M8S6
A	-7	TYR	-	expression tag	UNP Q9M8S6
A	-6	LYS	-	expression tag	UNP Q9M8S6
A	-5	ASP	-	expression tag	UNP Q9M8S6
A	-4	ASP	-	expression tag	UNP Q9M8S6
A	-3	ASP	-	expression tag	UNP Q9M8S6
A	-2	ASP	-	expression tag	UNP Q9M8S6
A	-1	LYS	-	expression tag	UNP Q9M8S6
A	0	HIS	-	expression tag	UNP Q9M8S6

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Chain	Residue	Modelled	Actual	Comment	Reference
A	271	PRO	LEU	engineered mutation	UNP Q9M8S6
A	312	ASN	ASP	engineered mutation	UNP Q9M8S6
D	-9	MET	-	initiating methionine	UNP Q9M8S6
D	-8	ASP	-	expression tag	UNP Q9M8S6
D	-7	TYR	-	expression tag	UNP Q9M8S6
D	-6	LYS	-	expression tag	UNP Q9M8S6
D	-5	ASP	-	expression tag	UNP Q9M8S6
D	-4	ASP	-	expression tag	UNP Q9M8S6
D	-3	ASP	-	expression tag	UNP Q9M8S6
D	-2	ASP	-	expression tag	UNP Q9M8S6
D	-1	LYS	-	expression tag	UNP Q9M8S6
D	0	HIS	-	expression tag	UNP Q9M8S6
D	271	PRO	LEU	engineered mutation	UNP Q9M8S6
D	312	ASN	ASP	engineered mutation	UNP Q9M8S6
C	-9	MET	-	initiating methionine	UNP Q9M8S6
C	-8	ASP	-	expression tag	UNP Q9M8S6
C	-7	TYR	-	expression tag	UNP Q9M8S6
C	-6	LYS	-	expression tag	UNP Q9M8S6
C	-5	ASP	-	expression tag	UNP Q9M8S6
C	-4	ASP	-	expression tag	UNP Q9M8S6
C	-3	ASP	-	expression tag	UNP Q9M8S6
C	-2	ASP	-	expression tag	UNP Q9M8S6
C	-1	LYS	-	expression tag	UNP Q9M8S6
C	0	HIS	-	expression tag	UNP Q9M8S6
C	271	PRO	LEU	engineered mutation	UNP Q9M8S6
C	312	ASN	ASP	engineered mutation	UNP Q9M8S6

- Molecule 2 is 1,2-DIACYL-SN-GLYCERO-3-PHOSPHOCHOLINE (CCD ID: PC1) (formula: C₄₄H₈₈NO₈P).

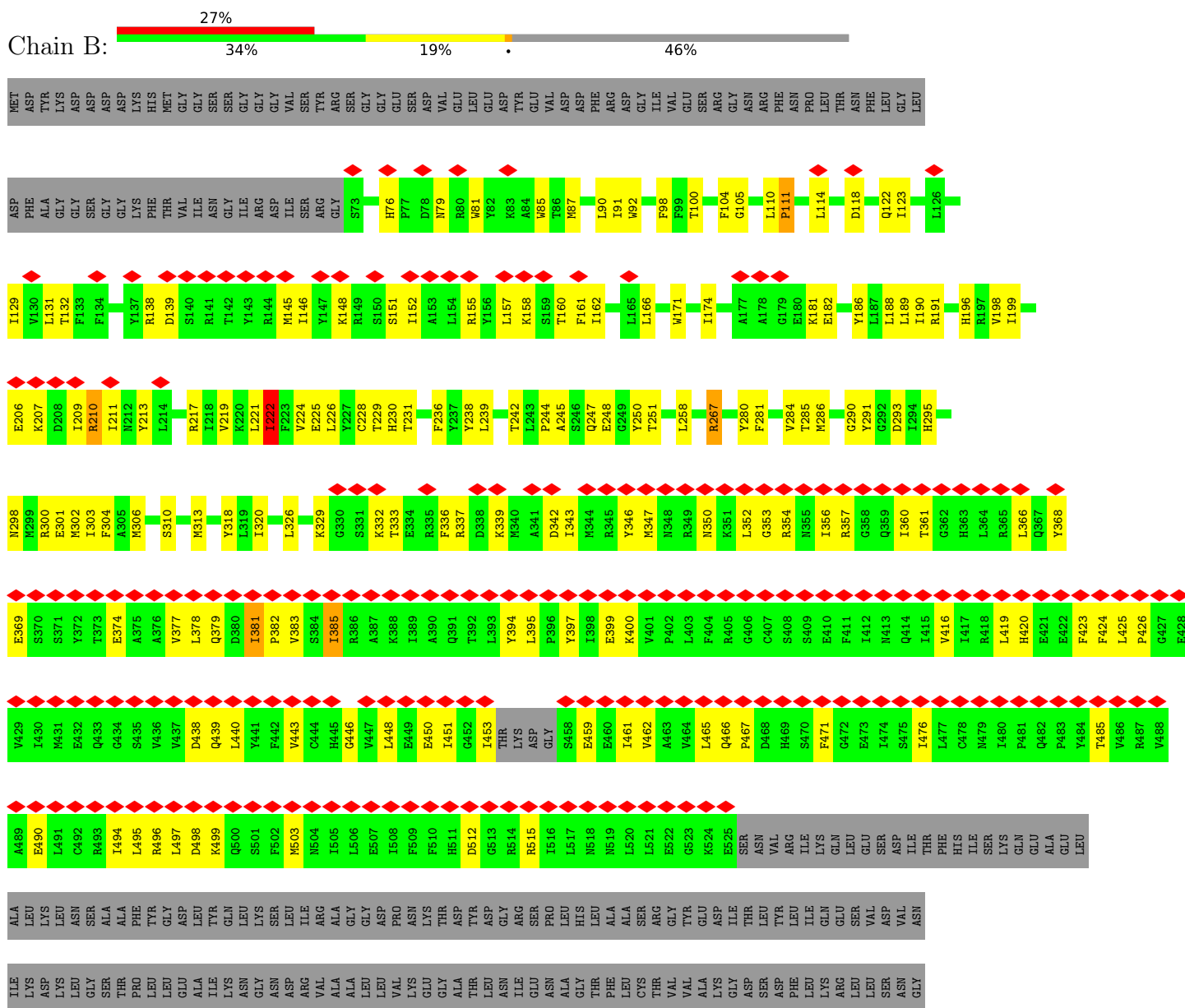


Mol	Chain	Residues	Atoms				AltConf
2	B	1	Total	C			0
			17	17			
2	B	1	Total	C			0
			17	17			
2	B	1	Total	C			0
			17	17			
2	A	1	Total	C			0
			17	17			
2	A	1	Total	C			0
			17	17			
2	A	1	Total	C	O	P	0
			30	21	8	1	
2	A	1	Total	C			0
			17	17			
2	D	1	Total	C			0
			17	17			
2	D	1	Total	C			0
			17	17			
2	D	1	Total	C			0
			17	17			
2	C	1	Total	C	O	P	0
			30	21	8	1	
2	C	1	Total	C			0
			17	17			
2	C	1	Total	C			0
			17	17			
2	C	1	Total	C			0
			17	17			

3 Residue-property plots

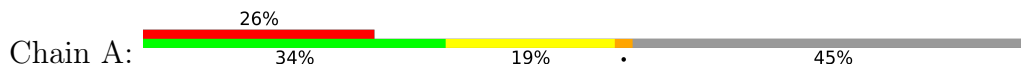
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Potassium channel SKOR



THR	ALA	LYS	GLU	GLN	LEU	ASN	VAL	PRO	GLU	ALA	SER	CYS	VAL	LEU	SER	GLU	ASP	GLU	ALA	LYS	ILE	ILE	ASP	VAL	ASP	LEU	ILE	SER	ASP	GLY	GLN	LYS	LEU	TYR	LEU	ALA	VAL	GLU	THR
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- Molecule 1: Potassium channel SKOR



NET	ASP	TYR	LYS	ASP	ASP	ASP	ASP	HIS	MET	GLY	GLY	SER	SER	GLY	GLY	VAL	SER	TYR	ARG	SER	GLY	GLY	GLU	GLU	LEU	GLU	ASP	ASP	PHE	ARG	ASP	GLY	ILE	VAL	GLU	SER	SER	ASN	PRO	LEU	THR	LEU	GLY	LEU
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ASP	PHE	ALA	GLY	GLY	SER	GLY	GLY	LYS	PHE	THR	VAL	ILE	ASN	GLY	ILE	ARG	ASP	ILE	SER	ARG	GLY	S73	P77	R60	W92	A93	S97	F98	F99	F104	G105	F106	F107	P111	A120	G121	I122	I123	A124	F125	L126	I129	L130	L131	T132	F133	A136	F137	R138	N140
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S140	R141	T142	R144	M145	T146	T147	R148	R149	S150	S151	T152	A153	L154	R155	T156	L157	F161	L165	L166	A167	W171	D172	T173	I174	L187	L188	L189	T190	R191	R194	L200	M205	E206	T209	R210	T211	N212	T216	L221	V224	E225	F236	L256	R257	T258
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G259	G260	G261	G271	G272	G273	G274	G279	G280	G281	G282	G283	G284	G285	G293	G294	G303	G304	G305	G306	G313	G320	G324	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	L352	G353	G354	G355	G356	G357
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Q358	Q359	Q360	Q361	Q362	Q363	Q364	Q365	Q366	Q367	Q368	Q369	Q370	Q371	Q372	Q373	Q374	Q375	Q376	Q377	Q378	Q379	Q380	Q381	Q382	Q383	Q384	Q385	Q386	Q387	Q388	Q389	Q390	Q391	Q392	Q393	Q394	Q395	Q396	Q397	Q398	Q399	Q400	Q401	Q402	Q403	Q404	Q405	Q406	Q407	Q408	Q409	Q410	Q411	Q412	Q413	Q414	Q415	Q416
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R418	L419	H420	E421	E422	F423	F424	L425	P426	G427	E428	V429	I430	M431	E432	G433	G434	S435	V436	V437	D438	Q439	L440	L441	F442	V443	C444	H445	G446	V447	L448	E449	E450	I451	G452	I453	THR	LYS	ASP	GLY	GLY	SER	GLU	GLU	I455	V462	A463	V464	L465	Q466	P467	D468	H469	S470	F471	G472	E473	I474	S475	I476	I477
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C478	M479	I480	P481	Q482	P483	I484	T485	V486	R487	V488	A489	E490	L491	C492	R493	I494	L495	R496	L497	D498	K499	Q500	S501	F502	M503	N504	I505	L506	E507	F508	F509	F510	H511	D512	G513	G514	R515	I516	L517	N518	M519	L520	L521	E522	G523	K524	K525	E526	N527	V528	R529	I530	K531	Q532	Q533	L534	E534	S535	D536	L537
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[illegible]

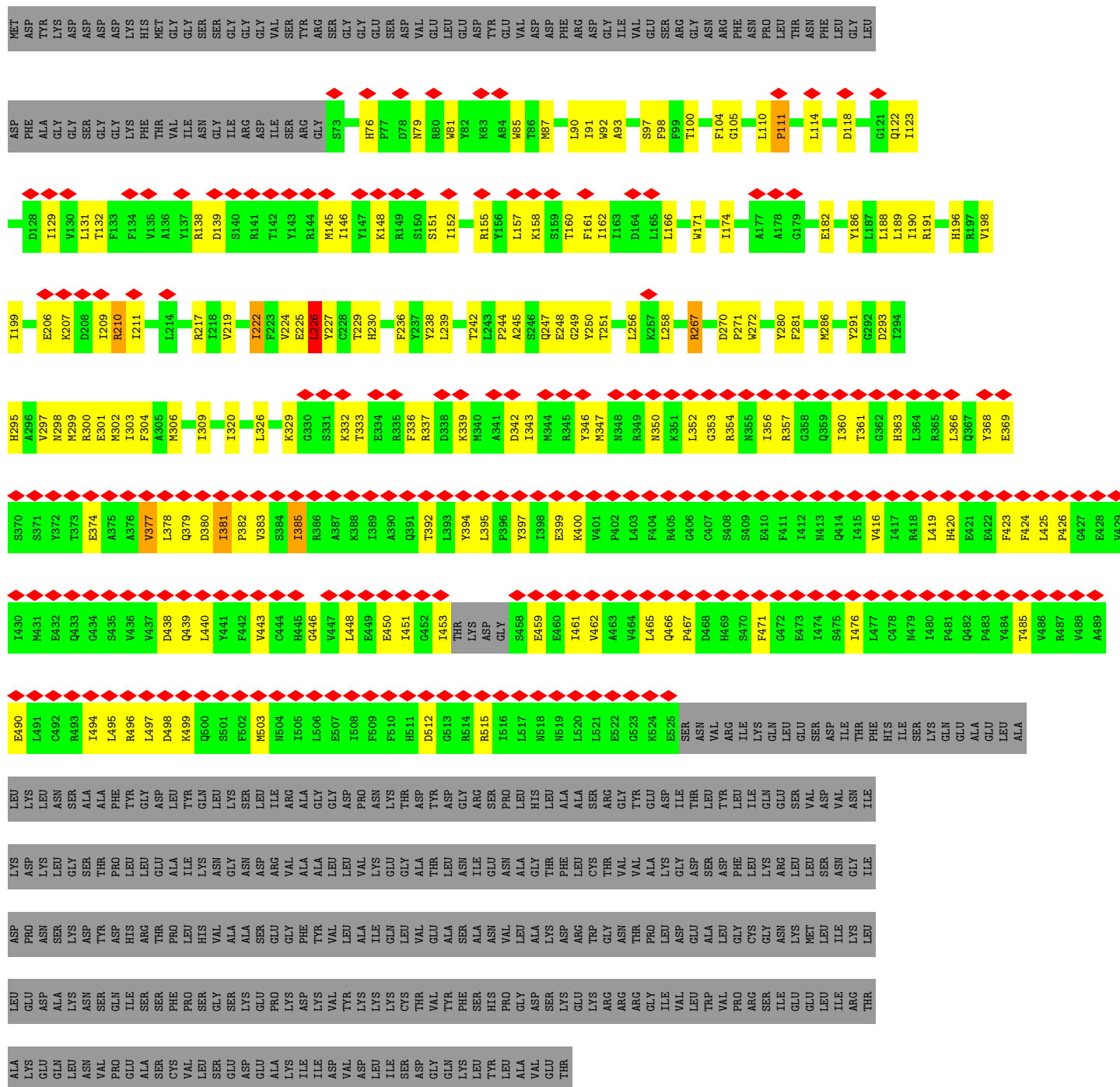
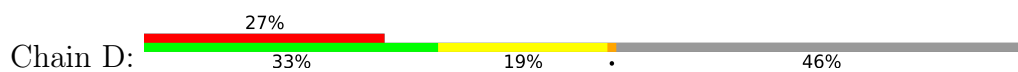
LEU TYR LEU LEU ILE GLN SER VAL ASP VAL ASN ILE LYS ASP LYS LEU LEU LEU LEU GLY THR PRO LEU LEU LEU GLU ALA ILE LYS ASN GLY GLY ASN ASP ARG VAL ALA ALA ALA LEU VAL LYS GLU GLY GLY ASN THR LEU LEU ASN ILE THR PHE LEU LEU CYS THR VAL VAL ALA ALA LYS GLY

SER	ASP	PHE	LEU	LYS	ARG	LEU	LEU	SER	ASN	GLY	ILE	ASP	PRO	ASN	SER	LYS	ASP	THR	PRO	LEU	HIS	VAL	ALA	ALA	SER	GLY	GLY	PHE	TYR	VAL	VAL	LEU	ALA	ALA	GLU	ALA	SER	ASN	VAL	LEU	LEU	GLN	ILE	GLN	THR	ASP	LYS	ALA	LEU	LEU	TRP	ARG	ASN	GLY	THR	PRO	PRO	LEU	LEU	ASP	ASP	GLN
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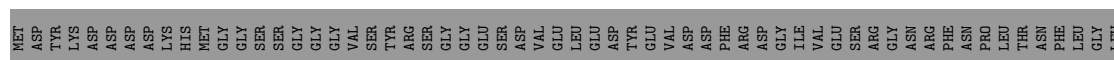
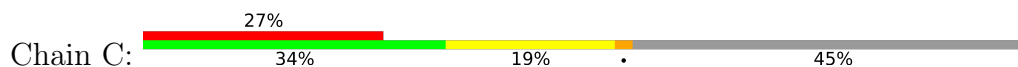
ALA LEU GLY CYS ASN LYS MET LEU ILE LYS LEU LEU ASP ASP ALA LYS ASN SER GLN ILE SER SER PHE PRO SER GLY LYS GLU PRO LYS ASP LYS LYS VAL TYR LYS LYS LYS LYS THR TYR PHE SER HIS PRO GLY ASP SER LYS GLU LYS ARG ARG ARG GLY ILE VAL LEU

TRP	VAL	PRO	ARG	SER	ILE	GLU	GLU	LEU	ILE	ARG	THR	ALA	LYS	GLU	GLN	LEU	ASN	VAL	PRO	GLU	ALA	CYS	VAL	LEU	SER	GLU	ASP	GLU	ALA	LYS	ILE	ILE	ASP	VAL	ASP	LEU	ILE	SER	ASP	GLY	GLN	LYS	LEU	TYR	LEU	LEU	ALA	VAL	GLU	THR
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- Molecule 1: Potassium channel SKOR



• Molecule 1: Potassium channel SKOR





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	97040	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)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.795	Depositor
Minimum map value	-1.079	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.184	Depositor
Map size (Å)	291.19998, 291.19998, 291.19998	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PC1

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	0.42	1/3925 (0.0%)	0.62	7/5307 (0.1%)
1	B	0.27	0/3797	0.45	1/5136 (0.0%)
1	C	0.42	1/3925 (0.0%)	0.62	6/5307 (0.1%)
1	D	0.26	0/3797	0.48	4/5136 (0.1%)
All	All	0.35	2/15444 (0.0%)	0.55	18/20886 (0.1%)

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	1
1	C	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	355	ASN	C-O	5.93	1.31	1.24
1	C	355	ASN	C-O	5.87	1.31	1.24

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	348	ASN	N-CA-C	-8.17	101.94	112.23
1	C	348	ASN	N-CA-C	-8.15	101.96	112.23
1	D	226	LEU	N-CA-C	-7.48	104.00	113.72
1	C	332	LYS	N-CA-C	-7.47	103.08	111.14
1	A	332	LYS	N-CA-C	-7.44	103.11	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	222	ILE	N-CA-C	-7.21	104.24	111.88
1	D	227	TYR	N-CA-C	-6.88	104.52	113.12
1	A	271	PRO	CA-N-CD	-6.41	103.03	112.00
1	C	271	PRO	CA-N-CD	-6.39	103.06	112.00
1	C	342	ASP	N-CA-C	-5.58	104.83	111.69
1	A	342	ASP	N-CA-C	-5.55	104.86	111.69
1	B	368	TYR	CB-CA-C	5.38	117.67	109.34
1	D	368	TYR	CB-CA-C	5.37	117.66	109.34
1	C	271	PRO	N-CD-CG	-5.31	95.23	103.20
1	A	271	PRO	N-CD-CG	-5.30	95.25	103.20
1	A	225	GLU	N-CA-C	-5.28	106.90	113.55
1	C	131	LEU	CA-CB-CG	5.12	134.21	116.30
1	A	131	LEU	CA-CB-CG	5.12	134.20	116.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	380	ASP	Mainchain
1	C	380	ASP	Mainchain

5.2 Too-close contacts

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	3832	0	3881	230	0
1	B	3706	0	3754	189	0
1	C	3832	0	3881	210	0
1	D	3706	0	3754	195	0
2	A	81	0	123	34	0
2	B	51	0	90	24	0
2	C	81	0	123	36	0
2	D	51	0	90	20	0
All	All	15340	0	15696	672	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 22.

All (672) 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:B:304:PHE:CD1	2:B:901:PC1:H2E1	1.15	1.66
1:C:272:TRP:HD1	2:C:902:PC1:C21	1.00	1.65
1:C:107:PHE:CE1	2:C:901:PC1:H11	1.16	1.62
1:A:346:TYR:CE2	1:D:378:LEU:HD22	1.33	1.57
1:C:107:PHE:CZ	2:C:901:PC1:H11	1.38	1.55
1:C:107:PHE:CE1	2:C:901:PC1:C1	1.89	1.53
1:A:364:LEU:CD2	1:D:382:PRO:HD3	1.38	1.51
1:C:272:TRP:CD1	2:C:902:PC1:C21	1.93	1.49
1:A:364:LEU:CD2	1:D:382:PRO:CD	1.92	1.48
1:A:346:TYR:CD2	1:D:378:LEU:HD13	1.47	1.46
1:B:304:PHE:CD1	2:B:901:PC1:C2E	2.02	1.42
1:A:189:LEU:CD1	2:A:902:PC1:H2D1	1.48	1.40
1:A:106:PHE:CD2	2:A:903:PC1:O22	1.75	1.38
1:B:304:PHE:HD1	2:B:901:PC1:C2E	1.35	1.37
1:A:107:PHE:CZ	2:A:903:PC1:H32	1.64	1.31
1:B:382:PRO:HD3	1:C:364:LEU:CD2	1.58	1.31
1:A:346:TYR:CE2	1:D:378:LEU:CD2	2.14	1.28
1:D:304:PHE:CD1	2:D:902:PC1:H2G1	1.69	1.24
1:B:209:ILE:HG21	1:C:344:MET:CE	1.69	1.21
1:B:378:LEU:HD13	1:C:346:TYR:CD2	1.74	1.20
1:A:364:LEU:CD2	1:D:382:PRO:CG	2.23	1.18
1:B:378:LEU:HD22	1:C:346:TYR:CE2	1.77	1.17
1:A:364:LEU:CG	1:D:382:PRO:HD3	1.74	1.17
1:D:189:LEU:CD1	2:D:903:PC1:C2H	2.21	1.16
1:A:346:TYR:CZ	1:D:378:LEU:HD22	1.79	1.16
1:A:189:LEU:CD1	2:A:902:PC1:C2D	2.24	1.14
1:A:364:LEU:HD21	1:D:382:PRO:CD	1.65	1.13
1:B:304:PHE:HE1	2:B:901:PC1:H2F2	1.09	1.12
1:B:382:PRO:CD	1:C:364:LEU:CD2	2.25	1.12
1:B:382:PRO:HD3	1:C:364:LEU:HD21	1.15	1.12
1:A:364:LEU:HD23	1:D:382:PRO:CD	1.68	1.12
1:D:304:PHE:CE1	2:D:902:PC1:H2G1	1.84	1.10
1:B:209:ILE:CG2	1:C:344:MET:HE3	1.82	1.10
1:A:346:TYR:HE2	1:D:378:LEU:CD2	1.59	1.10
1:D:189:LEU:HD13	2:D:903:PC1:C2H	1.82	1.09
1:A:106:PHE:CE2	2:A:903:PC1:O22	2.06	1.08
1:B:209:ILE:HG21	1:C:344:MET:HE2	1.35	1.08
1:B:304:PHE:CE1	2:B:901:PC1:C2E	2.39	1.05
1:A:364:LEU:HD21	1:D:382:PRO:CG	1.85	1.05
1:A:346:TYR:CD2	1:D:378:LEU:CD1	2.39	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:378:LEU:HD13	1:C:346:TYR:CE2	1.93	1.04
1:A:107:PHE:CE1	2:A:903:PC1:H2	1.93	1.03
1:A:189:LEU:HD11	2:A:902:PC1:H2D1	1.07	1.02
1:B:304:PHE:CE1	2:B:901:PC1:H2E1	1.93	1.02
1:B:209:ILE:HG21	1:C:344:MET:HE3	1.41	1.01
1:B:382:PRO:CD	1:C:364:LEU:HD21	1.90	1.01
1:A:364:LEU:HD23	1:D:382:PRO:CG	1.87	1.01
1:A:364:LEU:HD21	1:D:382:PRO:HD3	1.11	1.01
1:C:107:PHE:CE1	2:C:901:PC1:H12	1.94	1.01
1:A:107:PHE:HZ	2:A:903:PC1:C3	1.73	1.00
1:A:346:TYR:HE2	1:D:378:LEU:CG	1.73	1.00
1:B:304:PHE:HE1	2:B:901:PC1:C2F	1.74	1.00
1:A:189:LEU:HD13	2:A:902:PC1:H2F2	1.42	0.99
1:B:304:PHE:CE1	2:B:901:PC1:C2F	2.46	0.99
1:A:189:LEU:HD13	2:A:902:PC1:C2F	1.93	0.98
1:B:304:PHE:CE1	2:B:901:PC1:H2F2	2.00	0.97
1:A:346:TYR:CE2	1:D:378:LEU:HD13	1.99	0.96
1:A:189:LEU:HD12	2:A:902:PC1:C2D	1.95	0.96
1:B:382:PRO:CD	1:C:364:LEU:HD23	1.93	0.96
1:B:329:LYS:HZ3	1:C:334:GLU:HB3	1.28	0.95
1:B:209:ILE:CG2	1:C:344:MET:CE	2.42	0.94
1:A:334:GLU:HG2	1:D:329:LYS:HZ2	1.33	0.93
1:D:304:PHE:HD1	2:D:902:PC1:H2G1	1.27	0.92
1:A:107:PHE:CZ	2:A:903:PC1:C3	2.49	0.92
1:A:107:PHE:HZ	2:A:903:PC1:H32	0.79	0.92
1:A:334:GLU:CG	1:D:329:LYS:HZ2	1.82	0.92
1:A:346:TYR:CE2	1:D:378:LEU:CG	2.51	0.92
1:C:107:PHE:CZ	2:C:901:PC1:C1	2.32	0.92
1:B:378:LEU:HD13	1:C:346:TYR:HD2	1.33	0.91
1:D:304:PHE:CD1	2:D:902:PC1:C2G	2.53	0.91
1:B:329:LYS:HZ3	1:C:334:GLU:CB	1.84	0.90
2:B:901:PC1:H2A1	2:B:902:PC1:H2C2	1.52	0.90
1:A:304:PHE:HE1	2:A:901:PC1:H2D1	1.35	0.90
1:D:304:PHE:CE1	2:D:902:PC1:C2G	2.54	0.90
1:A:346:TYR:HE2	1:D:378:LEU:HD22	1.10	0.89
1:B:329:LYS:NZ	1:C:334:GLU:CB	2.35	0.88
1:A:364:LEU:HG	1:D:381:ILE:HA	1.56	0.87
1:B:378:LEU:CD2	1:C:346:TYR:CE2	2.56	0.87
1:A:304:PHE:CE1	2:A:901:PC1:H2D1	2.10	0.87
1:B:378:LEU:HD22	1:C:346:TYR:CZ	2.10	0.86
1:A:189:LEU:HD12	2:A:902:PC1:H2D1	1.51	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:LEU:HG	1:D:382:PRO:HD3	1.55	0.86
1:B:329:LYS:NZ	1:C:334:GLU:HB3	1.89	0.85
1:A:346:TYR:CE2	1:D:378:LEU:CD1	2.59	0.85
1:D:189:LEU:HD12	2:D:903:PC1:C2H	2.05	0.84
1:A:334:GLU:CG	1:D:329:LYS:NZ	2.40	0.84
1:B:378:LEU:HD22	1:C:346:TYR:HE2	1.38	0.84
1:C:107:PHE:HE1	2:C:901:PC1:C1	1.48	0.84
1:A:107:PHE:HE1	2:A:903:PC1:H2	1.43	0.83
1:A:346:TYR:HE2	1:D:378:LEU:CB	1.91	0.83
1:A:364:LEU:HD21	1:D:382:PRO:HG3	1.60	0.82
1:A:334:GLU:OE1	1:D:329:LYS:NZ	2.15	0.80
1:A:106:PHE:HD2	2:A:903:PC1:O22	1.55	0.79
1:A:364:LEU:HD23	1:D:382:PRO:HG2	1.62	0.79
1:A:364:LEU:HD23	1:D:382:PRO:HD2	1.65	0.79
1:B:229:THR:HG21	1:B:286:MET:HE2	1.63	0.78
1:B:378:LEU:CD1	1:C:346:TYR:CE2	2.67	0.78
1:A:189:LEU:HD12	2:A:902:PC1:H2D2	1.66	0.78
1:A:346:TYR:HD2	1:D:378:LEU:CD1	1.84	0.77
1:B:378:LEU:CD2	1:C:346:TYR:HE2	1.96	0.77
1:C:189:LEU:CD1	2:C:903:PC1:H2G1	2.14	0.77
1:A:344:MET:CE	1:D:209:ILE:HG21	2.15	0.77
1:A:346:TYR:CE2	1:D:378:LEU:HB2	2.20	0.76
1:B:329:LYS:NZ	1:C:334:GLU:CG	2.48	0.76
1:A:274:ARG:NH2	2:A:903:PC1:O14	2.18	0.76
1:B:378:LEU:CG	1:C:346:TYR:HE2	2.00	0.75
1:B:329:LYS:HZ3	1:C:334:GLU:CG	2.00	0.74
1:A:331:SER:HA	1:A:334:GLU:HB2	1.69	0.74
1:A:346:TYR:HE2	1:D:378:LEU:HB2	1.52	0.74
1:C:331:SER:HA	1:C:334:GLU:HB2	1.69	0.74
2:B:901:PC1:C2A	2:B:902:PC1:H2C2	2.17	0.74
1:C:107:PHE:HE1	2:C:901:PC1:H12	1.36	0.74
1:C:341:ALA:HA	1:C:344:MET:HB2	1.70	0.73
1:A:341:ALA:HA	1:A:344:MET:HB2	1.70	0.73
1:A:527:ASN:O	1:A:531:LYS:N	2.19	0.73
1:A:271:PRO:HB3	2:A:903:PC1:H12	1.71	0.72
1:A:345:ARG:NH1	1:D:374:GLU:HB3	2.03	0.72
1:B:306:MET:HG2	1:C:283:VAL:HB	1.71	0.72
1:A:259:GLY:HA3	1:D:297:VAL:HG11	1.71	0.72
1:B:382:PRO:HD3	1:C:364:LEU:CG	2.19	0.72
1:D:304:PHE:HD1	2:D:902:PC1:C2G	1.99	0.72
1:C:397:TYR:OH	1:C:493:ARG:NH2	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:334:GLU:CB	1:D:329:LYS:HZ2	2.04	0.71
1:A:334:GLU:HG2	1:D:329:LYS:NZ	2.05	0.71
1:C:189:LEU:HD12	2:C:903:PC1:H2G1	1.71	0.71
1:A:334:GLU:CB	1:D:329:LYS:NZ	2.54	0.71
1:C:107:PHE:HZ	2:C:901:PC1:H32	1.53	0.71
1:B:313:MET:HE3	1:C:319:LEU:HD22	1.74	0.70
1:A:397:TYR:OH	1:A:493:ARG:NH2	2.23	0.70
1:A:448:LEU:HB3	1:A:465:LEU:HB2	1.73	0.70
1:D:272:TRP:CE3	2:D:901:PC1:H221	2.27	0.70
1:D:304:PHE:HE1	2:D:902:PC1:C2G	2.02	0.70
1:B:382:PRO:CG	1:C:364:LEU:CD2	2.69	0.69
1:C:448:LEU:HB3	1:C:465:LEU:HB2	1.73	0.69
1:D:394:TYR:HB2	1:D:416:VAL:HG13	1.75	0.69
1:A:260:ASP:OD2	1:D:249:GLY:HA3	1.94	0.68
1:B:209:ILE:HG23	1:C:344:MET:HE3	1.76	0.68
1:B:336:PHE:HA	1:B:339:LYS:HG3	1.76	0.67
2:B:903:PC1:H2B1	1:A:306:MET:HB3	1.76	0.67
1:B:490:GLU:HB3	1:A:144:ARG:HE	1.59	0.67
1:B:394:TYR:HB2	1:B:416:VAL:HG13	1.75	0.67
1:A:344:MET:HE3	1:D:209:ILE:HG21	1.77	0.67
1:A:364:LEU:HG	1:D:382:PRO:CD	2.22	0.66
1:B:381:ILE:HA	1:C:364:LEU:HG	1.76	0.66
1:A:440:LEU:N	1:A:497:LEU:O	2.28	0.66
1:C:426:PRO:HG3	1:C:491:LEU:H	1.59	0.66
1:D:336:PHE:HA	1:D:339:LYS:HG3	1.76	0.66
1:A:426:PRO:HG3	1:A:491:LEU:H	1.59	0.66
1:D:490:GLU:HB3	1:C:144:ARG:HE	1.59	0.66
1:C:307:VAL:HG11	2:C:904:PC1:H2D1	1.78	0.66
1:C:440:LEU:N	1:C:497:LEU:O	2.28	0.66
1:A:346:TYR:HD2	1:D:378:LEU:HD13	0.89	0.66
1:C:527:ASN:O	1:C:531:LYS:N	2.19	0.65
1:B:476:ILE:HG12	1:B:499:LYS:HE2	1.78	0.65
1:D:226:LEU:HA	2:D:901:PC1:C2H	2.27	0.65
1:D:451:ILE:HG12	1:D:461:ILE:HG12	1.78	0.65
1:B:329:LYS:HZ3	1:C:334:GLU:HG2	1.61	0.65
1:D:272:TRP:HE3	2:D:901:PC1:H221	1.62	0.64
1:A:344:MET:HE3	1:D:209:ILE:CG2	2.27	0.64
1:B:453:ILE:HG12	1:B:459:GLU:HG2	1.78	0.64
1:D:453:ILE:HG12	1:D:459:GLU:HG2	1.78	0.64
1:A:189:LEU:CD1	2:A:902:PC1:C2F	2.74	0.64
1:B:378:LEU:HB2	1:C:346:TYR:HE2	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:148:LYS:HG2	1:D:151:SER:H	1.62	0.63
1:D:476:ILE:HG12	1:D:499:LYS:HE2	1.78	0.63
1:B:451:ILE:HG12	1:B:461:ILE:HG12	1.78	0.63
1:A:344:MET:HE2	1:D:209:ILE:HG21	1.79	0.63
1:A:526:SER:HB3	1:A:530:ILE:HD12	1.80	0.63
1:C:526:SER:HB3	1:C:530:ILE:HD12	1.80	0.63
1:A:107:PHE:CE1	2:A:903:PC1:C2	2.77	0.63
1:A:345:ARG:HH12	1:D:374:GLU:HB3	1.63	0.63
1:B:148:LYS:HG2	1:B:151:SER:H	1.63	0.63
1:B:378:LEU:CG	1:C:346:TYR:CE2	2.82	0.62
1:B:382:PRO:CG	1:C:364:LEU:HD21	2.28	0.62
1:A:450:GLU:O	1:A:462:VAL:N	2.32	0.62
1:C:450:GLU:O	1:C:462:VAL:N	2.32	0.62
1:C:383:VAL:HA	1:C:386:ARG:HE	1.65	0.62
1:C:419:LEU:HB3	1:C:495:LEU:HD22	1.82	0.62
1:A:205:MET:HE2	1:A:216:THR:HB	1.83	0.61
1:D:352:LEU:HB3	1:D:356:ILE:HD12	1.83	0.61
1:B:352:LEU:HB3	1:B:356:ILE:HD12	1.83	0.61
1:C:148:LYS:HZ2	1:C:150:SER:H	1.47	0.61
1:A:419:LEU:HB3	1:A:495:LEU:HD22	1.82	0.61
1:D:448:LEU:HB2	1:D:465:LEU:HB2	1.83	0.61
1:B:189:LEU:CD1	2:B:902:PC1:C2H	2.79	0.61
1:B:448:LEU:HB2	1:B:465:LEU:HB2	1.83	0.61
1:A:343:ILE:O	1:A:347:MET:HG2	2.01	0.61
1:A:356:ILE:HD11	1:D:392:THR:HG21	1.83	0.61
1:A:383:VAL:HA	1:A:386:ARG:HE	1.65	0.61
1:C:205:MET:HE2	1:C:216:THR:HB	1.83	0.61
1:A:107:PHE:CZ	2:A:903:PC1:C2	2.84	0.60
1:A:167:ALA:O	1:A:194:ARG:NH2	2.35	0.60
1:B:382:PRO:CG	1:C:364:LEU:HD23	2.30	0.60
1:A:345:ARG:NH2	1:D:374:GLU:CB	2.63	0.60
1:C:107:PHE:CE1	2:C:901:PC1:C2	2.81	0.60
1:C:189:LEU:CD1	2:C:903:PC1:C2G	2.79	0.60
1:C:343:ILE:O	1:C:347:MET:HG2	2.01	0.60
1:A:366:LEU:HB2	1:A:425:LEU:HD11	1.84	0.59
1:A:438:ASP:O	1:A:499:LYS:N	2.28	0.59
1:C:366:LEU:HB2	1:C:425:LEU:HD11	1.84	0.59
1:C:99:PHE:CD1	2:C:901:PC1:H342	2.38	0.59
1:C:167:ALA:O	1:C:194:ARG:NH2	2.35	0.59
1:C:307:VAL:CG1	2:C:904:PC1:H2D1	2.33	0.59
1:C:383:VAL:HG12	1:C:386:ARG:HH21	1.68	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:VAL:HB	1:D:306:MET:HG2	1.84	0.59
1:D:258:LEU:HD11	1:D:293:ASP:HB3	1.85	0.59
1:B:352:LEU:HB2	1:B:357:ARG:HH12	1.67	0.59
1:A:334:GLU:CD	1:D:329:LYS:NZ	2.61	0.59
1:A:418:ARG:NH2	1:A:501:SER:O	2.36	0.59
1:D:352:LEU:HB2	1:D:357:ARG:HH12	1.67	0.59
1:D:366:LEU:HD21	1:D:423:PHE:HB2	1.85	0.59
1:D:160:THR:O	1:D:162:ILE:N	2.36	0.59
1:B:378:LEU:CB	1:C:346:TYR:HE2	2.15	0.59
1:A:334:GLU:HB3	1:D:329:LYS:HZ2	1.67	0.59
1:B:160:THR:O	1:B:162:ILE:N	2.36	0.58
1:B:139:ASP:OD1	1:B:155:ARG:NH2	2.36	0.58
1:C:448:LEU:HD23	1:C:465:LEU:HD13	1.85	0.58
1:B:258:LEU:HD11	1:B:293:ASP:HB3	1.85	0.58
1:D:466:GLN:HG3	1:D:467:PRO:HD2	1.84	0.58
1:A:383:VAL:HG12	1:A:386:ARG:HH21	1.68	0.58
1:D:419:LEU:HD13	1:D:495:LEU:HD13	1.85	0.58
1:B:302:MET:SD	1:C:280:TYR:CG	2.96	0.58
1:C:418:ARG:NH2	1:C:501:SER:O	2.36	0.58
1:B:366:LEU:HD21	1:B:423:PHE:HB2	1.85	0.58
1:B:419:LEU:HD13	1:B:495:LEU:HD13	1.85	0.58
1:D:139:ASP:OD1	1:D:155:ARG:NH2	2.36	0.58
1:B:466:GLN:HG3	1:B:467:PRO:HD2	1.84	0.58
1:C:107:PHE:HE1	2:C:901:PC1:C2	2.16	0.57
1:D:98:PHE:HD1	1:D:230:HIS:HD2	1.51	0.57
1:C:211:ILE:HD12	1:C:212:ASN:H	1.70	0.57
1:C:419:LEU:HD13	1:C:495:LEU:HD13	1.86	0.57
1:A:448:LEU:HD23	1:A:465:LEU:HD13	1.85	0.57
1:B:250:TYR:CD1	1:C:261:TYR:HB2	2.39	0.57
1:B:306:MET:HG2	1:C:283:VAL:CB	2.34	0.57
1:A:107:PHE:CZ	2:A:903:PC1:H2	2.38	0.57
1:D:450:GLU:O	1:D:462:VAL:N	2.38	0.57
1:B:98:PHE:HD1	1:B:230:HIS:HD2	1.51	0.57
1:D:438:ASP:HA	1:D:499:LYS:HE3	1.87	0.57
1:A:419:LEU:HD13	1:A:495:LEU:HD13	1.86	0.57
1:D:298:ASN:ND2	1:D:301:GLU:OE2	2.32	0.57
1:B:374:GLU:OE1	1:C:346:TYR:CD2	2.57	0.57
1:A:211:ILE:HD12	1:A:212:ASN:H	1.70	0.57
1:D:219:VAL:HA	1:D:222:ILE:HG22	1.86	0.57
1:B:438:ASP:HA	1:B:499:LYS:HE3	1.87	0.56
1:D:110:LEU:HD11	1:D:114:LEU:HB2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:110:LEU:HD11	1:B:114:LEU:HB2	1.86	0.56
1:B:450:GLU:O	1:B:462:VAL:N	2.38	0.56
1:A:334:GLU:CD	1:D:329:LYS:HZ1	2.12	0.56
1:D:512:ASP:OD1	1:D:515:ARG:NH1	2.31	0.56
1:B:303:ILE:HA	1:B:306:MET:HE2	1.86	0.56
1:B:304:PHE:CD1	2:B:901:PC1:H2E2	2.26	0.56
1:A:484:TYR:OH	1:A:527:ASN:ND2	2.27	0.56
1:A:334:GLU:HB3	1:D:329:LYS:NZ	2.21	0.56
1:D:303:ILE:HA	1:D:306:MET:HE2	1.86	0.56
1:B:236:PHE:CZ	1:B:281:PHE:HE2	2.24	0.56
1:A:367:GLN:N	1:A:425:LEU:HD11	2.21	0.56
1:D:91:ILE:HG23	1:D:92:TRP:HD1	1.71	0.55
1:C:518:ASN:HA	1:C:521:LEU:HD12	1.88	0.55
1:A:261:TYR:HB2	1:D:250:TYR:HD1	1.72	0.55
1:A:394:TYR:HB2	1:A:416:VAL:HG23	1.88	0.55
1:C:367:GLN:N	1:C:425:LEU:HD11	2.21	0.55
1:B:91:ILE:HG23	1:B:92:TRP:HD1	1.71	0.55
1:A:518:ASN:HA	1:A:521:LEU:HD12	1.88	0.55
1:B:440:LEU:HG	1:B:476:ILE:HD12	1.89	0.55
1:B:512:ASP:OD1	1:B:515:ARG:NH1	2.31	0.55
1:A:364:LEU:CG	1:D:382:PRO:CD	2.55	0.55
1:B:291:TYR:OH	1:A:285:THR:OG1	2.25	0.55
1:C:394:TYR:HB2	1:C:416:VAL:HG23	1.88	0.55
1:C:438:ASP:O	1:C:499:LYS:N	2.28	0.55
1:A:364:LEU:HD11	1:D:380:ASP:O	2.06	0.54
1:B:329:LYS:NZ	1:C:334:GLU:HG2	2.18	0.54
1:A:444:CYS:HB2	1:A:493:ARG:HB3	1.89	0.54
1:D:440:LEU:HG	1:D:476:ILE:HD12	1.89	0.54
1:C:189:LEU:HD11	2:C:903:PC1:H2G1	1.87	0.54
1:D:236:PHE:CZ	1:D:281:PHE:HE2	2.24	0.54
1:B:300:ARG:HH12	2:B:902:PC1:H271	1.73	0.54
1:C:256:LEU:HD11	1:C:294:ILE:HG12	1.90	0.54
1:D:360:ILE:HG13	1:D:361:THR:N	2.23	0.54
1:C:444:CYS:HB2	1:C:493:ARG:HB3	1.89	0.54
1:B:213:TYR:OH	1:C:337:ARG:NH1	2.41	0.53
1:A:520:LEU:HA	1:A:524:LYS:HE3	1.91	0.53
1:B:360:ILE:HG13	1:B:361:THR:N	2.23	0.53
1:A:165:LEU:HD12	1:A:166:LEU:HG	1.91	0.53
1:B:378:LEU:HB2	1:C:346:TYR:CE2	2.42	0.53
1:C:439:GLN:HA	1:C:498:ASP:HA	1.91	0.53
1:C:165:LEU:HD12	1:C:166:LEU:HG	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:439:GLN:HE21	1:B:496:ARG:HG2	1.74	0.53
1:A:414:GLN:HG3	1:A:509:PHE:HE2	1.74	0.53
1:D:298:ASN:O	1:D:302:MET:HB2	2.08	0.53
1:B:298:ASN:O	1:B:302:MET:HB2	2.08	0.53
1:C:123:ILE:HA	1:C:126:LEU:HB2	1.90	0.53
1:A:346:TYR:OH	1:D:378:LEU:HD22	2.08	0.53
1:A:256:LEU:HD11	1:A:294:ILE:HG12	1.89	0.53
1:C:414:GLN:HG3	1:C:509:PHE:HE2	1.74	0.52
1:D:189:LEU:CD1	2:D:903:PC1:C2G	2.86	0.52
1:D:320:ILE:HD12	1:C:320:ILE:HG21	1.91	0.52
1:C:520:LEU:HA	1:C:524:LYS:HE3	1.91	0.52
1:B:250:TYR:O	1:B:298:ASN:ND2	2.42	0.52
1:C:517:LEU:HD22	1:C:537:ILE:HG23	1.92	0.52
1:B:157:LEU:HD12	1:B:158:LYS:HE2	1.92	0.52
1:D:244:PRO:HG2	1:D:247:GLN:HG3	1.92	0.52
1:D:342:ASP:OD1	1:D:342:ASP:N	2.42	0.52
1:B:424:PHE:HE2	1:B:494:ILE:HB	1.75	0.52
1:A:189:LEU:HD13	2:A:902:PC1:H2F1	1.87	0.52
1:A:439:GLN:HA	1:A:498:ASP:HA	1.91	0.52
1:B:104:PHE:HE2	2:B:902:PC1:H2F2	1.73	0.52
1:D:226:LEU:CA	2:D:901:PC1:C2H	2.87	0.52
1:B:320:ILE:HD12	1:A:320:ILE:HG21	1.91	0.52
1:D:157:LEU:HD12	1:D:158:LYS:HE2	1.92	0.52
1:D:217:ARG:HG3	1:D:326:LEU:HD11	1.92	0.52
1:B:182:GLU:OE2	1:B:186:TYR:OH	2.28	0.52
1:B:300:ARG:HH11	2:B:902:PC1:H282	1.74	0.52
1:B:347:MET:HE3	1:B:360:ILE:CD1	2.40	0.52
1:D:239:LEU:O	1:D:242:THR:OG1	2.24	0.52
1:B:217:ARG:HG3	1:B:326:LEU:HD11	1.92	0.52
1:D:439:GLN:HE21	1:D:496:ARG:HG2	1.74	0.52
1:C:172:ASP:OD1	1:C:172:ASP:N	2.42	0.52
1:A:123:ILE:HA	1:A:126:LEU:HB2	1.90	0.51
1:D:250:TYR:O	1:D:298:ASN:ND2	2.42	0.51
1:A:172:ASP:OD1	1:A:172:ASP:N	2.42	0.51
1:A:342:ASP:CG	1:D:377:VAL:HG11	2.36	0.51
1:D:347:MET:HE3	1:D:360:ILE:CD1	2.40	0.51
1:A:189:LEU:CD1	2:A:902:PC1:H2F2	2.27	0.51
1:D:248:GLU:O	1:D:251:THR:OG1	2.26	0.51
1:C:484:TYR:OH	1:C:527:ASN:ND2	2.27	0.51
1:A:517:LEU:HD22	1:A:537:ILE:HG23	1.92	0.51
1:D:424:PHE:HE2	1:D:494:ILE:HB	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:244:PRO:HG2	1:B:247:GLN:HG3	1.92	0.51
1:A:148:LYS:HZ2	1:A:150:SER:H	1.58	0.51
1:A:446:GLY:H	1:A:467:PRO:HG3	1.76	0.51
1:B:378:LEU:HD22	1:C:346:TYR:OH	2.11	0.51
1:C:430:ILE:HG22	1:C:431:MET:SD	2.51	0.50
1:B:229:THR:HG21	1:B:286:MET:CE	2.37	0.50
1:B:239:LEU:O	1:B:242:THR:OG1	2.24	0.50
1:B:382:PRO:HD2	1:C:364:LEU:HD23	1.85	0.50
1:A:272:TRP:HB3	1:D:299:MET:HE1	1.93	0.50
1:B:342:ASP:OD1	1:B:342:ASP:N	2.42	0.50
1:A:293:ASP:HB3	1:D:295:HIS:CD2	2.47	0.50
1:C:521:LEU:HD23	1:C:534:GLU:HG3	1.94	0.50
1:C:446:GLY:H	1:C:467:PRO:HG3	1.76	0.50
1:B:209:ILE:O	1:B:211:ILE:N	2.45	0.50
1:B:439:GLN:NE2	1:B:498:ASP:OD1	2.41	0.50
1:B:79:ASN:HD21	1:B:81:TRP:HB2	1.76	0.50
1:B:286:MET:HE1	1:A:313:MET:HE1	1.94	0.50
1:A:99:PHE:CE1	2:A:903:PC1:H341	2.47	0.50
1:A:261:TYR:HB2	1:D:250:TYR:CD1	2.47	0.50
1:A:443:VAL:N	1:A:469:HIS:O	2.40	0.50
1:D:209:ILE:O	1:D:211:ILE:N	2.45	0.50
1:C:189:LEU:CD1	2:C:903:PC1:C2H	2.89	0.50
1:A:368:TYR:O	1:A:369:GLU:C	2.54	0.50
1:D:100:THR:HG21	1:D:191:ARG:HB2	1.94	0.50
1:C:366:LEU:HB2	1:C:425:LEU:CD1	2.42	0.50
1:B:300:ARG:HH12	2:B:902:PC1:C27	2.24	0.50
1:B:360:ILE:HG13	1:B:361:THR:H	1.77	0.50
1:A:77:PRO:HD3	1:A:136:ALA:HB3	1.93	0.50
1:C:189:LEU:HD12	2:C:903:PC1:C2G	2.40	0.50
1:A:430:ILE:HG22	1:A:431:MET:SD	2.51	0.49
1:D:360:ILE:HG13	1:D:361:THR:H	1.77	0.49
1:B:248:GLU:O	1:B:251:THR:OG1	2.26	0.49
1:B:300:ARG:NH1	2:B:902:PC1:H282	2.27	0.49
1:B:87:MET:HE2	1:B:87:MET:N	2.28	0.49
1:D:79:ASN:HD21	1:D:81:TRP:HB2	1.76	0.49
1:A:334:GLU:HG3	1:A:337:ARG:HH21	1.78	0.49
1:C:400:LYS:O	1:C:405:ARG:NH2	2.36	0.49
1:D:439:GLN:NE2	1:D:498:ASP:OD1	2.41	0.49
1:C:77:PRO:HD3	1:C:136:ALA:HB3	1.93	0.49
1:A:346:TYR:CE2	1:D:378:LEU:CB	2.77	0.49
1:D:286:MET:HE1	1:C:313:MET:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:148:LYS:NZ	1:C:150:SER:H	2.10	0.49
1:B:298:ASN:ND2	1:B:301:GLU:OE2	2.32	0.49
1:A:521:LEU:HD23	1:A:534:GLU:HG3	1.94	0.49
1:D:451:ILE:HA	1:D:461:ILE:HA	1.93	0.49
1:A:366:LEU:HB2	1:A:425:LEU:CD1	2.42	0.49
1:C:368:TYR:O	1:C:369:GLU:C	2.54	0.49
1:C:443:VAL:N	1:C:469:HIS:O	2.40	0.49
1:B:250:TYR:HD1	1:C:261:TYR:HB2	1.78	0.49
1:B:451:ILE:HA	1:B:461:ILE:HA	1.93	0.49
1:A:271:PRO:CB	2:A:903:PC1:H12	2.40	0.49
1:C:171:TRP:CE3	1:C:174:ILE:HD12	2.48	0.49
1:B:302:MET:SD	1:C:280:TYR:CD2	3.06	0.48
1:B:499:LYS:O	1:B:503:MET:HG2	2.13	0.48
1:A:187:LEU:O	1:A:190:ILE:HG12	2.14	0.48
1:D:87:MET:HE2	1:D:87:MET:N	2.28	0.48
1:B:100:THR:HG21	1:B:191:ARG:HB2	1.94	0.48
1:A:148:LYS:NZ	1:A:150:SER:H	2.10	0.48
1:A:364:LEU:HA	1:A:364:LEU:HD22	1.70	0.48
1:D:209:ILE:HG23	1:D:210:ARG:H	1.78	0.48
1:A:534:GLU:HA	1:A:537:ILE:HD12	1.96	0.48
1:B:374:GLU:HG2	1:C:346:TYR:CE2	2.49	0.48
2:B:901:PC1:C2A	2:B:902:PC1:C2C	2.91	0.48
1:A:171:TRP:CE3	1:A:174:ILE:HD12	2.48	0.48
1:C:187:LEU:O	1:C:190:ILE:HG12	2.14	0.48
1:B:90:LEU:HD21	1:B:198:VAL:HG23	1.96	0.48
1:A:343:ILE:HD13	1:A:343:ILE:HA	1.71	0.48
1:B:209:ILE:HG23	1:B:210:ARG:H	1.78	0.48
1:A:153:ALA:O	1:A:157:LEU:HD23	2.14	0.48
1:B:329:LYS:NZ	1:C:334:GLU:OE1	2.44	0.47
1:A:345:ARG:CZ	1:D:374:GLU:HB3	2.44	0.47
1:C:534:GLU:HA	1:C:537:ILE:HD12	1.96	0.47
1:B:245:ALA:HA	1:B:267:ARG:HH22	1.79	0.47
1:A:364:LEU:CD2	1:D:382:PRO:HG2	2.25	0.47
1:A:364:LEU:CD2	1:D:382:PRO:HG3	2.23	0.47
1:D:499:LYS:O	1:D:503:MET:HG2	2.13	0.47
1:C:320:ILE:O	1:C:324:THR:HG22	2.14	0.47
1:C:334:GLU:HG3	1:C:337:ARG:HH21	1.78	0.47
1:A:331:SER:CA	1:A:334:GLU:HB2	2.44	0.47
1:A:320:ILE:O	1:A:324:THR:HG22	2.14	0.47
1:D:245:ALA:HA	1:D:267:ARG:HH22	1.79	0.47
1:D:350:ASN:HB3	1:C:393:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:PHE:CD1	1:B:230:HIS:HD2	2.31	0.47
1:C:498:ASP:O	1:C:501:SER:OG	2.29	0.47
1:B:104:PHE:CE2	2:B:902:PC1:H2F2	2.50	0.47
1:B:207:LYS:HA	1:B:207:LYS:HD2	1.66	0.47
1:B:354:ARG:HA	1:B:357:ARG:HD2	1.96	0.47
1:B:385:ILE:HG21	1:C:360:ILE:HD12	1.23	0.47
1:A:391:GLN:HG3	1:A:395:LEU:HD22	1.96	0.47
1:D:182:GLU:OE2	1:D:186:TYR:OH	2.28	0.47
1:D:298:ASN:O	1:D:302:MET:HE2	2.15	0.47
1:D:337:ARG:NH1	1:C:206:GLU:O	2.48	0.47
1:C:153:ALA:O	1:C:157:LEU:HD23	2.14	0.47
1:C:343:ILE:HD13	1:C:343:ILE:HA	1.71	0.47
1:A:258:LEU:C	1:D:297:VAL:HG13	2.39	0.47
1:A:284:VAL:HG12	1:D:309:ILE:CD1	2.44	0.47
1:D:90:LEU:HD21	1:D:198:VAL:HG23	1.96	0.47
1:C:331:SER:CA	1:C:334:GLU:HB2	2.44	0.47
1:B:295:HIS:CD2	1:C:293:ASP:HB3	2.50	0.47
1:C:279:MET:HE1	2:C:902:PC1:H2C2	1.95	0.47
1:C:343:ILE:HD12	1:C:347:MET:HE2	1.97	0.47
1:A:133:PHE:HE2	1:A:157:LEU:HD21	1.80	0.47
1:A:191:ARG:HD3	1:A:194:ARG:NH1	2.29	0.47
1:D:354:ARG:HA	1:D:357:ARG:HD2	1.96	0.47
1:C:191:ARG:HD3	1:C:194:ARG:NH1	2.29	0.47
1:B:158:LYS:HA	1:B:158:LYS:HD3	1.65	0.46
1:C:503:MET:HA	1:C:506:LEU:HD12	1.97	0.46
1:B:280:TYR:HA	1:A:306:MET:CE	2.45	0.46
1:B:298:ASN:O	1:B:302:MET:HE2	2.15	0.46
1:B:356:ILE:O	1:B:360:ILE:HG12	2.15	0.46
1:A:343:ILE:HD12	1:A:347:MET:HE2	1.97	0.46
2:B:902:PC1:H2D2	2:B:902:PC1:H2G2	1.39	0.46
1:A:410:GLU:OE2	1:A:410:GLU:N	2.31	0.46
1:C:106:PHE:HD2	2:C:901:PC1:H12	1.80	0.46
1:C:133:PHE:HE2	1:C:157:LEU:HD21	1.80	0.46
1:B:285:THR:HG1	1:C:291:TYR:HH	1.56	0.46
1:B:397:TYR:HA	1:B:400:LYS:NZ	2.30	0.46
1:D:98:PHE:CD1	1:D:230:HIS:HD2	2.31	0.46
1:B:350:ASN:HB3	1:A:393:LEU:HD22	1.97	0.46
1:D:356:ILE:O	1:D:360:ILE:HG12	2.15	0.46
1:D:397:TYR:HA	1:D:400:LYS:NZ	2.30	0.46
1:D:471:PHE:HZ	1:D:494:ILE:HD13	1.81	0.46
1:C:99:PHE:HD1	2:C:901:PC1:H342	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:LEU:HD13	2:C:901:PC1:H221	1.98	0.46
1:C:148:LYS:HD2	1:C:148:LYS:HA	1.76	0.46
1:D:346:TYR:O	1:D:350:ASN:N	2.40	0.46
1:B:337:ARG:NH1	1:A:206:GLU:O	2.48	0.46
2:B:903:PC1:H221	2:B:903:PC1:H251	1.60	0.46
1:A:498:ASP:O	1:A:501:SER:OG	2.29	0.46
1:C:391:GLN:HG3	1:C:395:LEU:HD22	1.96	0.46
1:B:451:ILE:O	1:B:485:THR:N	2.49	0.46
1:A:380:ASP:O	1:A:386:ARG:NH1	2.49	0.46
1:D:158:LYS:HA	1:D:158:LYS:HD3	1.65	0.46
1:C:189:LEU:HD12	2:C:903:PC1:C2H	2.46	0.46
1:A:279:MET:HE1	2:A:904:PC1:C2C	2.46	0.46
1:D:256:LEU:HD23	1:D:256:LEU:HA	1.81	0.46
1:B:219:VAL:HA	1:B:222:ILE:HG22	1.97	0.46
1:A:129:ILE:HD11	1:A:161:PHE:CE1	2.51	0.46
1:D:280:TYR:HA	1:C:306:MET:CE	2.45	0.46
1:D:332:LYS:HE2	1:D:332:LYS:HB2	1.85	0.46
1:C:129:ILE:HD11	1:C:161:PHE:CE1	2.51	0.46
2:C:903:PC1:H242	2:C:903:PC1:H272	1.71	0.46
1:C:520:LEU:HD12	1:C:524:LYS:HE3	1.99	0.45
1:D:451:ILE:O	1:D:485:THR:N	2.49	0.45
1:C:226:LEU:HA	2:C:902:PC1:H2E2	1.98	0.45
1:C:380:ASP:O	1:C:386:ARG:NH1	2.49	0.45
1:B:206:GLU:OE2	1:C:337:ARG:NH1	2.47	0.45
1:A:395:LEU:N	1:A:396:PRO:HD2	2.32	0.45
1:A:503:MET:HA	1:A:506:LEU:HD12	1.97	0.45
1:B:329:LYS:HZ2	1:C:334:GLU:CG	2.30	0.45
1:B:353:GLY:O	1:B:357:ARG:NH1	2.50	0.45
1:C:395:LEU:N	1:C:396:PRO:HD2	2.32	0.45
2:C:903:PC1:H261	2:C:903:PC1:H291	1.62	0.45
1:D:353:GLY:O	1:D:357:ARG:NH1	2.50	0.45
1:C:304:PHE:CE1	2:C:904:PC1:H2D2	2.52	0.45
2:B:902:PC1:H242	2:B:902:PC1:H272	1.68	0.45
1:A:520:LEU:HD12	1:A:524:LYS:HE3	1.99	0.45
1:C:99:PHE:CE1	2:C:901:PC1:H342	2.52	0.45
1:C:303:ILE:O	1:C:306:MET:HB2	2.17	0.45
1:B:329:LYS:HZ2	1:C:334:GLU:CD	2.24	0.45
1:B:332:LYS:HE2	1:B:332:LYS:HB2	1.85	0.45
1:A:92:TRP:HB3	1:A:125:PHE:HE1	1.82	0.45
1:A:148:LYS:HD2	1:A:148:LYS:HA	1.76	0.45
1:A:430:ILE:HB	1:A:486:VAL:HB	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:145:MET:SD	1:D:146:ILE:N	2.90	0.45
1:D:343:ILE:HG22	1:C:377:VAL:HB	1.98	0.45
1:C:528:VAL:O	1:C:532:GLN:HB2	2.16	0.45
1:B:145:MET:SD	1:B:146:ILE:N	2.90	0.45
1:B:471:PHE:HZ	1:B:494:ILE:HD13	1.81	0.45
1:A:345:ARG:CZ	1:D:374:GLU:CB	2.94	0.45
1:A:400:LYS:O	1:A:405:ARG:NH2	2.36	0.45
1:D:118:ASP:OD1	1:D:122:GLN:NE2	2.50	0.45
1:D:425:LEU:HD12	1:D:426:PRO:HD2	1.99	0.45
1:C:389:ILE:HG13	1:C:390:ALA:N	2.32	0.45
1:A:339:LYS:H	1:A:339:LYS:HG2	1.68	0.45
1:D:385:ILE:O	1:D:385:ILE:HG13	2.16	0.45
1:C:225:GLU:HB3	2:C:902:PC1:C2F	2.47	0.44
1:A:346:TYR:CD2	1:D:374:GLU:OE1	2.70	0.44
1:B:385:ILE:O	1:B:385:ILE:HG13	2.16	0.44
1:A:356:ILE:H	1:A:356:ILE:HG13	1.36	0.44
1:A:528:VAL:O	1:A:532:GLN:HB2	2.16	0.44
1:C:92:TRP:HB3	1:C:125:PHE:HE1	1.82	0.44
1:B:118:ASP:OD1	1:B:122:GLN:NE2	2.50	0.44
1:A:303:ILE:O	1:A:306:MET:HB2	2.17	0.44
1:C:107:PHE:CZ	2:C:901:PC1:H32	2.43	0.44
1:C:529:ARG:HG3	1:C:530:ILE:HG13	2.00	0.44
1:B:343:ILE:HG22	1:A:377:VAL:HB	1.98	0.44
1:B:425:LEU:HD12	1:B:426:PRO:HD2	1.98	0.44
1:D:166:LEU:HB3	1:D:190:ILE:HD11	2.00	0.44
1:D:207:LYS:HD2	1:D:207:LYS:HA	1.66	0.44
1:C:236:PHE:CZ	1:C:281:PHE:HE2	2.36	0.44
1:C:477:LEU:HD12	1:C:540:HIS:HE1	1.83	0.44
1:D:395:LEU:O	1:D:399:GLU:HG2	2.18	0.44
1:B:110:LEU:HD21	1:B:114:LEU:HB2	2.00	0.44
1:B:286:MET:SD	1:A:313:MET:HE1	2.58	0.44
1:D:129:ILE:O	1:D:132:THR:OG1	2.36	0.44
1:A:236:PHE:CZ	1:A:281:PHE:HE2	2.36	0.44
2:D:902:PC1:H292	2:D:902:PC1:H262	1.54	0.44
1:C:373:THR:O	1:C:377:VAL:HG12	2.18	0.44
1:C:430:ILE:HB	1:C:486:VAL:HB	1.99	0.44
1:B:302:MET:CG	1:C:280:TYR:HB2	2.48	0.44
1:B:318:TYR:CE1	1:C:327:ILE:HD11	2.52	0.44
1:B:395:LEU:O	1:B:399:GLU:HG2	2.18	0.44
1:D:85:TRP:CE2	1:D:131:LEU:HD21	2.53	0.44
2:C:903:PC1:H2C1	2:C:903:PC1:H292	1.75	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:ILE:HG22	1:B:148:LYS:H	1.82	0.43
1:D:110:LEU:HD21	1:D:114:LEU:HB2	2.00	0.43
1:D:146:ILE:HG22	1:D:148:LYS:H	1.82	0.43
1:D:171:TRP:HA	1:D:174:ILE:HG22	2.00	0.43
1:B:228:CYS:HA	1:B:231:THR:HG22	1.99	0.43
1:A:189:LEU:CD1	2:A:902:PC1:C2E	2.94	0.43
1:A:426:PRO:HB3	1:A:490:GLU:HA	1.99	0.43
1:C:396:PRO:O	1:C:400:LYS:NZ	2.51	0.43
1:A:279:MET:HE1	2:A:904:PC1:H2C2	2.00	0.43
1:A:354:ARG:HA	1:A:357:ARG:HB2	1.99	0.43
1:A:402:PRO:HD2	1:A:469:HIS:HA	2.01	0.43
1:A:424:PHE:CZ	1:A:430:ILE:HG23	2.53	0.43
1:C:335:ARG:O	1:C:339:LYS:HG2	2.18	0.43
1:B:129:ILE:O	1:B:132:THR:OG1	2.36	0.43
1:C:424:PHE:CZ	1:C:430:ILE:HG23	2.53	0.43
1:B:85:TRP:CE2	1:B:131:LEU:HD21	2.53	0.43
1:B:382:PRO:HD3	1:C:364:LEU:HG	1.98	0.43
1:D:286:MET:SD	1:C:313:MET:HE1	2.58	0.43
1:C:354:ARG:HA	1:C:357:ARG:HB2	1.99	0.43
1:A:145:MET:HG3	1:A:147:TYR:CE1	2.54	0.43
1:A:335:ARG:O	1:A:339:LYS:HG2	2.18	0.43
1:A:352:LEU:HD22	1:A:352:LEU:HA	1.79	0.43
1:A:359:GLN:NE2	1:D:385:ILE:HD13	2.34	0.43
1:A:529:ARG:HG3	1:A:530:ILE:HG13	2.00	0.43
1:C:125:PHE:CD1	1:C:125:PHE:N	2.87	0.43
1:B:171:TRP:HB2	1:B:188:LEU:HD12	2.00	0.43
1:B:306:MET:O	1:B:310:SER:OG	2.31	0.43
1:B:329:LYS:HZ1	1:C:334:GLU:CB	2.26	0.43
1:A:93:ALA:O	1:A:97:SER:OG	2.32	0.43
1:A:389:ILE:HG13	1:A:390:ALA:N	2.32	0.43
1:D:229:THR:HG21	1:D:286:MET:HE2	2.01	0.43
1:C:145:MET:HG3	1:C:147:TYR:CE1	2.54	0.43
1:C:426:PRO:HB3	1:C:490:GLU:HA	1.99	0.43
1:A:146:ILE:HG22	1:A:148:LYS:H	1.84	0.43
1:A:221:LEU:HA	1:A:224:VAL:HG12	2.01	0.43
1:A:448:LEU:HD11	1:A:486:VAL:HG12	2.01	0.43
1:D:446:GLY:HA2	1:C:144:ARG:HH22	1.84	0.43
1:B:166:LEU:HB3	1:B:190:ILE:HD11	2.00	0.43
1:C:448:LEU:HD11	1:C:486:VAL:HG12	2.01	0.43
1:B:171:TRP:HA	1:B:174:ILE:HG22	2.00	0.42
1:B:420:HIS:HD2	1:B:496:ARG:NH2	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:396:PRO:O	1:A:400:LYS:NZ	2.51	0.42
1:D:171:TRP:HB2	1:D:188:LEU:HD12	2.00	0.42
1:C:146:ILE:HG22	1:C:148:LYS:H	1.84	0.42
1:A:373:THR:O	1:A:377:VAL:HG12	2.18	0.42
1:C:361:THR:O	1:C:362:GLY:C	2.62	0.42
1:C:402:PRO:HD2	1:C:469:HIS:HA	2.01	0.42
1:B:76:HIS:CD2	1:B:145:MET:HE3	2.54	0.42
1:B:123:ILE:C	1:B:123:ILE:HD12	2.44	0.42
1:A:260:ASP:OD2	1:D:249:GLY:CA	2.67	0.42
1:A:361:THR:O	1:A:362:GLY:C	2.62	0.42
1:A:386:ARG:HA	1:A:389:ILE:HG12	2.01	0.42
1:A:415:ILE:O	1:A:419:LEU:HG	2.19	0.42
1:B:443:VAL:HG22	1:B:471:PHE:HE1	1.85	0.42
1:B:446:GLY:HA2	1:A:144:ARG:HH22	1.84	0.42
1:D:206:GLU:HG3	1:D:217:ARG:NH1	2.35	0.42
1:D:440:LEU:HB2	1:D:497:LEU:HB3	2.01	0.42
1:C:386:ARG:HA	1:C:389:ILE:HG12	2.01	0.42
1:D:300:ARG:HH12	2:D:903:PC1:H271	1.84	0.42
1:A:125:PHE:N	1:A:125:PHE:HD1	2.18	0.42
1:A:141:ARG:H	1:A:141:ARG:HG3	1.65	0.42
1:C:131:LEU:O	1:C:131:LEU:HD23	2.19	0.42
1:B:225:GLU:O	1:B:229:THR:HG23	2.19	0.42
1:B:284:VAL:O	1:B:290:GLY:N	2.48	0.42
1:A:104:PHE:CD2	1:A:189:LEU:HD21	2.55	0.42
1:A:125:PHE:N	1:A:125:PHE:CD1	2.87	0.42
1:D:104:PHE:CE2	2:D:903:PC1:H2E2	2.55	0.42
1:D:291:TYR:CE1	1:C:281:PHE:HE1	2.38	0.42
1:A:339:LYS:HD2	1:A:368:TYR:CE2	2.55	0.42
1:D:76:HIS:CD2	1:D:145:MET:HE3	2.54	0.42
1:A:477:LEU:HD12	1:A:540:HIS:HE1	1.83	0.42
1:C:364:LEU:HD22	1:C:364:LEU:HA	1.70	0.42
1:A:444:CYS:O	1:A:445:HIS:ND1	2.51	0.41
1:D:420:HIS:HD2	1:D:496:ARG:NH2	2.17	0.41
1:C:432:GLU:HA	1:C:485:THR:HA	2.02	0.41
1:B:280:TYR:HA	1:A:306:MET:HE1	2.02	0.41
1:A:131:LEU:O	1:A:131:LEU:HD23	2.19	0.41
1:A:418:ARG:HH22	1:A:504:ASN:HB2	1.85	0.41
1:D:123:ILE:C	1:D:123:ILE:HD12	2.45	0.41
1:D:443:VAL:HG22	1:D:471:PHE:HE1	1.85	0.41
1:C:104:PHE:CD2	1:C:189:LEU:HD21	2.55	0.41
1:C:125:PHE:N	1:C:125:PHE:HD1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:201:PHE:CD1	1:C:201:PHE:C	2.99	0.41
1:C:360:ILE:HD13	1:C:360:ILE:HA	1.95	0.41
1:B:291:TYR:CE1	1:A:281:PHE:HE1	2.38	0.41
1:B:206:GLU:HG3	1:B:217:ARG:NH1	2.35	0.41
1:B:440:LEU:HB2	1:B:497:LEU:HB3	2.01	0.41
1:A:200:LEU:HD23	1:A:200:LEU:HA	1.92	0.41
1:A:274:ARG:H	1:A:274:ARG:HG2	1.62	0.41
1:A:356:ILE:CD1	1:D:392:THR:HG21	2.50	0.41
1:D:245:ALA:HA	1:D:267:ARG:NH2	2.36	0.41
1:C:444:CYS:O	1:C:445:HIS:ND1	2.51	0.41
1:B:181:LYS:HE2	1:B:181:LYS:HB2	1.90	0.41
1:D:270:ASP:HA	1:D:271:PRO:HD2	1.95	0.41
1:C:339:LYS:HD2	1:C:368:TYR:CE2	2.55	0.41
1:C:415:ILE:O	1:C:419:LEU:HG	2.19	0.41
1:C:418:ARG:HH22	1:C:504:ASN:HB2	1.85	0.41
1:A:138:ARG:HB2	1:A:145:MET:HE2	2.03	0.41
1:D:196:HIS:HA	1:D:199:ILE:HG22	2.02	0.41
1:C:332:LYS:O	1:C:335:ARG:HB2	2.21	0.41
1:B:110:LEU:HD23	1:B:111:PRO:HD2	2.02	0.41
1:B:196:HIS:HA	1:B:199:ILE:HG22	2.02	0.41
1:A:332:LYS:O	1:A:335:ARG:HB2	2.21	0.41
1:D:337:ARG:NH2	1:C:211:ILE:O	2.54	0.41
1:C:107:PHE:CZ	2:C:901:PC1:C2	2.99	0.41
1:C:299:MET:HE3	2:C:904:PC1:C21	2.51	0.41
1:B:217:ARG:O	1:B:221:LEU:HG	2.21	0.41
1:B:337:ARG:HA	1:A:209:ILE:HD11	2.02	0.41
1:B:337:ARG:NH2	1:A:211:ILE:O	2.54	0.41
1:B:440:LEU:HD23	1:B:440:LEU:HA	1.91	0.41
1:D:93:ALA:O	1:D:97:SER:OG	2.27	0.41
1:D:280:TYR:HA	1:C:306:MET:HE1	2.02	0.41
1:C:138:ARG:HB2	1:C:145:MET:HE2	2.03	0.41
1:A:401:VAL:HG22	1:A:402:PRO:HD2	2.03	0.41
1:D:304:PHE:HE1	2:D:902:PC1:C2H	2.33	0.41
1:D:333:THR:HA	1:D:336:PHE:HD1	1.85	0.41
2:D:901:PC1:H252	2:D:901:PC1:H222	1.70	0.41
1:C:401:VAL:HG22	1:C:402:PRO:HD2	2.03	0.41
1:B:105:GLY:HA2	1:B:238:TYR:HB2	2.03	0.41
1:B:333:THR:HA	1:B:336:PHE:HD1	1.85	0.41
1:B:346:TYR:O	1:B:350:ASN:N	2.40	0.41
1:A:174:ILE:H	1:A:174:ILE:HG13	1.58	0.41
1:A:212:ASN:O	1:A:216:THR:HG22	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:ASP:CG	1:D:249:GLY:HA3	2.46	0.41
1:B:250:TYR:CE1	1:C:261:TYR:HB2	2.56	0.40
1:B:378:LEU:CD1	1:C:346:TYR:CD2	2.70	0.40
1:D:337:ARG:HA	1:C:209:ILE:HD11	2.02	0.40
1:A:432:GLU:HA	1:A:485:THR:HA	2.02	0.40
1:D:105:GLY:HA2	1:D:238:TYR:HB2	2.04	0.40
1:C:243:LEU:HD11	1:C:298:ASN:HD22	1.86	0.40
1:B:138:ARG:HG2	1:B:145:MET:HA	2.03	0.40
1:A:304:PHE:CE1	2:A:901:PC1:C2D	2.96	0.40
1:D:110:LEU:HD23	1:D:111:PRO:HD2	2.02	0.40
1:D:138:ARG:HG2	1:D:145:MET:HA	2.03	0.40
1:D:363:HIS:HA	1:D:366:LEU:HB3	2.04	0.40
1:A:122:GLN:HE22	1:A:194:ARG:HH12	1.69	0.40
1:A:279:MET:CE	2:A:904:PC1:H2C2	2.51	0.40
1:B:245:ALA:HA	1:B:267:ARG:NH2	2.36	0.40
1:C:212:ASN:O	1:C:216:THR:HG22	2.21	0.40
1:C:394:TYR:CZ	1:C:495:LEU:HD21	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	460/838 (55%)	422 (92%)	35 (8%)	3 (1%)	18	47
1	B	445/838 (53%)	418 (94%)	23 (5%)	4 (1%)	14	42
1	C	460/838 (55%)	425 (92%)	32 (7%)	3 (1%)	18	47
1	D	445/838 (53%)	419 (94%)	23 (5%)	3 (1%)	18	47
All	All	1810/3352 (54%)	1684 (93%)	113 (6%)	13 (1%)	20	47

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	161	PHE
1	D	161	PHE
1	B	210	ARG
1	A	355	ASN
1	D	210	ARG
1	C	355	ASN
1	B	111	PRO
1	A	111	PRO
1	D	111	PRO
1	C	111	PRO
1	B	222	ILE
1	A	381	ILE
1	C	381	ILE

5.3.2 Protein sidechains ⓘ

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	415/727 (57%)	385 (93%)	30 (7%)	13	39
1	B	400/727 (55%)	389 (97%)	11 (3%)	38	60
1	C	415/727 (57%)	384 (92%)	31 (8%)	12	38
1	D	400/727 (55%)	389 (97%)	11 (3%)	38	60
All	All	1630/2908 (56%)	1547 (95%)	83 (5%)	23	48

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	152	ILE
1	B	222	ILE
1	B	224	VAL
1	B	226	LEU
1	B	267	ARG
1	B	369	GLU
1	B	377	VAL
1	B	379	GLN
1	B	381	ILE

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Mol	Chain	Res	Type
1	B	383	VAL
1	B	385	ILE
1	A	224	VAL
1	A	332	LYS
1	A	333	THR
1	A	334	GLU
1	A	336	PHE
1	A	337	ARG
1	A	339	LYS
1	A	340	MET
1	A	342	ASP
1	A	343	ILE
1	A	344	MET
1	A	345	ARG
1	A	346	TYR
1	A	348	ASN
1	A	349	ARG
1	A	351	LYS
1	A	352	LEU
1	A	354	ARG
1	A	355	ASN
1	A	356	ILE
1	A	357	ARG
1	A	360	ILE
1	A	364	LEU
1	A	365	ARG
1	A	367	GLN
1	A	368	TYR
1	A	369	GLU
1	A	377	VAL
1	A	379	GLN
1	A	380	ASP
1	D	152	ILE
1	D	224	VAL
1	D	225	GLU
1	D	226	LEU
1	D	267	ARG
1	D	369	GLU
1	D	377	VAL
1	D	379	GLN
1	D	381	ILE
1	D	383	VAL

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Mol	Chain	Res	Type
1	D	385	ILE
1	C	224	VAL
1	C	225	GLU
1	C	332	LYS
1	C	333	THR
1	C	334	GLU
1	C	336	PHE
1	C	337	ARG
1	C	339	LYS
1	C	340	MET
1	C	342	ASP
1	C	343	ILE
1	C	344	MET
1	C	345	ARG
1	C	346	TYR
1	C	348	ASN
1	C	349	ARG
1	C	351	LYS
1	C	352	LEU
1	C	354	ARG
1	C	355	ASN
1	C	356	ILE
1	C	357	ARG
1	C	360	ILE
1	C	364	LEU
1	C	365	ARG
1	C	367	GLN
1	C	368	TYR
1	C	369	GLU
1	C	377	VAL
1	C	379	GLN
1	C	380	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	247	GLN
1	B	359	GLN
1	B	367	GLN
1	B	379	GLN
1	B	413	ASN
1	B	439	GLN

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Mol	Chain	Res	Type
1	A	359	GLN
1	A	363	HIS
1	A	479	ASN
1	A	482	GLN
1	A	519	ASN
1	D	247	GLN
1	D	295	HIS
1	D	359	GLN
1	D	367	GLN
1	D	379	GLN
1	D	413	ASN
1	D	439	GLN
1	C	359	GLN
1	C	363	HIS
1	C	479	ASN
1	C	482	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

14 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PC1	D	901	-	16,16,53	0.17	0	15,15,61	0.09	0
2	PC1	B	903	-	16,16,53	0.17	0	15,15,61	0.08	0
2	PC1	C	902	-	16,16,53	0.16	0	15,15,61	0.09	0
2	PC1	C	903	-	16,16,53	0.17	0	15,15,61	0.11	0
2	PC1	B	901	-	16,16,53	0.15	0	15,15,61	0.08	0
2	PC1	C	904	-	16,16,53	0.15	0	15,15,61	0.07	0
2	PC1	A	903	-	29,29,53	0.46	0	32,34,61	0.57	1 (3%)
2	PC1	A	904	-	16,16,53	0.16	0	15,15,61	0.09	0
2	PC1	D	903	-	16,16,53	0.15	0	15,15,61	0.08	0
2	PC1	B	902	-	16,16,53	0.15	0	15,15,61	0.09	0
2	PC1	A	901	-	16,16,53	0.12	0	15,15,61	0.06	0
2	PC1	A	902	-	16,16,53	0.15	0	15,15,61	0.07	0
2	PC1	D	902	-	16,16,53	0.15	0	15,15,61	0.07	0
2	PC1	C	901	-	29,29,53	0.47	0	32,34,61	0.70	1 (3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PC1	D	901	-	-	8/14/14/57	-
2	PC1	B	903	-	-	9/14/14/57	-
2	PC1	C	902	-	-	7/14/14/57	-
2	PC1	C	903	-	-	11/14/14/57	-
2	PC1	B	901	-	-	9/14/14/57	-
2	PC1	C	904	-	-	10/14/14/57	-
2	PC1	A	903	-	-	14/31/31/57	-
2	PC1	A	904	-	-	6/14/14/57	-
2	PC1	D	903	-	-	8/14/14/57	-
2	PC1	B	902	-	-	11/14/14/57	-
2	PC1	A	901	-	-	6/14/14/57	-
2	PC1	A	902	-	-	10/14/14/57	-
2	PC1	D	902	-	-	8/14/14/57	-
2	PC1	C	901	-	-	14/31/31/57	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	903	PC1	O12-P-O14	2.43	120.31	110.83
2	C	901	PC1	O12-P-O14	2.22	119.48	110.83

There are no chirality outliers.

All (131) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	903	PC1	C1-O11-P-O12
2	A	903	PC1	C1-O11-P-O14
2	A	903	PC1	C1-O11-P-O13
2	C	901	PC1	C1-O11-P-O14
2	C	901	PC1	C22-C21-O21-C2
2	C	901	PC1	O22-C21-O21-C2
2	C	903	PC1	C2D-C2E-C2F-C2G
2	C	901	PC1	C32-C31-O31-C3
2	B	902	PC1	C2D-C2E-C2F-C2G
2	C	901	PC1	O32-C31-O31-C3
2	D	902	PC1	C22-C23-C24-C25
2	B	902	PC1	C24-C25-C26-C27
2	B	903	PC1	C22-C23-C24-C25
2	C	903	PC1	C26-C27-C28-C29
2	D	901	PC1	C22-C23-C24-C25
2	D	901	PC1	C24-C25-C26-C27
2	D	902	PC1	C26-C27-C28-C29
2	C	903	PC1	C2B-C2C-C2D-C2E
2	B	902	PC1	C28-C29-C2A-C2B
2	D	903	PC1	C2C-C2D-C2E-C2F
2	C	903	PC1	C24-C25-C26-C27
2	B	902	PC1	C21-C22-C23-C24
2	C	903	PC1	C29-C2A-C2B-C2C
2	A	903	PC1	C22-C21-O21-C2
2	C	904	PC1	C27-C28-C29-C2A
2	A	901	PC1	C22-C23-C24-C25
2	D	902	PC1	C28-C29-C2A-C2B
2	C	904	PC1	C2C-C2D-C2E-C2F
2	C	904	PC1	C24-C25-C26-C27
2	A	903	PC1	C1-C2-C3-O31
2	A	902	PC1	C24-C25-C26-C27
2	A	903	PC1	C31-C32-C33-C34
2	B	901	PC1	C27-C28-C29-C2A
2	C	903	PC1	C21-C22-C23-C24
2	B	903	PC1	C26-C27-C28-C29
2	B	903	PC1	C25-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
2	A	903	PC1	O22-C21-O21-C2
2	A	902	PC1	C2B-C2C-C2D-C2E
2	A	903	PC1	C32-C33-C34-C35
2	A	904	PC1	C24-C25-C26-C27
2	B	901	PC1	C25-C26-C27-C28
2	D	902	PC1	C2B-C2C-C2D-C2E
2	C	902	PC1	C24-C25-C26-C27
2	D	901	PC1	C27-C28-C29-C2A
2	D	902	PC1	C27-C28-C29-C2A
2	C	902	PC1	C23-C24-C25-C26
2	B	903	PC1	C28-C29-C2A-C2B
2	A	904	PC1	C23-C24-C25-C26
2	D	901	PC1	C28-C29-C2A-C2B
2	C	902	PC1	C22-C23-C24-C25
2	A	901	PC1	C23-C24-C25-C26
2	C	903	PC1	C22-C23-C24-C25
2	C	903	PC1	C28-C29-C2A-C2B
2	A	903	PC1	O21-C2-C3-O31
2	A	902	PC1	C22-C23-C24-C25
2	A	902	PC1	C23-C24-C25-C26
2	C	903	PC1	C2A-C2B-C2C-C2D
2	B	902	PC1	C2C-C2D-C2E-C2F
2	A	904	PC1	C22-C23-C24-C25
2	B	903	PC1	C24-C25-C26-C27
2	A	902	PC1	C29-C2A-C2B-C2C
2	D	903	PC1	C24-C25-C26-C27
2	C	904	PC1	C21-C22-C23-C24
2	A	902	PC1	C2A-C2B-C2C-C2D
2	B	901	PC1	C2A-C2B-C2C-C2D
2	C	904	PC1	C2A-C2B-C2C-C2D
2	D	903	PC1	C23-C24-C25-C26
2	A	903	PC1	C25-C26-C27-C28
2	A	902	PC1	C21-C22-C23-C24
2	C	904	PC1	C2E-C2F-C2G-C2H
2	B	901	PC1	C2D-C2E-C2F-C2G
2	B	901	PC1	C28-C29-C2A-C2B
2	D	902	PC1	C2C-C2D-C2E-C2F
2	A	901	PC1	C2A-C2B-C2C-C2D
2	A	903	PC1	C27-C28-C29-C2A
2	C	903	PC1	C2C-C2D-C2E-C2F
2	D	902	PC1	C29-C2A-C2B-C2C
2	C	903	PC1	C25-C26-C27-C28

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Mol	Chain	Res	Type	Atoms
2	C	902	PC1	C27-C28-C29-C2A
2	A	903	PC1	C26-C27-C28-C29
2	B	901	PC1	C21-C22-C23-C24
2	D	901	PC1	C25-C26-C27-C28
2	D	903	PC1	C2D-C2E-C2F-C2G
2	D	903	PC1	C29-C2A-C2B-C2C
2	C	904	PC1	C2D-C2E-C2F-C2G
2	D	901	PC1	C21-C22-C23-C24
2	A	904	PC1	C27-C28-C29-C2A
2	B	901	PC1	C29-C2A-C2B-C2C
2	B	902	PC1	C29-C2A-C2B-C2C
2	C	901	PC1	C22-C23-C24-C25
2	A	904	PC1	C2D-C2E-C2F-C2G
2	B	902	PC1	C27-C28-C29-C2A
2	B	901	PC1	C2E-C2F-C2G-C2H
2	B	902	PC1	C25-C26-C27-C28
2	C	901	PC1	C27-C28-C29-C2A
2	A	903	PC1	C23-C24-C25-C26
2	D	901	PC1	C2D-C2E-C2F-C2G
2	C	902	PC1	C2D-C2E-C2F-C2G
2	C	904	PC1	C25-C26-C27-C28
2	A	903	PC1	C22-C23-C24-C25
2	C	901	PC1	C31-C32-C33-C34
2	C	902	PC1	C29-C2A-C2B-C2C
2	B	902	PC1	C2E-C2F-C2G-C2H
2	B	902	PC1	C2B-C2C-C2D-C2E
2	A	902	PC1	C2E-C2F-C2G-C2H
2	A	904	PC1	C2E-C2F-C2G-C2H
2	A	902	PC1	C28-C29-C2A-C2B
2	D	903	PC1	C2E-C2F-C2G-C2H
2	A	901	PC1	C26-C27-C28-C29
2	C	904	PC1	C22-C23-C24-C25
2	B	903	PC1	C29-C2A-C2B-C2C
2	C	901	PC1	C1-C2-C3-O31
2	B	903	PC1	C2E-C2F-C2G-C2H
2	C	901	PC1	C3-C2-O21-C21
2	B	903	PC1	C21-C22-C23-C24
2	A	901	PC1	C2E-C2F-C2G-C2H
2	C	901	PC1	C25-C26-C27-C28
2	D	902	PC1	C2A-C2B-C2C-C2D
2	C	904	PC1	C23-C24-C25-C26
2	D	903	PC1	C28-C29-C2A-C2B

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Mol	Chain	Res	Type	Atoms
2	D	901	PC1	C2C-C2D-C2E-C2F
2	A	902	PC1	C27-C28-C29-C2A
2	C	902	PC1	C2E-C2F-C2G-C2H
2	D	903	PC1	C2A-C2B-C2C-C2D
2	A	901	PC1	C24-C25-C26-C27
2	C	901	PC1	C1-O11-P-O13
2	B	903	PC1	C2A-C2B-C2C-C2D
2	C	901	PC1	C1-C2-O21-C21
2	B	902	PC1	C2A-C2B-C2C-C2D
2	C	901	PC1	C2-C1-O11-P
2	B	901	PC1	C24-C25-C26-C27

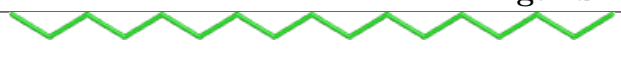
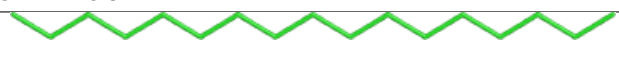
There are no ring outliers.

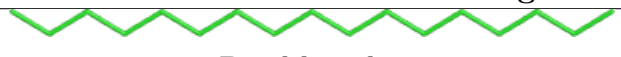
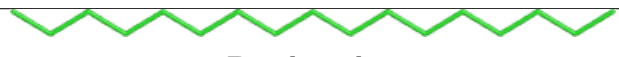
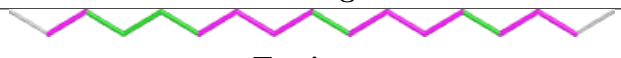
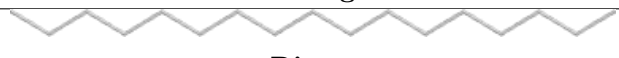
14 monomers are involved in 114 short contacts:

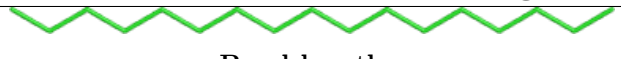
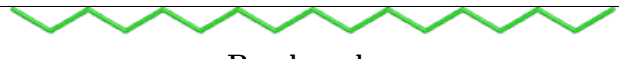
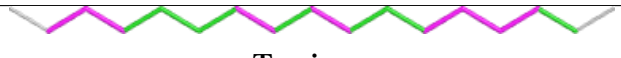
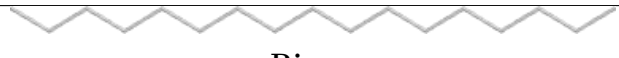
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	901	PC1	5	0
2	B	903	PC1	2	0
2	C	902	PC1	5	0
2	C	903	PC1	10	0
2	B	901	PC1	13	0
2	C	904	PC1	4	0
2	A	903	PC1	16	0
2	A	904	PC1	3	0
2	D	903	PC1	6	0
2	B	902	PC1	12	0
2	A	901	PC1	3	0
2	A	902	PC1	12	0
2	D	902	PC1	9	0
2	C	901	PC1	17	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient

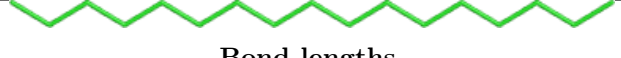
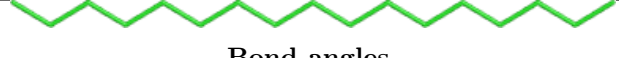
equivalents in the CSD to analyse the geometry.

Ligand PC1 D 901			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

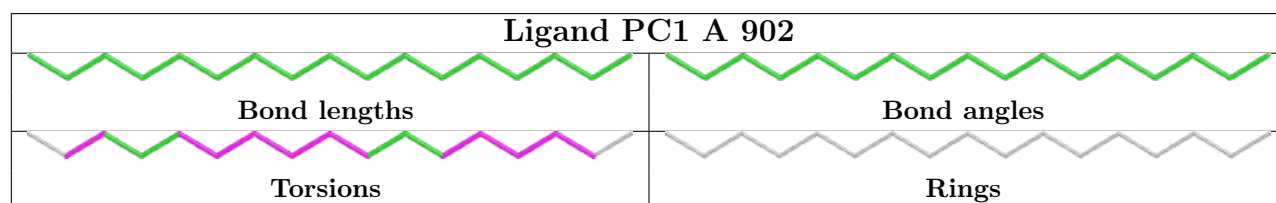
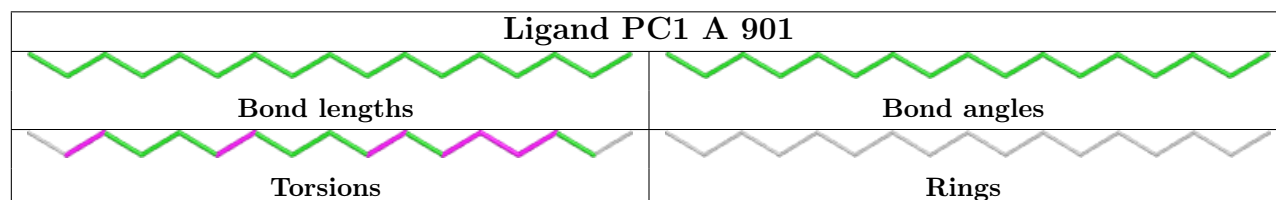
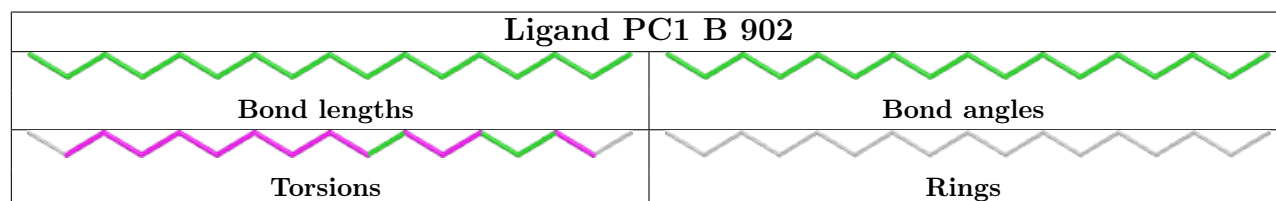
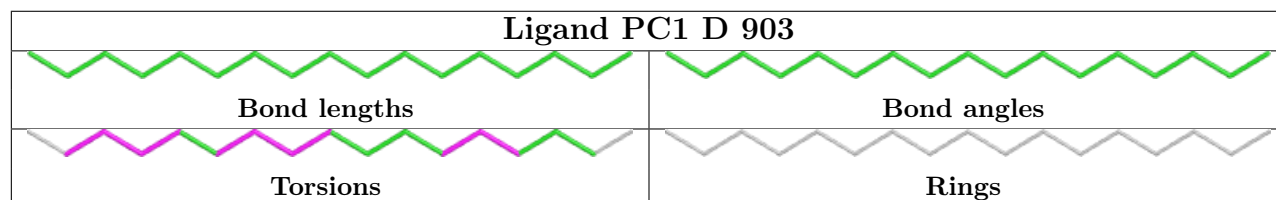
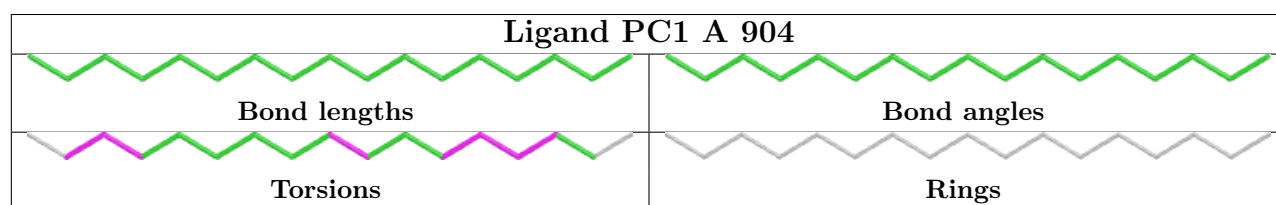
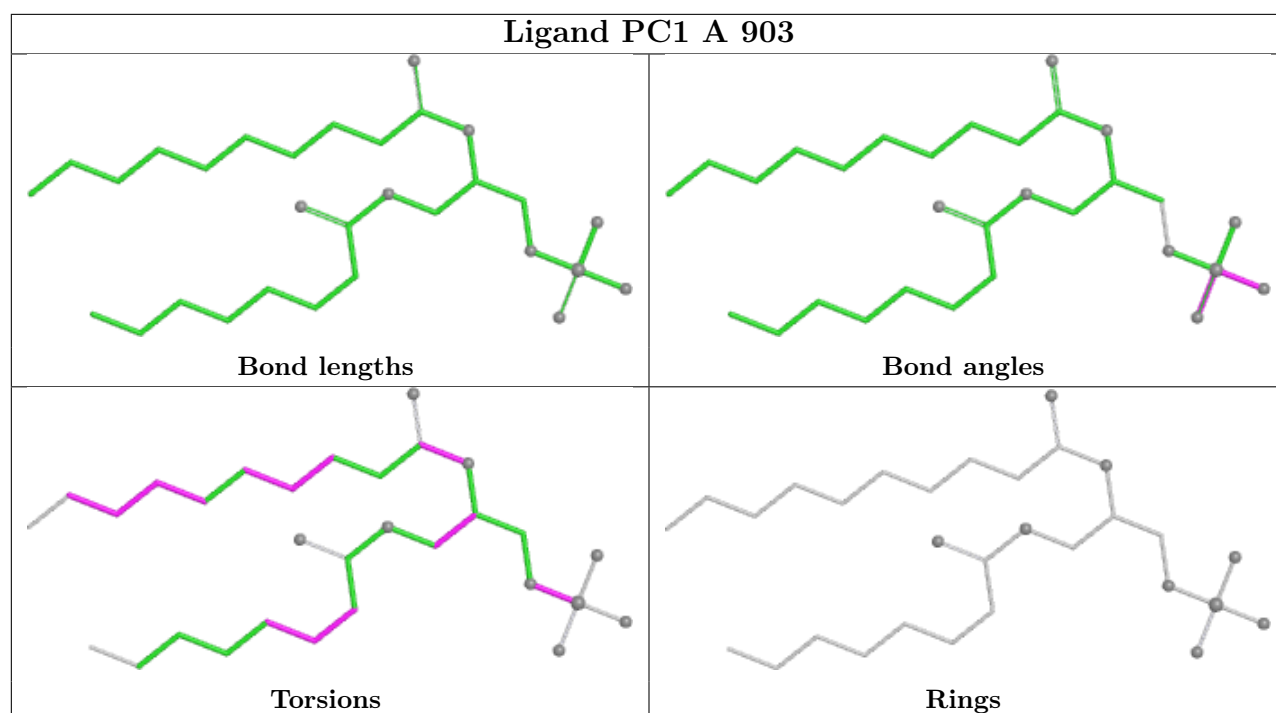
Ligand PC1 B 903			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

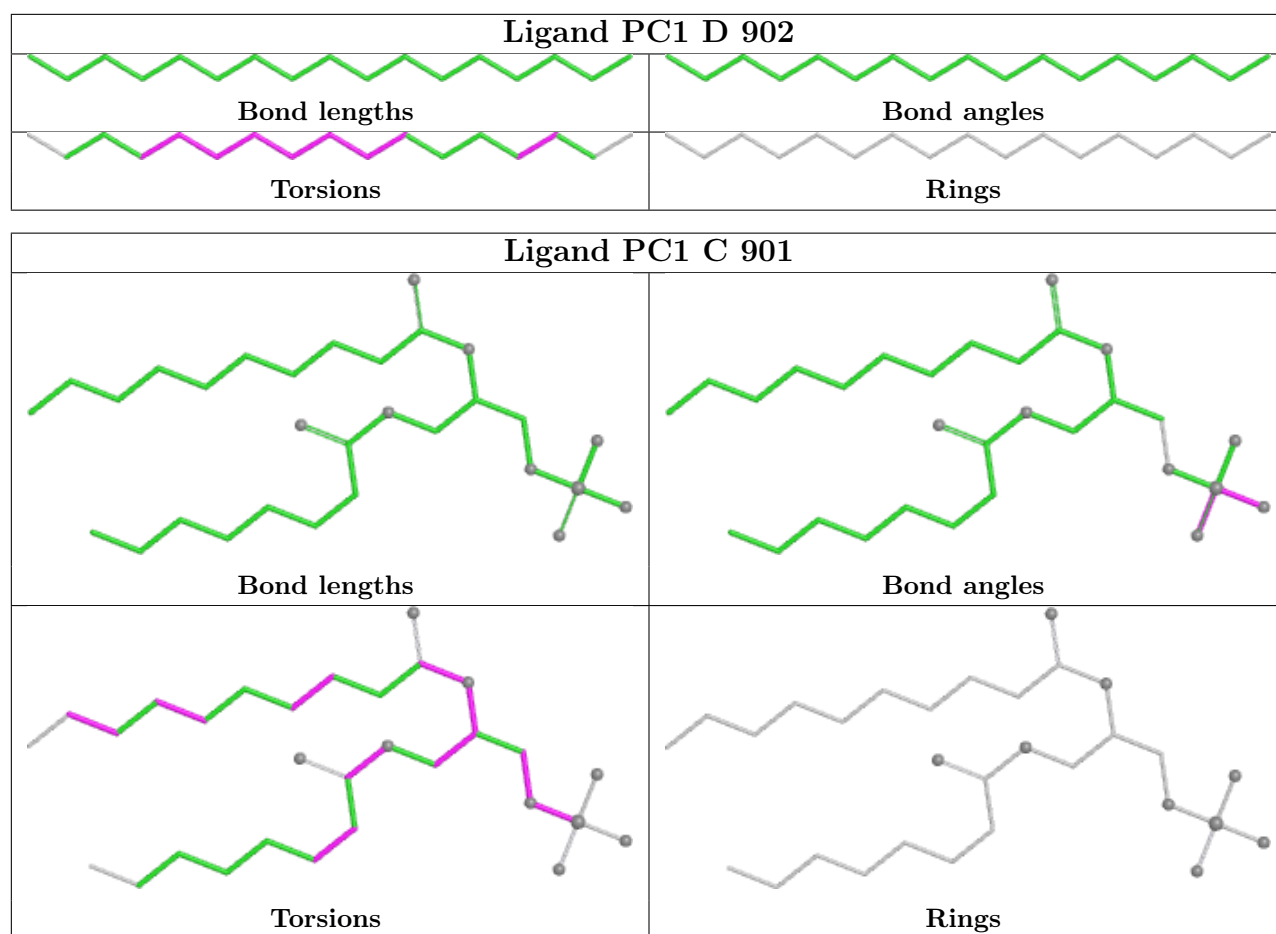
Ligand PC1 C 902			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

Ligand PC1 C 903			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

Ligand PC1 B 901			
 Bond lengths		 Bond angles	
 Torsions		 Rings	

Ligand PC1 C 904			
 Bond lengths		 Bond angles	
 Torsions		 Rings	





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

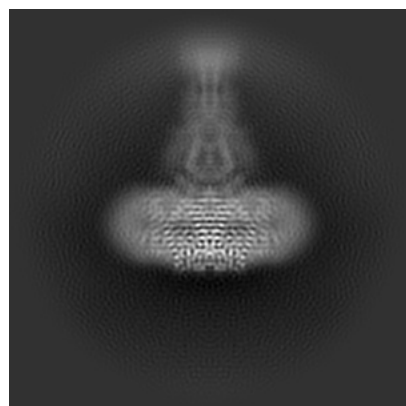
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37855. These allow visual inspection of the internal detail of the map and identification of artifacts.

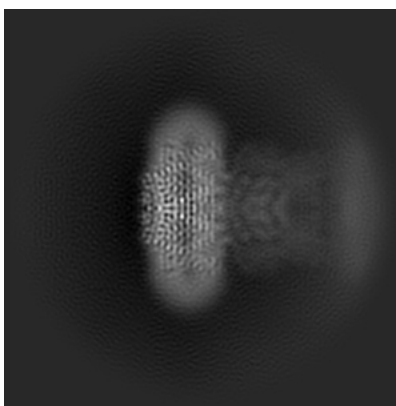
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

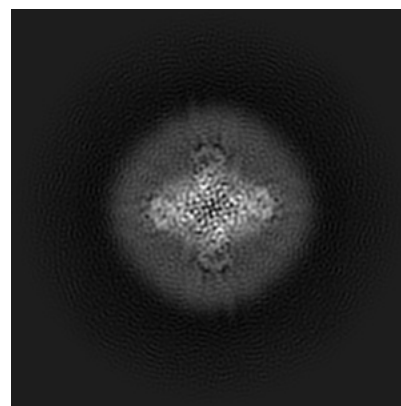
6.1.1 Primary map



X

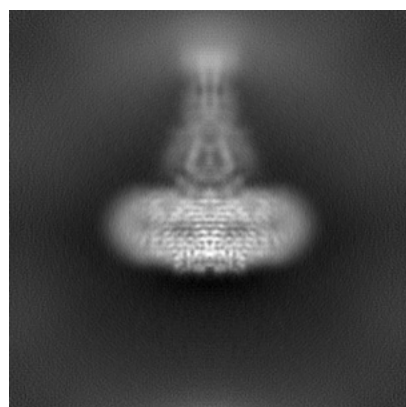


Y

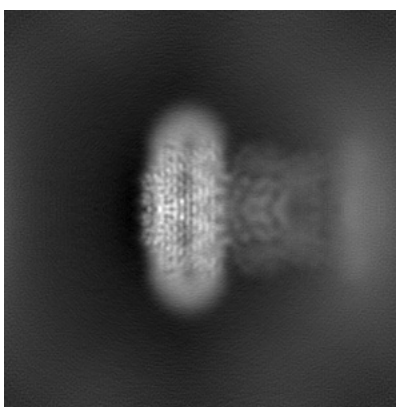


Z

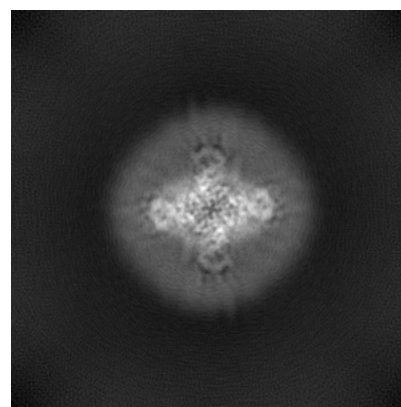
6.1.2 Raw map



X



Y

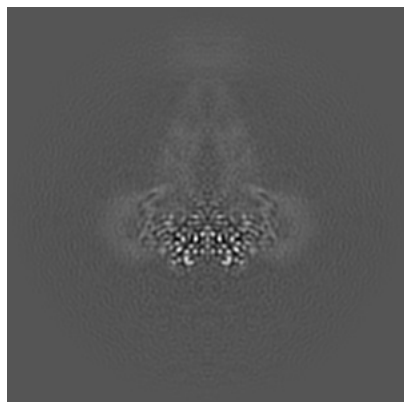


Z

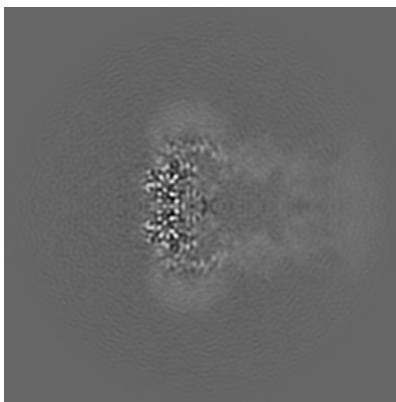
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

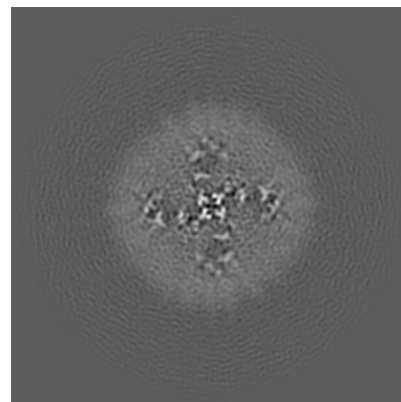
6.2.1 Primary map



X Index: 140

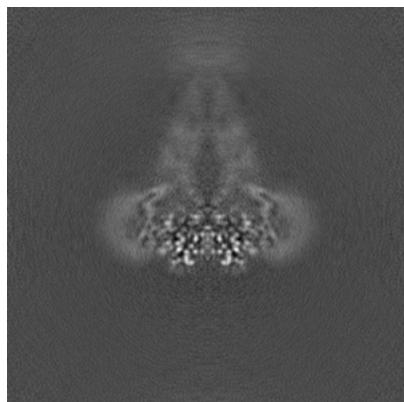


Y Index: 140

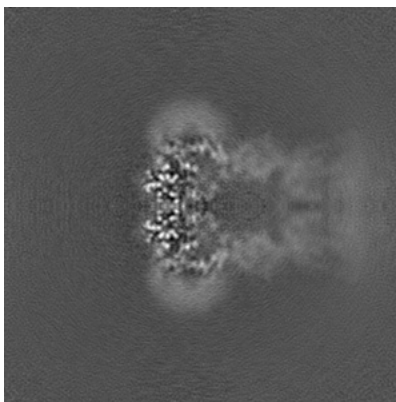


Z Index: 140

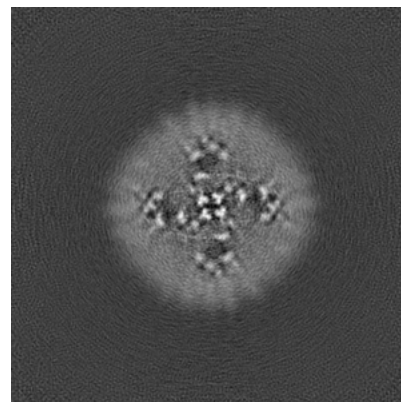
6.2.2 Raw map



X Index: 140



Y Index: 140

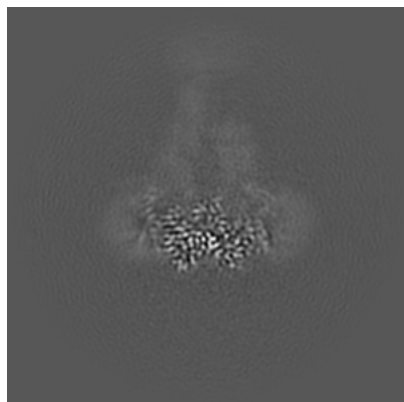


Z Index: 140

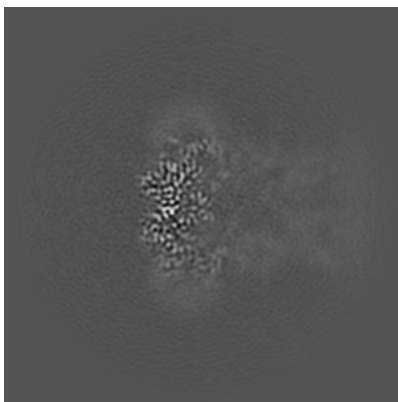
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

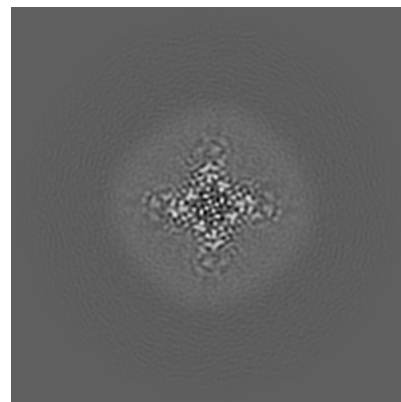
6.3.1 Primary map



X Index: 143

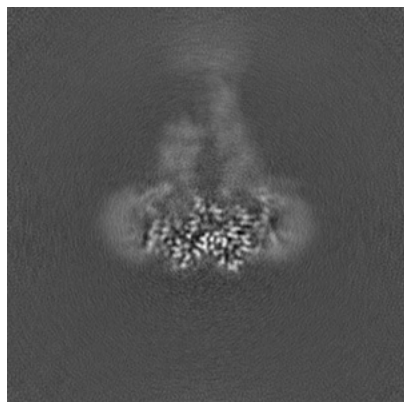


Y Index: 143

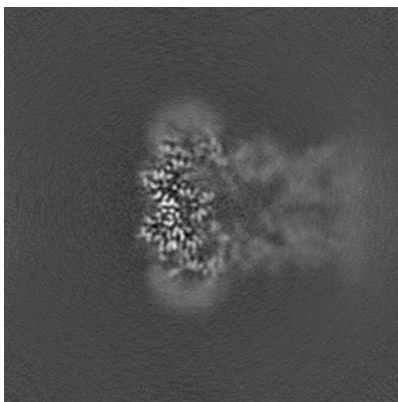


Z Index: 115

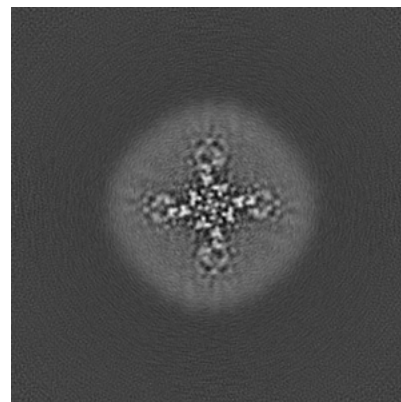
6.3.2 Raw map



X Index: 137



Y Index: 137

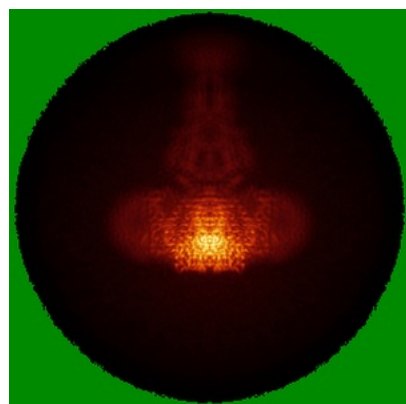


Z Index: 119

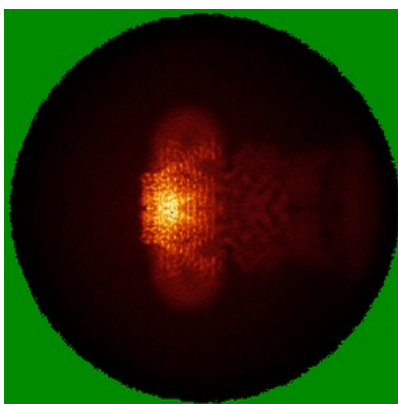
The images above show the largest variance slices of the map in three orthogonal directions.

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

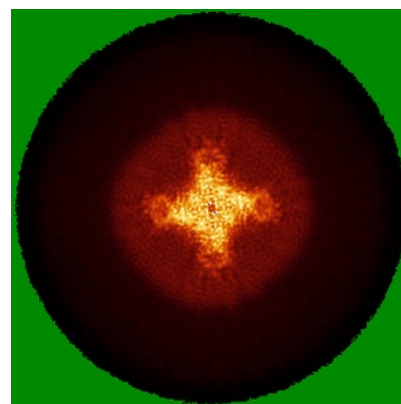
6.4.1 Primary map



X

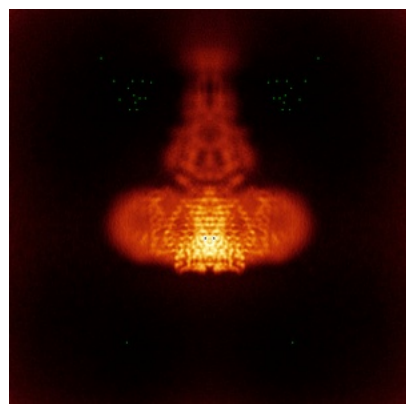


Y

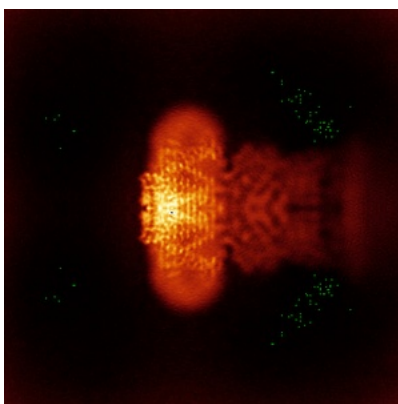


Z

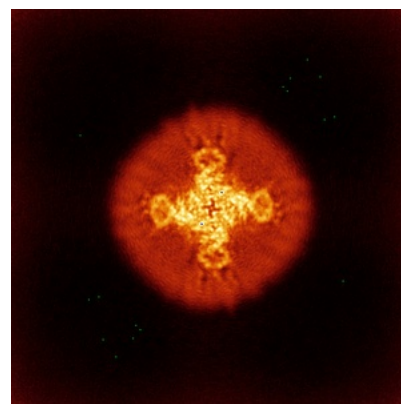
6.4.2 Raw map



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 0.184. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

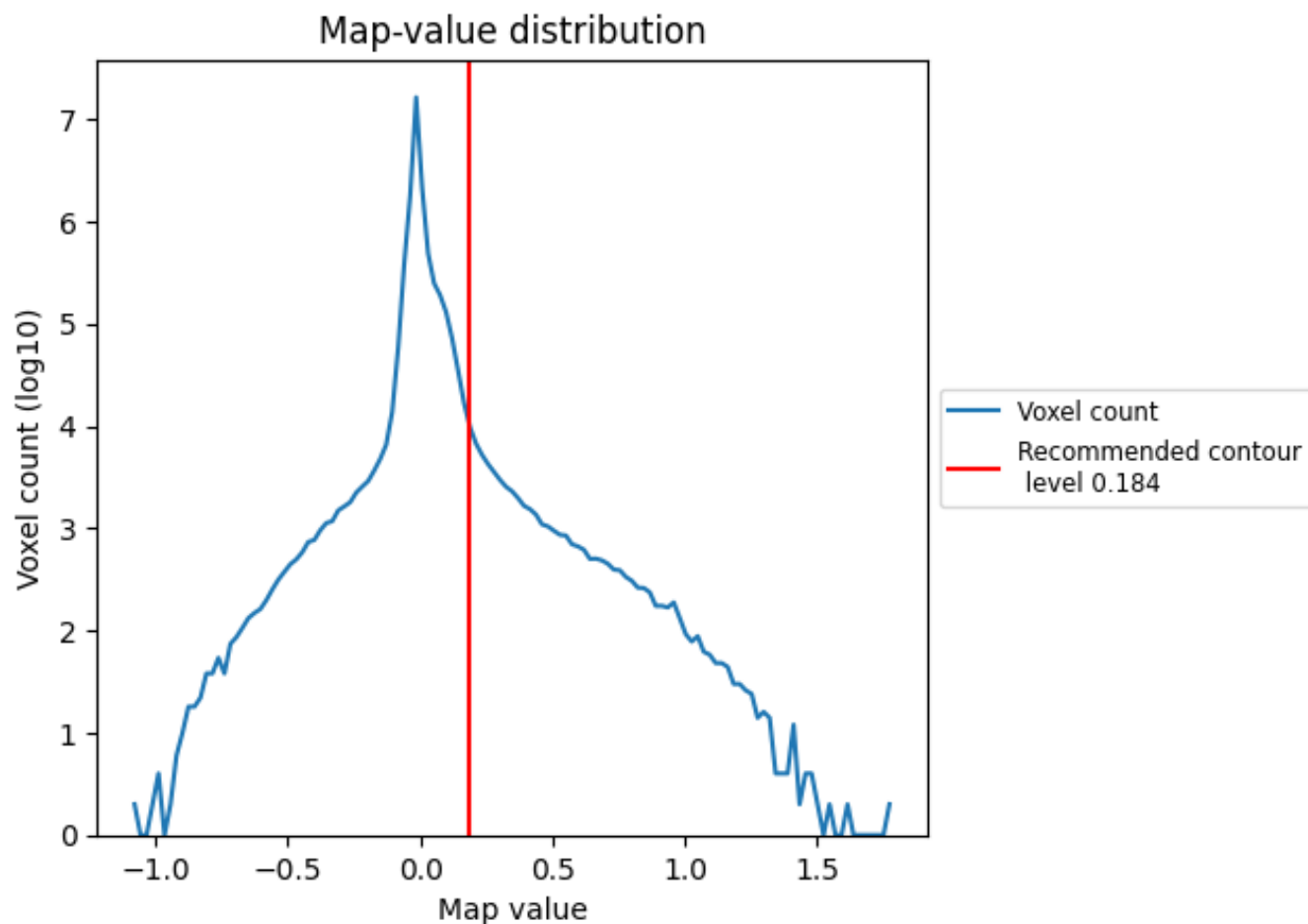
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

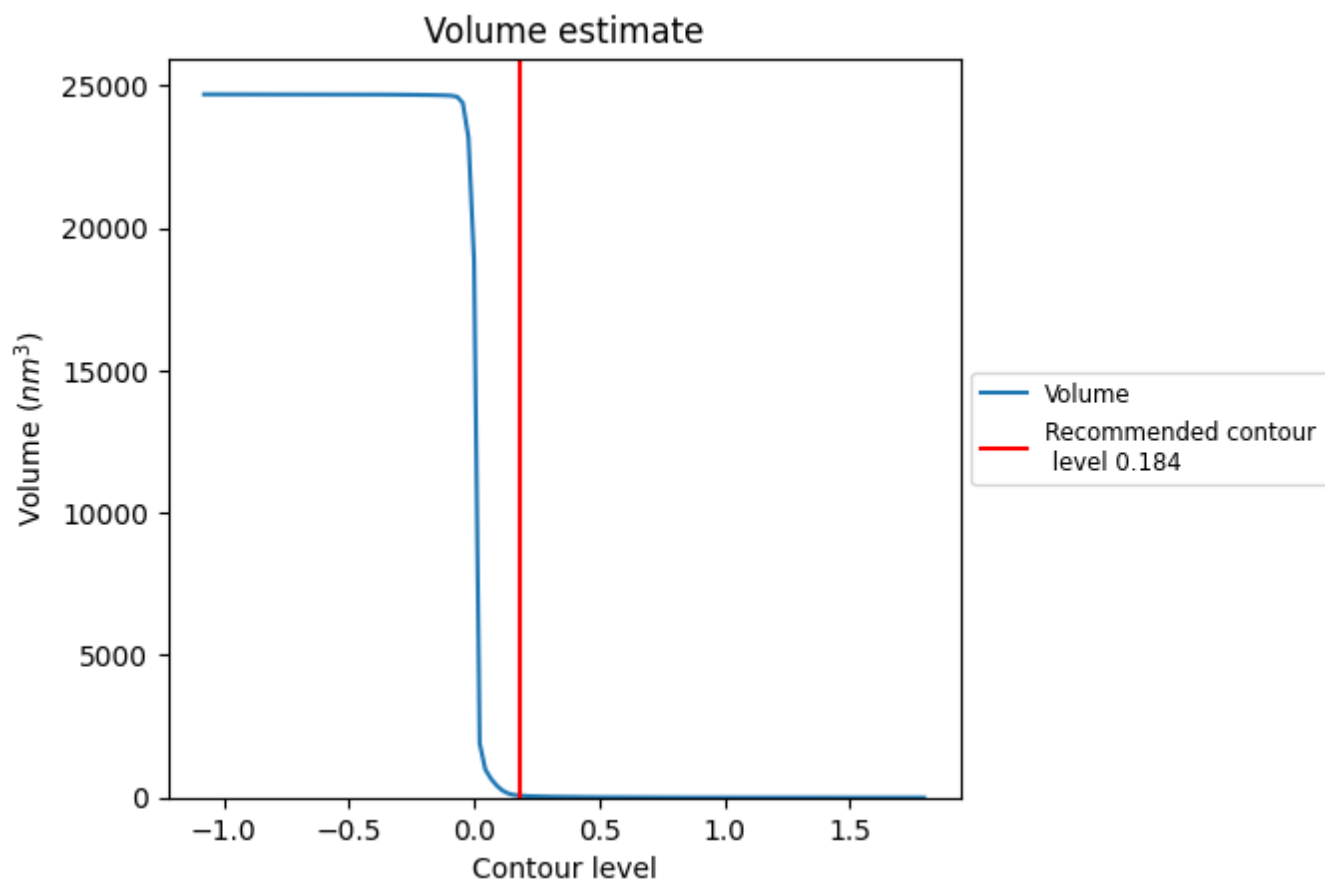
This section contains the results of statistical analysis of the map.

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.

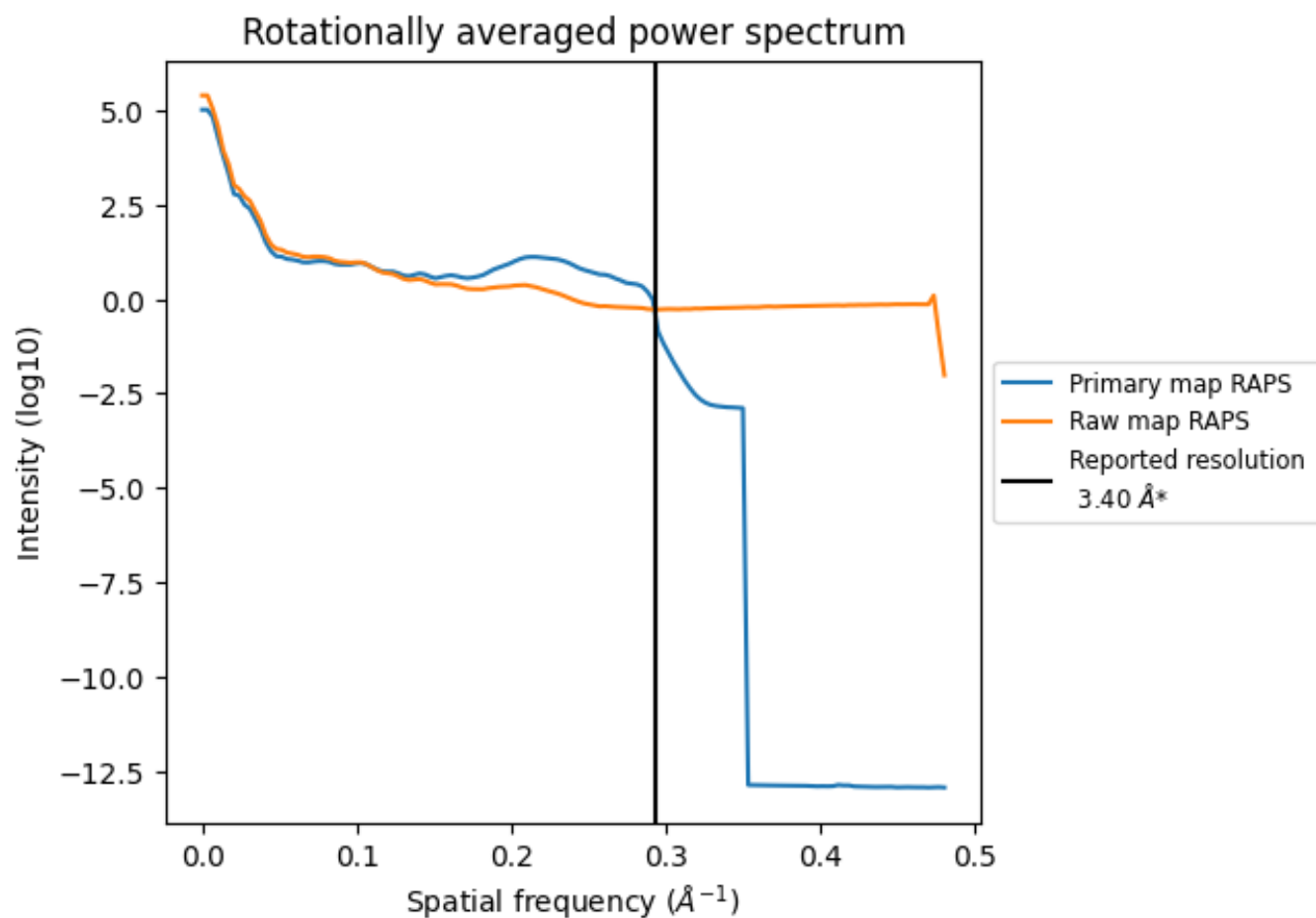
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 67 nm³; this corresponds to an approximate mass of 60 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 ⓘ

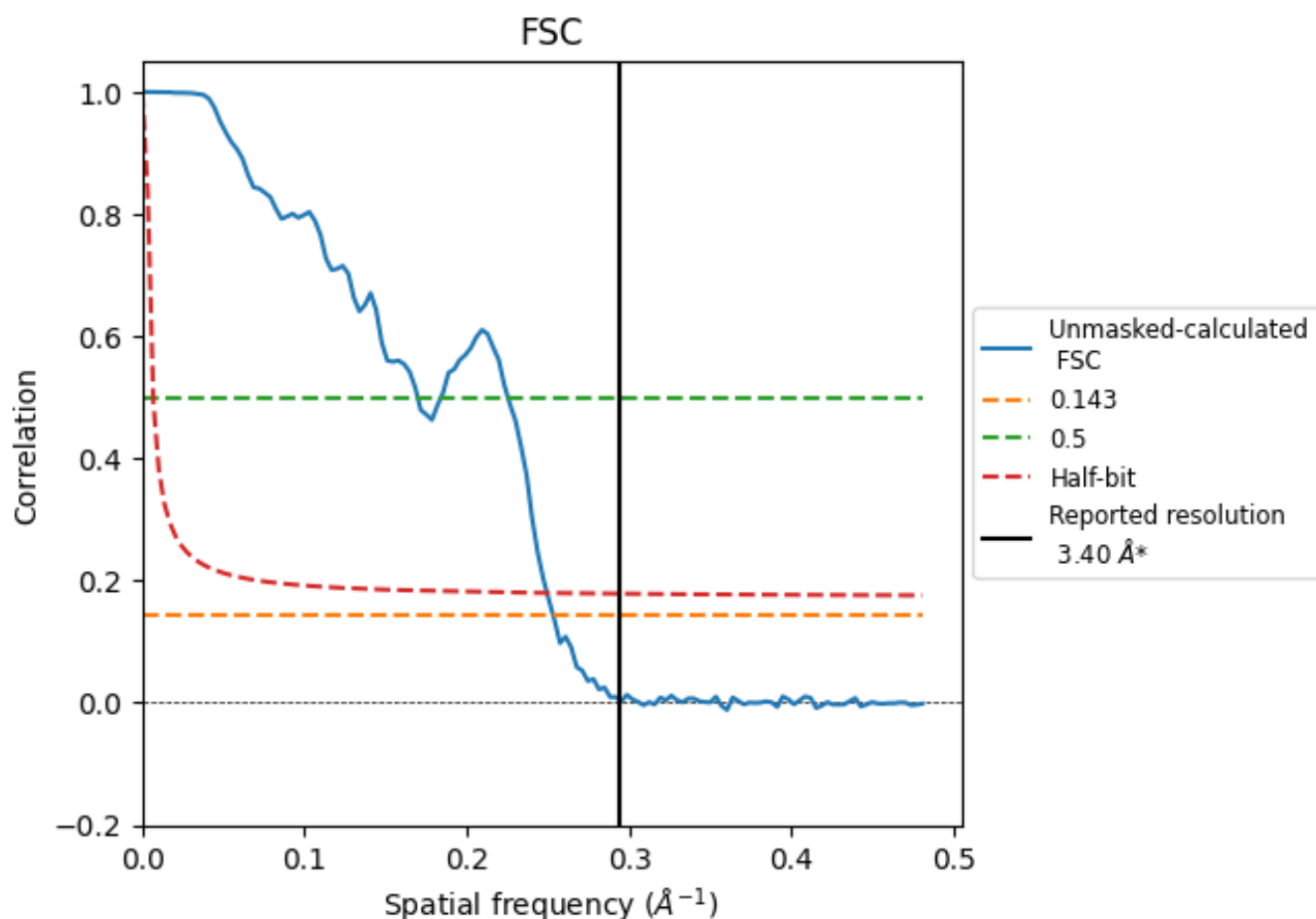


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

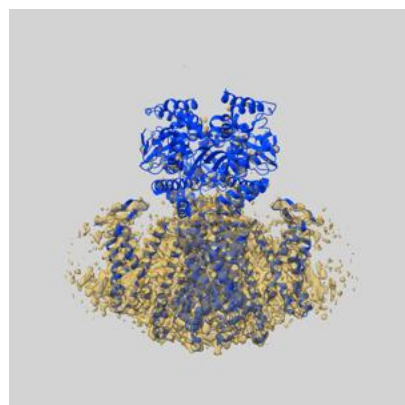
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.95	5.89	4.01

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.95 differs from the reported value 3.4 by more than 10 %

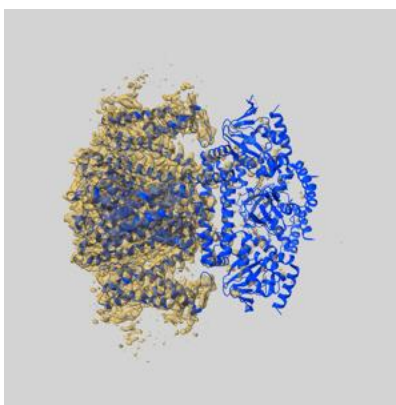
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-37855 and PDB model 8WUI. Per-residue inclusion information can be found in section 3 on page 6.

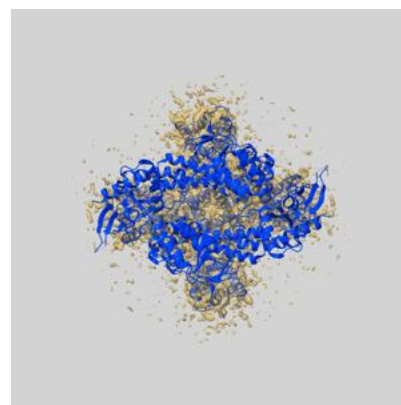
9.1 Map-model overlay [i](#)



X



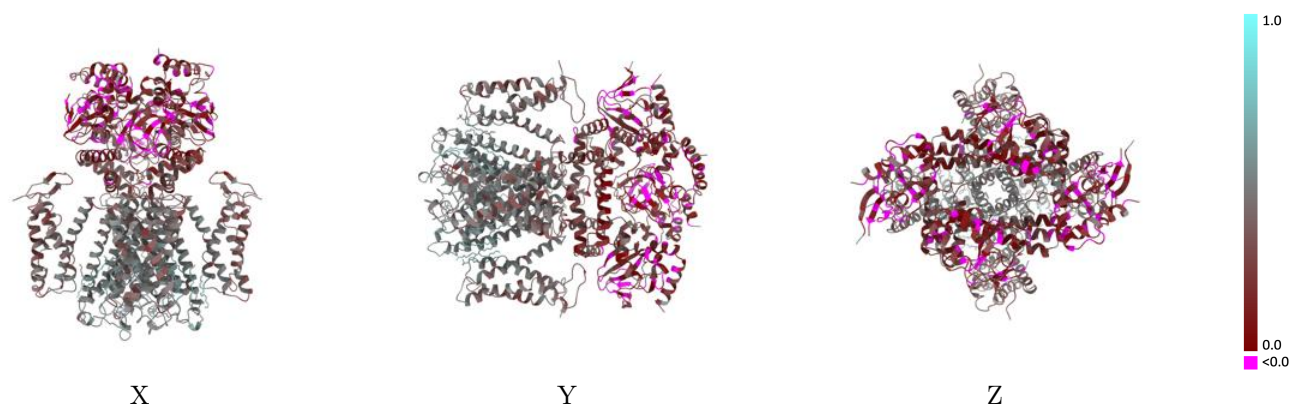
Y



Z

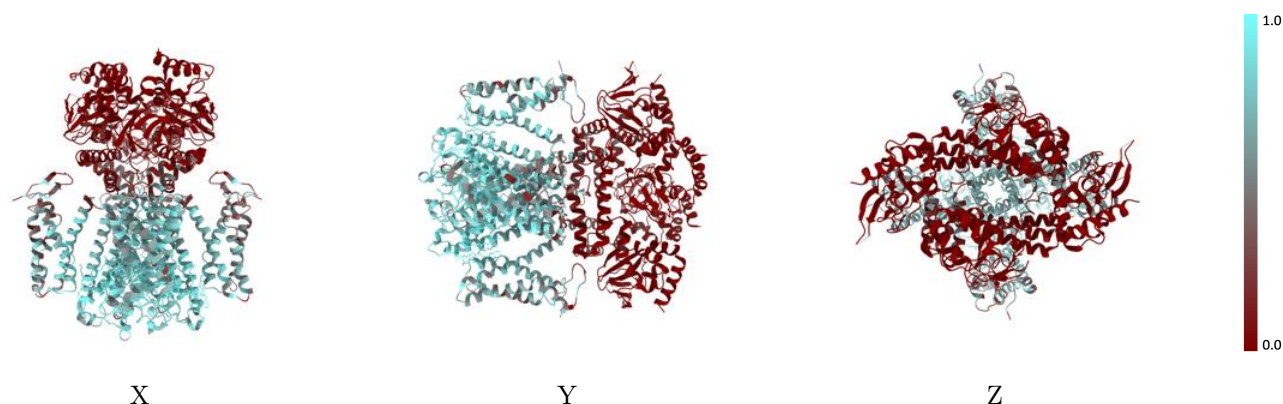
The images above show the 3D surface view of the map at the recommended contour level 0.184 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



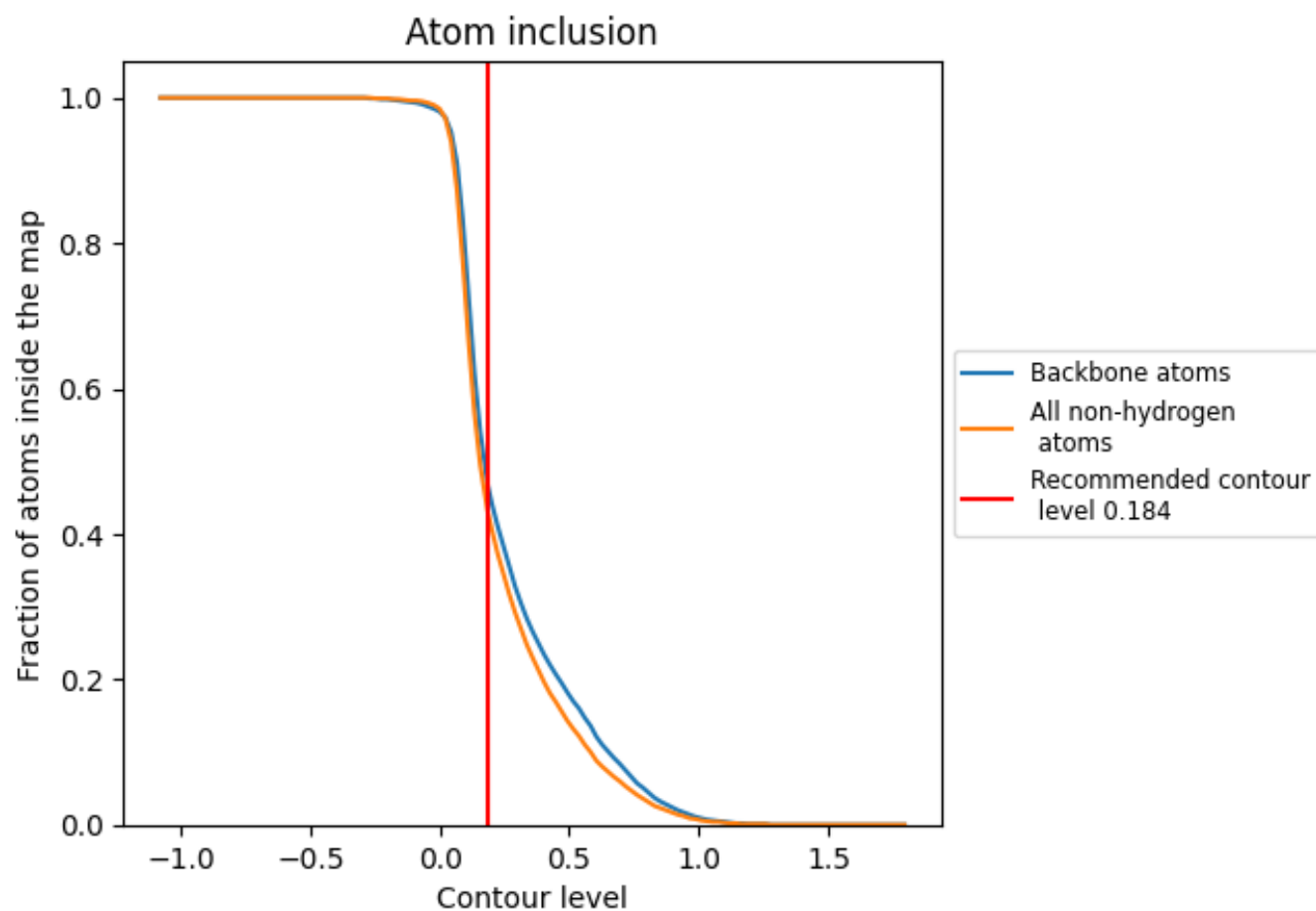
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.184).

9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 43% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.184) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4320	0.3320
A	0.4370	0.3420
B	0.4290	0.3350
C	0.4310	0.3280
D	0.4290	0.3220

