Full wwPDB EM Validation Report

May 26, 2025 – 11:41 PM EDT

PDB ID	:	9DXA / pdb_00009dxa
EMDB ID	:	EMD-47283
Title	:	LRRC8A:D Conformation 2
Authors	:	Lurie, A.; Brohawn, S.G.
Deposited on	:	2024-10-11
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:

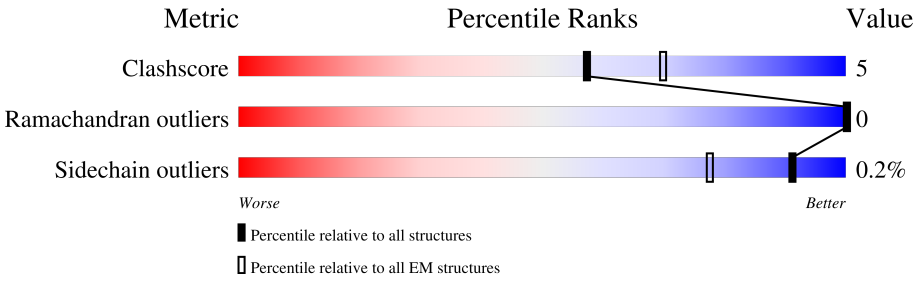
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0rc1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 <=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	911	31% · 65%
1	B	911	30% 5% 65%
1	C	911	31% · 65%
1	D	911	32% · 65%
2	E	868	6% 32% · 64%
2	F	868	5% 30% 6% 64%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 16291 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 Volume-regulated anion channel subunit LRRC8A,Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	315	Total	C	N	O	S	0	0
			2654	1753	426	458	17		
1	B	316	Total	C	N	O	S	0	0
			2658	1755	427	459	17		
1	C	315	Total	C	N	O	S	0	0
			2654	1753	426	458	17		
1	D	316	Total	C	N	O	S	0	0
			2658	1755	427	459	17		

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	68O	TRP	MET	conflict	UNP P0ABE8
A	68Y	ILE	VAL	conflict	UNP P0ABE8
A	72D	ALA	SER	conflict	UNP P0ABE8
A	72F	ILE	HIS	conflict	UNP P0ABE8
A	72G	GLN	LYS	conflict	UNP P0ABE8
A	72J	LEU	-	linker	UNP P0ABE8
A	811	SER	-	expression tag	UNP Q80WG5
A	812	ASN	-	expression tag	UNP Q80WG5
A	813	SER	-	expression tag	UNP Q80WG5
A	814	LEU	-	expression tag	UNP Q80WG5
A	815	GLU	-	expression tag	UNP Q80WG5
A	816	VAL	-	expression tag	UNP Q80WG5
A	817	LEU	-	expression tag	UNP Q80WG5
A	818	PHE	-	expression tag	UNP Q80WG5
A	819	GLN	-	expression tag	UNP Q80WG5
B	68O	TRP	MET	conflict	UNP P0ABE8
B	68Y	ILE	VAL	conflict	UNP P0ABE8
B	72D	ALA	SER	conflict	UNP P0ABE8
B	72F	ILE	HIS	conflict	UNP P0ABE8
B	72G	GLN	LYS	conflict	UNP P0ABE8
B	72J	LEU	-	linker	UNP P0ABE8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	811	SER	-	expression tag	UNP Q80WG5
B	812	ASN	-	expression tag	UNP Q80WG5
B	813	SER	-	expression tag	UNP Q80WG5
B	814	LEU	-	expression tag	UNP Q80WG5
B	815	GLU	-	expression tag	UNP Q80WG5
B	816	VAL	-	expression tag	UNP Q80WG5
B	817	LEU	-	expression tag	UNP Q80WG5
B	818	PHE	-	expression tag	UNP Q80WG5
B	819	GLN	-	expression tag	UNP Q80WG5
C	68O	TRP	MET	conflict	UNP P0ABE8
C	68Y	ILE	VAL	conflict	UNP P0ABE8
C	72D	ALA	SER	conflict	UNP P0ABE8
C	72F	ILE	HIS	conflict	UNP P0ABE8
C	72G	GLN	LYS	conflict	UNP P0ABE8
C	72J	LEU	-	linker	UNP P0ABE8
C	811	SER	-	expression tag	UNP Q80WG5
C	812	ASN	-	expression tag	UNP Q80WG5
C	813	SER	-	expression tag	UNP Q80WG5
C	814	LEU	-	expression tag	UNP Q80WG5
C	815	GLU	-	expression tag	UNP Q80WG5
C	816	VAL	-	expression tag	UNP Q80WG5
C	817	LEU	-	expression tag	UNP Q80WG5
C	818	PHE	-	expression tag	UNP Q80WG5
C	819	GLN	-	expression tag	UNP Q80WG5
D	68O	TRP	MET	conflict	UNP P0ABE8
D	68Y	ILE	VAL	conflict	UNP P0ABE8
D	72D	ALA	SER	conflict	UNP P0ABE8
D	72F	ILE	HIS	conflict	UNP P0ABE8
D	72G	GLN	LYS	conflict	UNP P0ABE8
D	72J	LEU	-	linker	UNP P0ABE8
D	811	SER	-	expression tag	UNP Q80WG5
D	812	ASN	-	expression tag	UNP Q80WG5
D	813	SER	-	expression tag	UNP Q80WG5
D	814	LEU	-	expression tag	UNP Q80WG5
D	815	GLU	-	expression tag	UNP Q80WG5
D	816	VAL	-	expression tag	UNP Q80WG5
D	817	LEU	-	expression tag	UNP Q80WG5
D	818	PHE	-	expression tag	UNP Q80WG5
D	819	GLN	-	expression tag	UNP Q80WG5

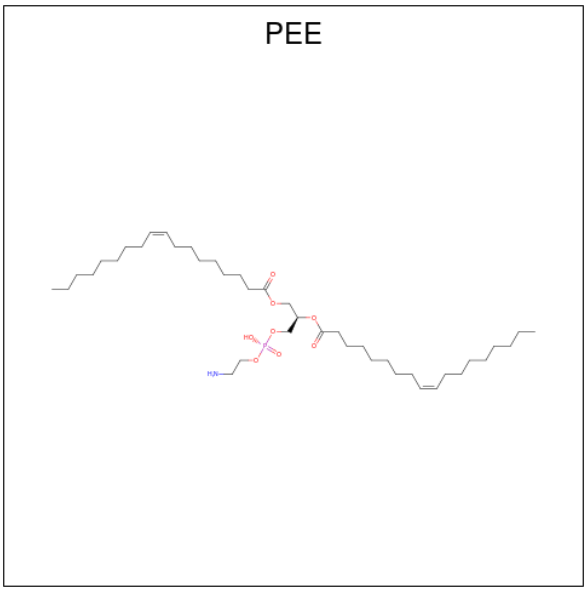
- Molecule 2 is a protein called Volume-regulated anion channel subunit LRRC8D.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	E	309	Total	C	N	O	S	0	0
			2580	1715	402	445	18		
2	F	309	Total	C	N	O	S	0	0
			2580	1715	402	445	18		

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	860	SER	-	expression tag	UNP Q8BGR2
E	861	ASN	-	expression tag	UNP Q8BGR2
E	862	SER	-	expression tag	UNP Q8BGR2
E	863	GLU	-	expression tag	UNP Q8BGR2
E	864	ASN	-	expression tag	UNP Q8BGR2
E	865	LEU	-	expression tag	UNP Q8BGR2
E	866	TYR	-	expression tag	UNP Q8BGR2
E	867	PHE	-	expression tag	UNP Q8BGR2
E	868	GLN	-	expression tag	UNP Q8BGR2
F	860	SER	-	expression tag	UNP Q8BGR2
F	861	ASN	-	expression tag	UNP Q8BGR2
F	862	SER	-	expression tag	UNP Q8BGR2
F	863	GLU	-	expression tag	UNP Q8BGR2
F	864	ASN	-	expression tag	UNP Q8BGR2
F	865	LEU	-	expression tag	UNP Q8BGR2
F	866	TYR	-	expression tag	UNP Q8BGR2
F	867	PHE	-	expression tag	UNP Q8BGR2
F	868	GLN	-	expression tag	UNP Q8BGR2

- Molecule 3 is 1,2-dioleoyl-sn-glycero-3-phosphoethanolamine (CCD ID: PEE) (formula: $C_{41}H_{78}NO_8P$).



Mol	Chain	Residues	Atoms	AltConf
3	A	1	Total C N O P 51 41 1 8 1	0
3	A	1	Total C N O P 39 29 1 8 1	0
3	A	1	Total C O 14 12 2	0
3	A	1	Total C O 13 11 2	0
3	B	1	Total C O 14 12 2	0
3	B	1	Total C O 13 11 2	0
3	B	1	Total C N O P 39 29 1 8 1	0
3	C	1	Total C O 14 12 2	0
3	C	1	Total C O 13 11 2	0
3	C	1	Total C N O P 39 29 1 8 1	0
3	D	1	Total C N O P 51 41 1 8 1	0
3	D	1	Total C O 14 12 2	0
3	D	1	Total C N O P 39 29 1 8 1	0
3	E	1	Total C O 14 12 2	0

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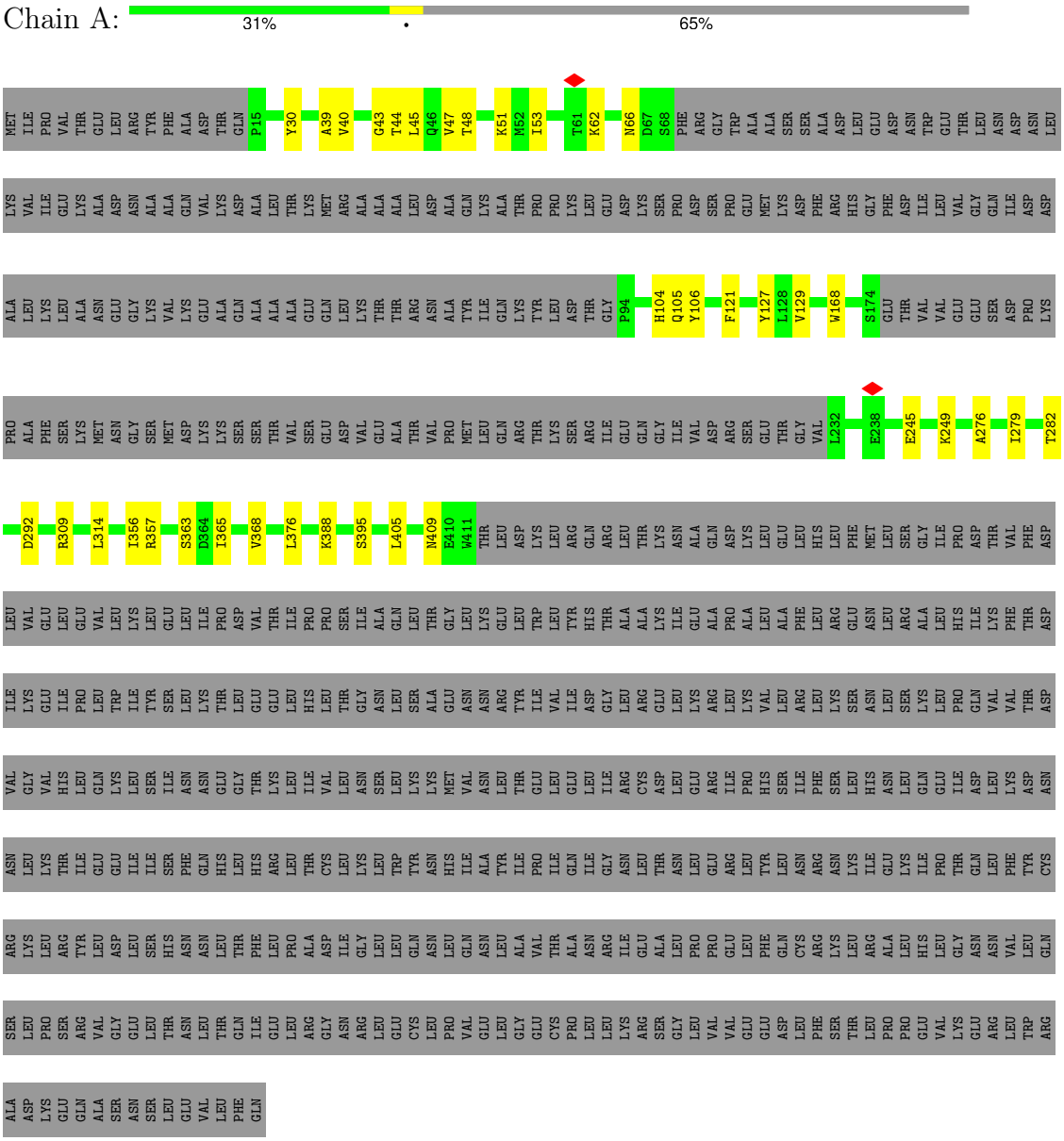
Mol	Chain	Residues	Atoms	AltConf
3	E	1	Total C N O P 39 29 1 8 1	0
3	F	1	Total C N O P 51 41 1 8 1	0
3	F	1	Total C O 11 9 2	0
3	F	1	Total C N O P 39 29 1 8 1	0

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.

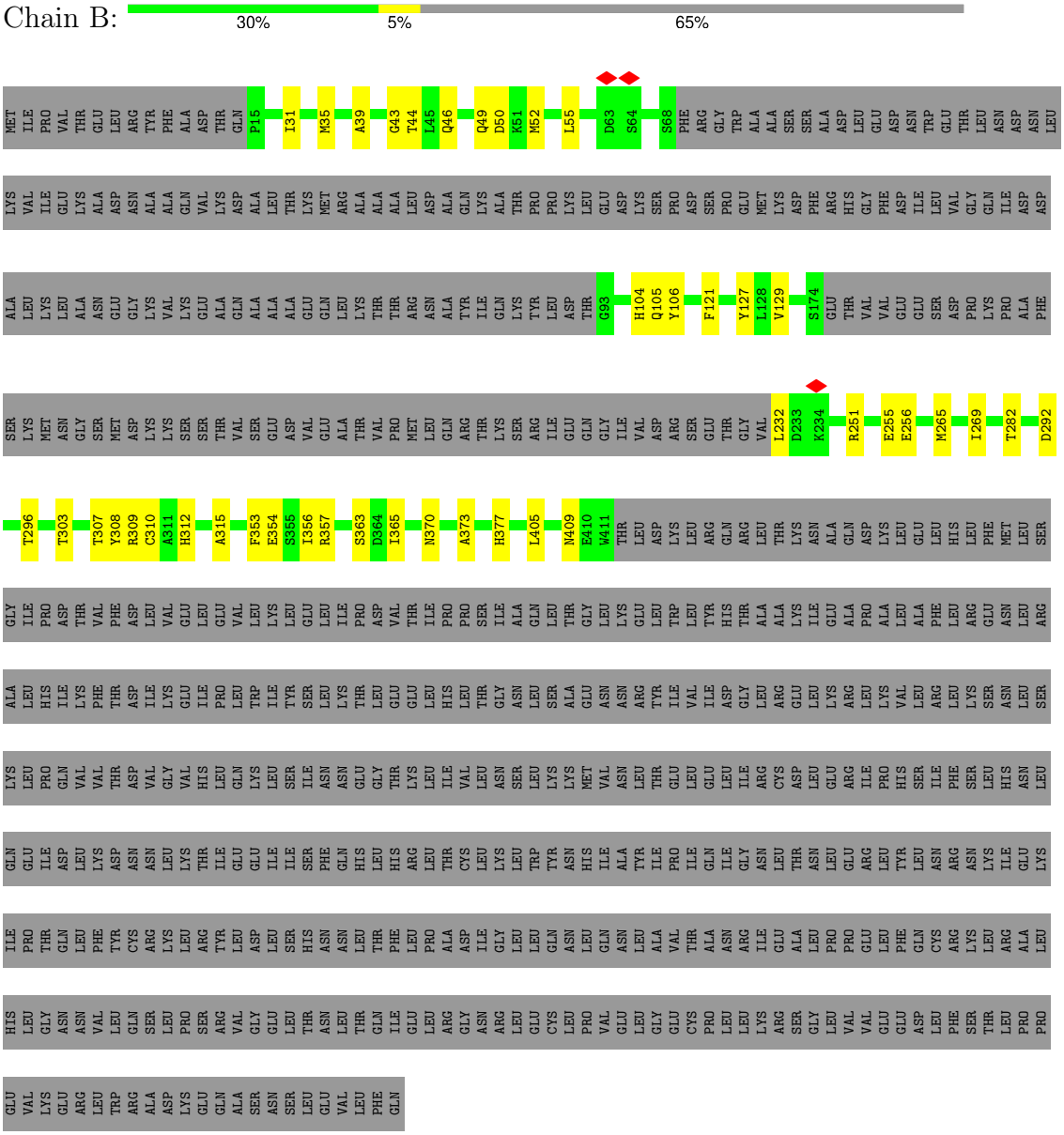
• Molecule 1: Volume-regulated anion channel subunit LRRC8A,Soluble cytochrome b562

Chain A:



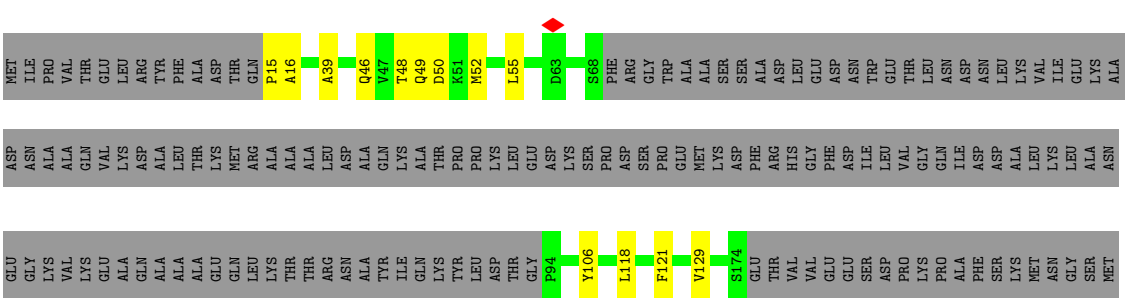
• Molecule 1: Volume-regulated anion channel subunit LRRC8A,Soluble cytochrome b562

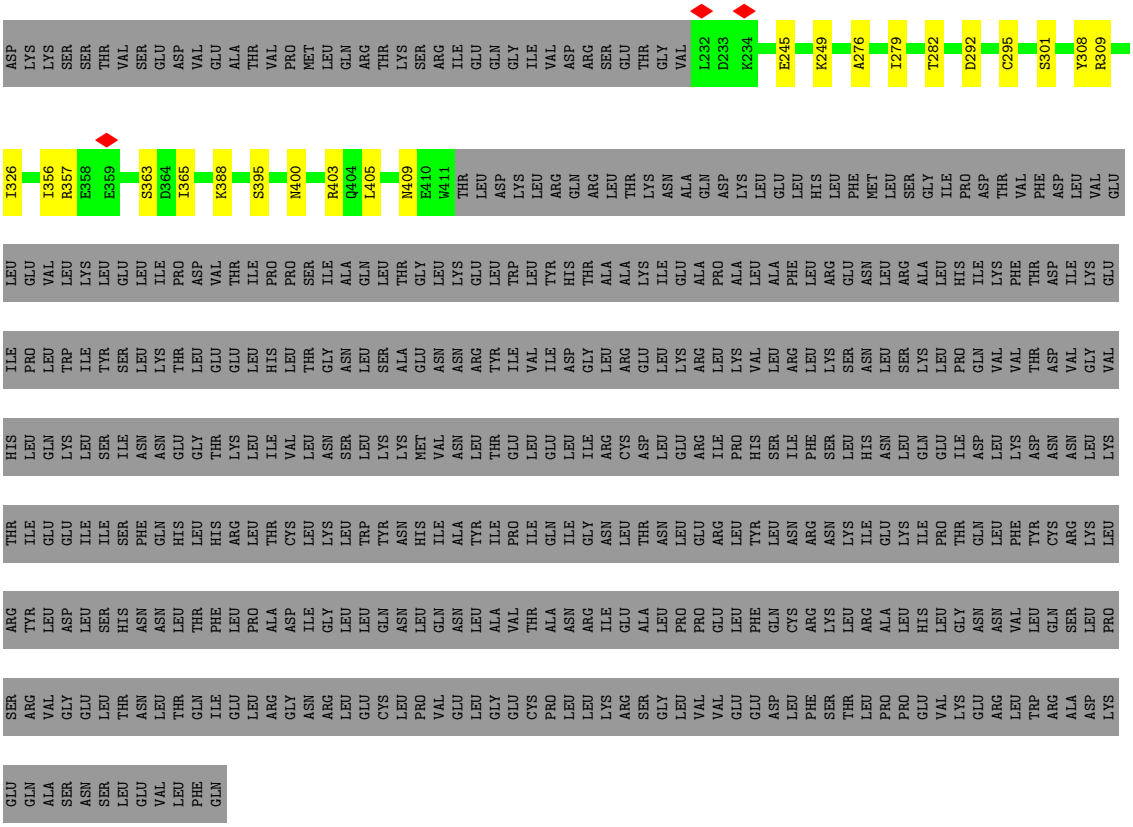
Chain B:



• Molecule 1: Volume-regulated anion channel subunit LRRC8A,Soluble cytochrome b562

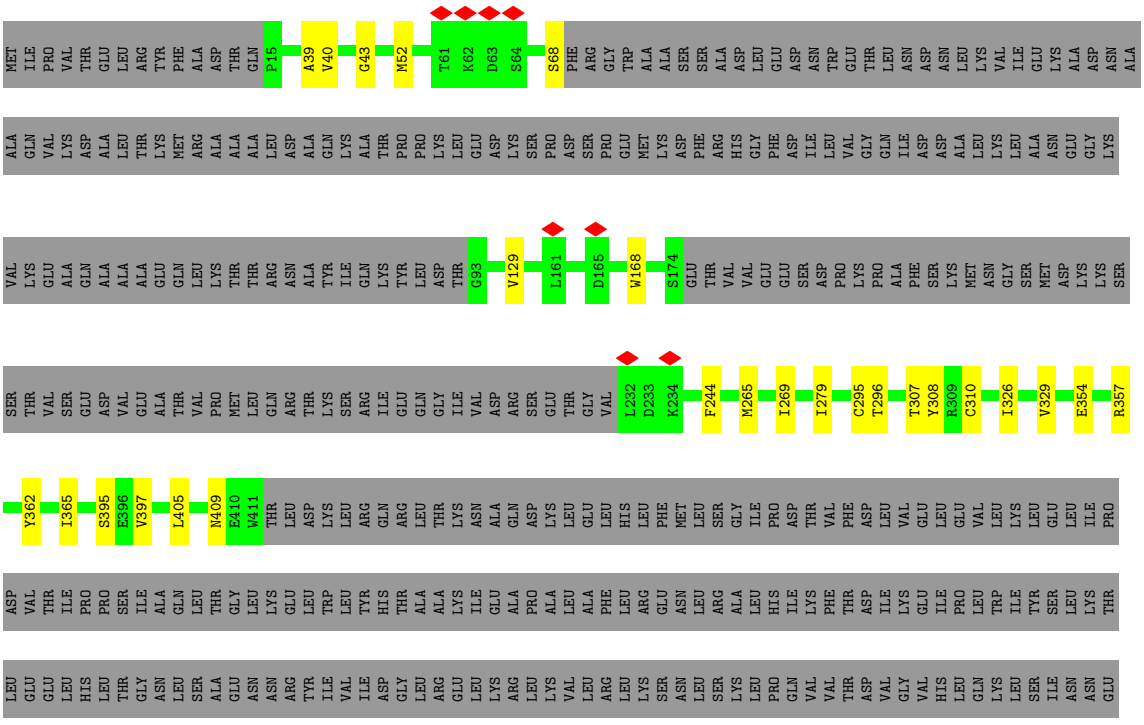
Chain C:

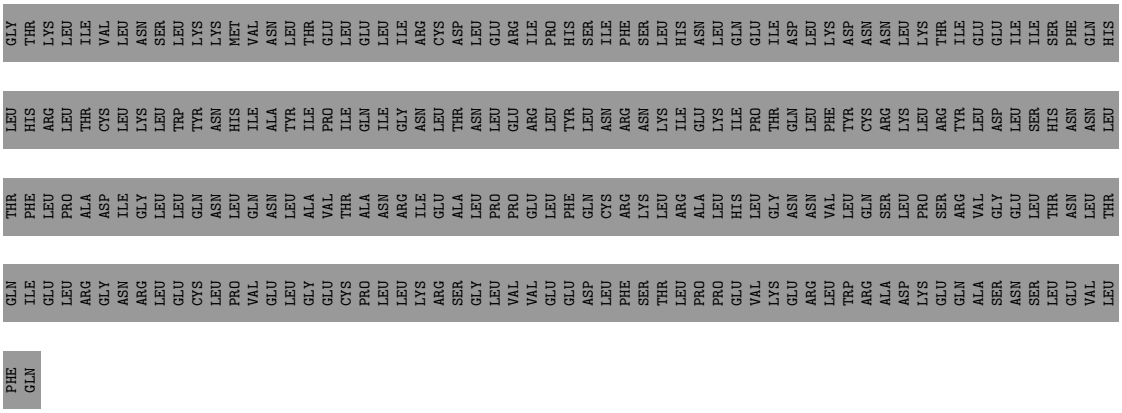




• Molecule 1: Volume-regulated anion channel subunit LRRC8A,Soluble cytochrome b562

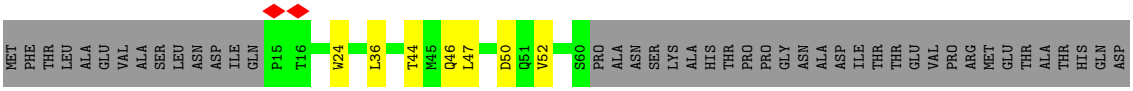
Chain D:

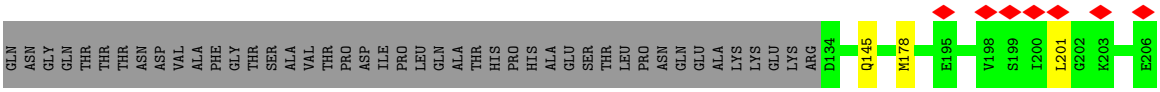


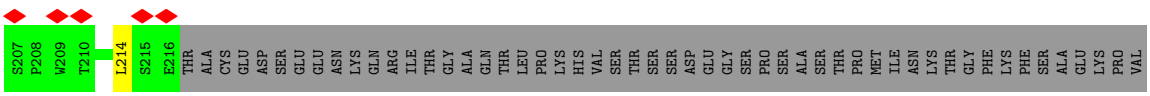


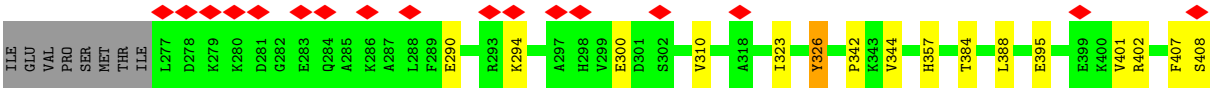
• Molecule 2: Volume-regulated anion channel subunit LRRC8D

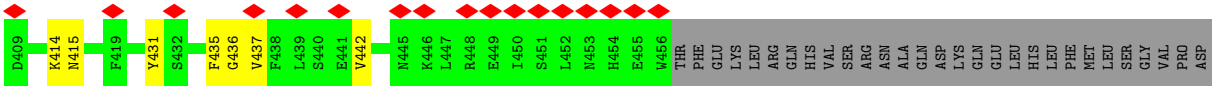
Chain E:

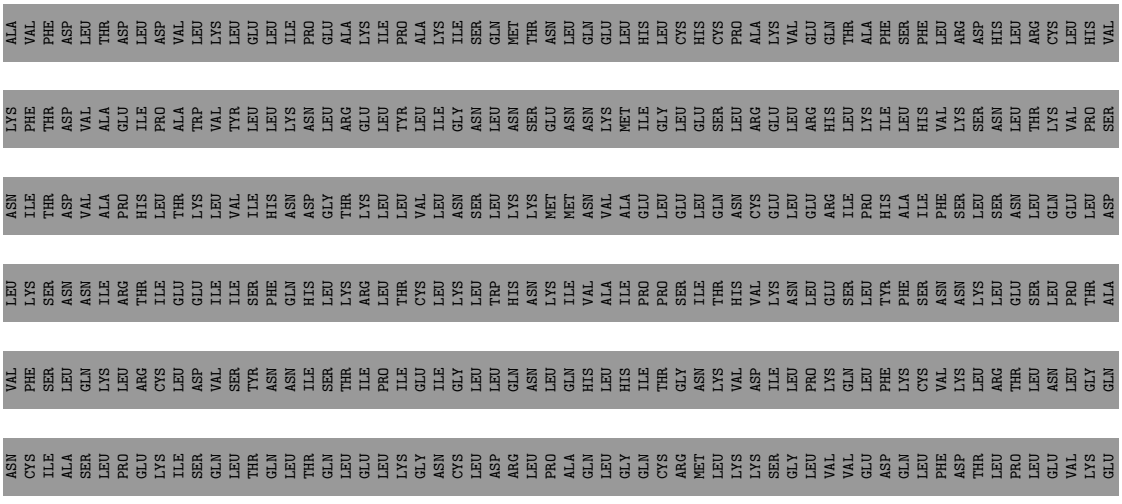






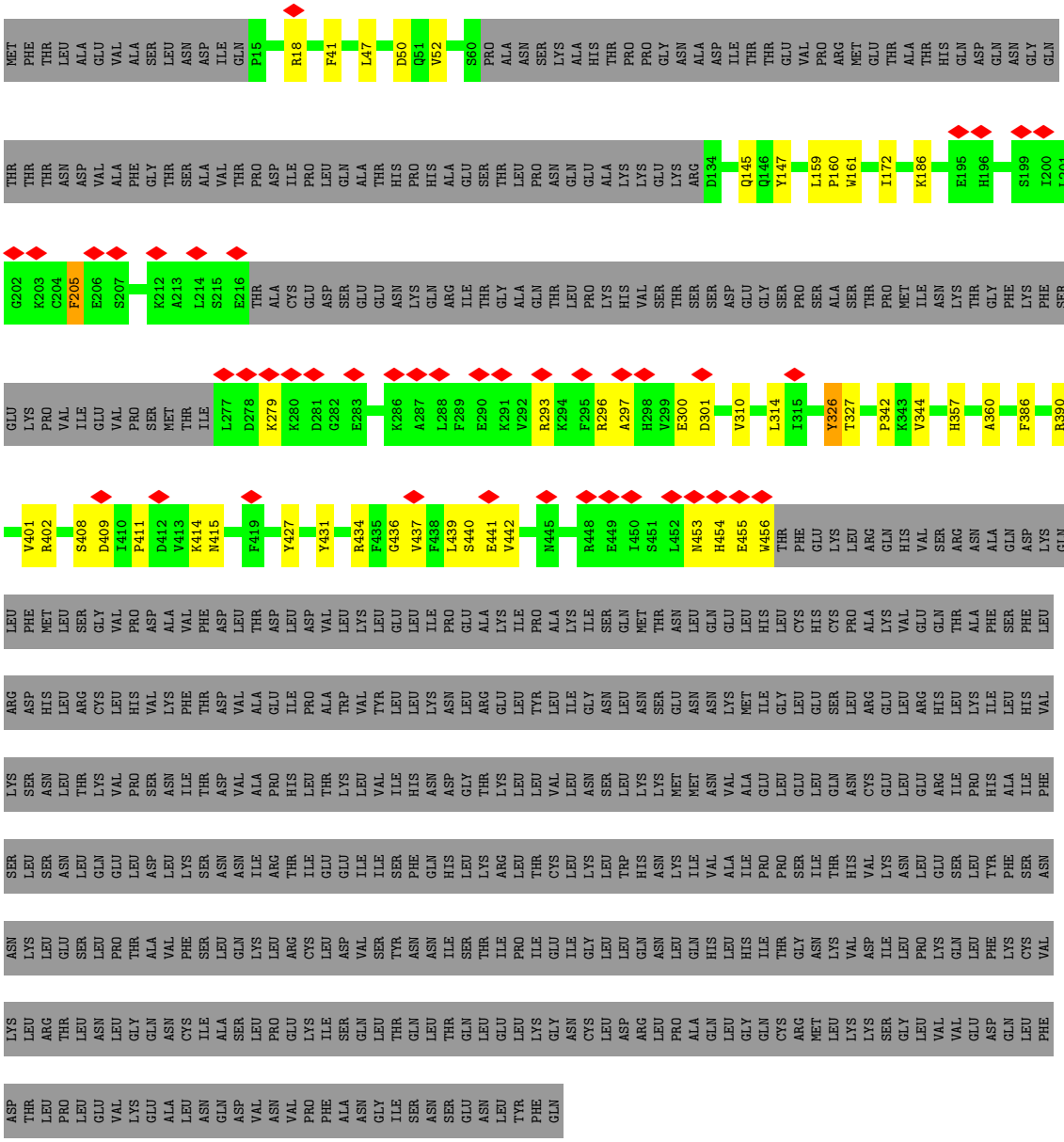






• Molecule 2: Volume-regulated anion channel subunit LRRC8D

Chain F:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46893	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	6000	Depositor
Maximum defocus (nm)	18000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.458	Depositor
Minimum map value	-0.826	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.12	Depositor
Map size (Å)	435.968, 435.968, 435.968	wwPDB
Map dimensions	416, 416, 416	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.048, 1.048, 1.048	Depositor

5 Model quality

5.1 Standard geometry

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

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	0.11	0/2731	0.25	0/3698
1	B	0.14	0/2735	0.25	0/3704
1	C	0.10	0/2731	0.24	0/3698
1	D	0.10	0/2735	0.24	0/3704
2	E	0.11	0/2656	0.23	0/3596
2	F	0.16	0/2656	0.35	0/3596
All	All	0.12	0/16244	0.26	0/21996

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2654	0	2643	26	0
1	B	2658	0	2645	29	0
1	C	2654	0	2643	21	0
1	D	2658	0	2645	18	0
2	E	2580	0	2580	24	0
2	F	2580	0	2580	38	0
3	A	117	0	168	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	66	0	82	2	0
3	C	66	0	90	2	0
3	D	104	0	146	3	0
3	E	53	0	72	0	0
3	F	101	0	144	7	0
All	All	16291	0	16438	150	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 5.

All (150) 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)
2:E:290:GLU:OE2	2:E:294:LYS:HE2	1.75	0.86
2:E:323:ILE:HA	2:E:326:TYR:CD1	2.10	0.85
2:F:439:LEU:O	2:F:439:LEU:HG	1.88	0.72
2:E:323:ILE:HA	2:E:326:TYR:HD1	1.54	0.69
2:E:323:ILE:HA	2:E:326:TYR:CE1	2.29	0.67
2:F:205:PHE:CD2	2:F:205:PHE:C	2.74	0.66
1:D:43:GLY:HA3	3:D:901:PEE:H81	1.77	0.65
1:A:47:VAL:O	1:B:49:GLN:NE2	2.30	0.65
1:C:48:THR:HG23	3:D:901:PEE:H14	1.80	0.64
2:F:402:ARG:NH1	2:F:408:SER:O	2.31	0.63
1:B:251:ARG:O	1:B:255:GLU:HB2	1.99	0.63
2:F:386:PHE:CE1	2:F:390:ARG:NH1	2.67	0.63
2:F:172:ILE:HD11	3:F:903:PEE:H27	1.80	0.62
1:C:292:ASP:HB2	1:C:309:ARG:HE	1.65	0.61
2:E:342:PRO:HG2	2:E:344:VAL:HG22	1.83	0.60
1:A:365:ILE:HG12	1:A:395:SER:HB3	1.83	0.60
1:B:405:LEU:O	1:B:409:ASN:ND2	2.35	0.60
2:E:201:LEU:HD11	2:E:431:TYR:HB3	1.83	0.60
1:B:296:THR:HG23	1:B:307:THR:HG22	1.84	0.59
1:C:365:ILE:HG13	1:C:395:SER:HB3	1.84	0.59
2:F:401:VAL:HG11	2:F:436:GLY:HA3	1.82	0.59
2:E:310:VAL:HG22	2:E:388:LEU:HD21	1.85	0.58
2:F:357:HIS:HB3	2:F:360:ALA:HB2	1.84	0.58
1:B:357:ARG:HB2	1:B:363:SER:HA	1.85	0.58
2:F:205:PHE:CD1	2:F:431:TYR:HA	2.39	0.57
1:C:405:LEU:O	1:C:409:ASN:ND2	2.37	0.57
1:D:40:VAL:HA	3:D:901:PEE:H79	1.85	0.57
1:A:405:LEU:O	1:A:409:ASN:ND2	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:VAL:HG21	1:A:376:LEU:HD12	1.87	0.56
1:B:292:ASP:OD2	1:B:309:ARG:NH2	2.38	0.56
1:B:373:ALA:O	1:B:377:HIS:ND1	2.38	0.56
1:D:405:LEU:O	1:D:409:ASN:ND2	2.39	0.56
2:F:296:ARG:HH21	2:F:297:ALA:HB2	1.71	0.56
2:E:47:LEU:HD11	2:F:41:PHE:HE1	1.71	0.56
2:F:47:LEU:HD12	3:F:901:PEE:H34	1.89	0.55
1:A:62:LYS:HG2	1:A:66:ASN:HB2	1.88	0.55
1:D:326:ILE:HA	1:D:329:VAL:HG12	1.88	0.55
2:F:455:GLU:HG2	2:F:455:GLU:O	2.07	0.55
2:F:50:ASP:OD1	2:F:357:HIS:NE2	2.36	0.55
1:A:48:THR:HG23	3:F:901:PEE:H15	1.87	0.55
1:C:301:SER:HB3	1:D:68:SER:H	1.71	0.55
2:F:411:PRO:HD3	2:F:441:GLU:H	1.72	0.55
1:A:44:THR:HG21	3:F:901:PEE:H38	1.89	0.54
1:A:245:GLU:OE2	1:A:249:LYS:NZ	2.42	0.53
1:A:127:TYR:HB3	3:A:902:PEE:H25	1.91	0.52
2:F:398:PHE:O	2:F:402:ARG:NE	2.41	0.52
1:B:292:ASP:OD1	1:B:292:ASP:N	2.42	0.52
1:C:245:GLU:OE2	1:C:249:LYS:NZ	2.42	0.52
2:F:342:PRO:HG2	2:F:344:VAL:HG22	1.90	0.52
2:F:18:ARG:NH1	2:F:427:TYR:OH	2.43	0.52
1:C:48:THR:HG22	1:C:49:GLN:HG3	1.93	0.51
2:F:436:GLY:O	2:F:440:SER:OG	2.29	0.51
1:D:365:ILE:HG12	1:D:395:SER:HB3	1.93	0.51
3:A:901:PEE:H79	1:B:43:GLY:HA3	1.91	0.51
1:B:357:ARG:NH2	1:B:365:ILE:O	2.43	0.50
1:D:296:THR:HG23	1:D:307:THR:HG22	1.93	0.50
1:A:104:HIS:CD2	1:B:106:TYR:HB3	2.47	0.49
1:A:357:ARG:HB2	1:A:363:SER:HA	1.94	0.49
2:F:205:PHE:HD1	2:F:431:TYR:HA	1.78	0.49
2:F:279:LYS:HB3	2:F:454:HIS:HB2	1.95	0.49
1:B:46:GLN:HA	1:B:50:ASP:HB2	1.94	0.49
2:E:401:VAL:HG11	2:E:436:GLY:HA3	1.94	0.49
2:F:300:GLU:HG3	2:F:414:LYS:H	1.78	0.48
1:A:51:LYS:HE2	1:A:53:ILE:HD11	1.95	0.48
1:A:121:PHE:HZ	1:A:282:THR:HG23	1.78	0.48
1:B:104:HIS:CD2	1:C:106:TYR:HB3	2.49	0.48
1:B:312:HIS:HB3	1:B:315:ALA:HB2	1.96	0.48
1:B:52:MET:HG2	1:B:310:CYS:HB3	1.96	0.48
2:E:290:GLU:O	2:E:294:LYS:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:300:GLU:O	2:E:415:ASN:ND2	2.47	0.47
1:B:265:MET:HE3	1:B:269:ILE:HD11	1.95	0.47
2:F:394:LYS:O	2:F:415:ASN:N	2.47	0.47
1:C:39:ALA:HB2	1:C:129:VAL:HG12	1.96	0.47
2:F:293:ARG:HH21	2:F:296:ARG:HH11	1.61	0.47
2:F:453:ASN:HD22	2:F:456:TRP:NE1	2.13	0.47
1:A:40:VAL:HG22	3:A:901:PEE:H39	1.97	0.47
1:D:326:ILE:O	1:D:329:VAL:HG12	2.13	0.47
2:F:159:LEU:HD12	2:F:160:PRO:HD2	1.97	0.47
1:A:106:TYR:HB3	2:F:145:GLN:HG3	1.96	0.46
2:F:326:TYR:CE1	2:F:327:THR:HG23	2.51	0.46
1:B:127:TYR:HB3	3:B:903:PEE:H26	1.96	0.46
2:E:145:GLN:HG3	2:F:147:TYR:HB3	1.97	0.46
3:A:901:PEE:H24	1:B:44:THR:HG21	1.98	0.46
1:A:292:ASP:OD1	1:A:292:ASP:N	2.44	0.45
1:C:356:ILE:HG23	1:C:388:LYS:HD3	1.98	0.45
2:F:453:ASN:HA	2:F:456:TRP:CD1	2.51	0.45
2:F:409:ASP:HB3	2:F:442:VAL:HG23	1.98	0.45
1:D:39:ALA:HB2	1:D:129:VAL:HG12	1.97	0.45
1:A:30:TYR:OH	2:F:186:LYS:NZ	2.36	0.45
1:B:105:GLN:HA	1:C:55:LEU:HD11	1.99	0.45
2:E:44:THR:HG23	3:F:901:PEE:H73	1.98	0.45
1:B:121:PHE:HZ	1:B:282:THR:HG23	1.82	0.45
1:A:39:ALA:HB2	1:A:129:VAL:HG12	2.00	0.44
1:B:353:PHE:HD2	1:B:356:ILE:HD12	1.83	0.44
1:D:265:MET:HE3	1:D:269:ILE:HD11	1.99	0.44
2:F:310:VAL:O	2:F:314:LEU:HG	2.18	0.44
2:F:434:ARG:HA	2:F:437:VAL:HG22	1.98	0.44
2:E:36:LEU:HD22	2:E:178:MET:HE1	2.00	0.44
2:F:52:VAL:HG12	2:F:357:HIS:HA	2.00	0.44
3:B:903:PEE:H8	3:B:903:PEE:H49	1.72	0.44
1:D:279:ILE:HD12	1:D:279:ILE:HA	1.87	0.44
1:C:121:PHE:HZ	1:C:282:THR:HG23	1.82	0.43
1:C:276:ALA:HA	1:C:279:ILE:HG22	2.00	0.43
2:E:24:TRP:CD1	2:E:384:THR:HG1	2.37	0.43
2:E:395:GLU:HA	2:E:414:LYS:HA	2.00	0.43
3:C:903:PEE:H49	3:C:903:PEE:H8	1.55	0.43
1:D:354:GLU:HA	1:D:357:ARG:HG2	2.01	0.43
2:F:411:PRO:HG3	2:F:441:GLU:HB2	2.00	0.43
1:A:292:ASP:OD2	1:A:309:ARG:NH2	2.44	0.43
1:C:400:ASN:OD1	1:C:403:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:402:ARG:HB2	2:E:408:SER:HA	1.99	0.43
2:E:46:GLN:NE2	2:E:50:ASP:OD2	2.52	0.43
1:A:105:GLN:HA	1:B:55:LEU:HD11	2.00	0.43
1:A:276:ALA:HA	1:A:279:ILE:HG22	2.00	0.43
1:B:31:ILE:HG22	1:B:35:MET:HE2	2.01	0.42
1:C:15:PRO:HB2	1:C:16:ALA:H	1.62	0.42
1:A:356:ILE:HG23	1:A:388:LYS:HD3	2.01	0.42
1:D:357:ARG:NH2	1:D:365:ILE:O	2.51	0.42
1:B:232:LEU:HD22	1:B:405:LEU:HD13	2.02	0.42
2:F:161:TRP:HB3	3:F:903:PEE:H3	2.01	0.42
1:C:52:MET:HE3	1:C:118:LEU:HD22	2.00	0.42
2:E:46:GLN:HA	2:E:50:ASP:HB2	2.00	0.42
1:B:303:THR:OG1	1:B:308:TYR:OH	2.29	0.42
3:F:903:PEE:H7	3:F:903:PEE:H49	1.30	0.42
2:E:214:LEU:HD21	2:E:437:VAL:HG11	2.02	0.42
1:C:276:ALA:O	1:C:279:ILE:HG22	2.19	0.42
2:E:52:VAL:HG12	2:E:357:HIS:HA	2.01	0.42
2:F:279:LYS:HD2	2:F:455:GLU:HB2	2.01	0.42
1:B:39:ALA:HB2	1:B:129:VAL:HG12	2.02	0.41
2:E:323:ILE:CA	2:E:326:TYR:HD1	2.26	0.41
2:F:301:ASP:OD1	2:F:301:ASP:N	2.54	0.41
3:A:901:PEE:H11	1:B:49:GLN:HE21	1.85	0.41
1:B:354:GLU:HA	1:B:357:ARG:HG2	2.01	0.41
1:C:357:ARG:HB2	1:C:363:SER:HA	2.02	0.41
1:D:52:MET:HG2	1:D:310:CYS:HB3	2.01	0.41
2:E:407:PHE:HB3	2:E:442:VAL:HB	2.03	0.41
1:A:43:GLY:HA3	3:A:901:PEE:H33	2.01	0.41
1:A:121:PHE:CZ	1:A:282:THR:HG23	2.55	0.41
1:C:46:GLN:HA	1:C:50:ASP:HB2	2.02	0.41
1:D:168:TRP:NE1	1:D:244:PHE:HE1	2.18	0.41
1:A:168:TRP:HZ3	1:A:405:LEU:HD12	1.85	0.41
1:C:295:CYS:SG	1:C:308:TYR:HB2	2.61	0.41
1:A:45:LEU:HB3	1:A:314:LEU:HD13	2.02	0.41
1:D:295:CYS:SG	1:D:308:TYR:HB2	2.62	0.40
1:B:256:GLU:O	1:B:370:ASN:ND2	2.54	0.40
2:E:323:ILE:O	2:E:326:TYR:CD1	2.74	0.40
3:A:903:PEE:H26	3:A:903:PEE:H32	1.94	0.40
1:D:326:ILE:CA	1:D:329:VAL:HG12	2.52	0.40
1:C:326:ILE:HG21	3:C:902:PEE:H21	2.03	0.40
1:D:362:TYR:HD1	1:D:397:VAL:HB	1.86	0.40

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	309/911 (34%)	298 (96%)	11 (4%)	0	100	100
1	B	310/911 (34%)	302 (97%)	8 (3%)	0	100	100
1	C	309/911 (34%)	301 (97%)	8 (3%)	0	100	100
1	D	310/911 (34%)	304 (98%)	6 (2%)	0	100	100
2	E	303/868 (35%)	297 (98%)	6 (2%)	0	100	100
2	F	303/868 (35%)	297 (98%)	6 (2%)	0	100	100
All	All	1844/5380 (34%)	1799 (98%)	45 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	294/830 (35%)	294 (100%)	0	100	100
1	B	294/830 (35%)	294 (100%)	0	100	100
1	C	294/830 (35%)	294 (100%)	0	100	100
1	D	294/830 (35%)	294 (100%)	0	100	100
2	E	288/798 (36%)	286 (99%)	2 (1%)	81	88
2	F	288/798 (36%)	286 (99%)	2 (1%)	81	88
All	All	1752/4916 (36%)	1748 (100%)	4 (0%)	91	96

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	E	326	TYR
2	E	435	PHE
2	F	205	PHE
2	F	326	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	ASN
1	B	49	GLN
1	B	104	HIS
1	B	288	ASN
1	B	409	ASN
1	C	377	HIS
1	C	409	ASN
1	D	404	GLN
1	D	409	ASN
2	E	46	GLN
2	E	358	ASN
2	F	338	HIS
2	F	445	ASN
2	F	453	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

18 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	$\#\|Z\| > 2$
3	PEE	A	903	-	13,13,50	0.41	0	13,13,55	0.24	0
3	PEE	F	903	-	38,38,50	0.34	0	41,43,55	0.37	0
3	PEE	A	901	-	50,50,50	0.30	0	53,55,55	0.39	0
3	PEE	C	901	-	13,13,50	0.41	0	13,13,55	0.25	0
3	PEE	E	901	-	13,13,50	0.41	0	13,13,55	0.26	0
3	PEE	B	901	-	13,13,50	0.41	0	13,13,55	0.27	0
3	PEE	E	902	-	38,38,50	0.33	0	41,43,55	0.44	0
3	PEE	D	903	-	38,38,50	0.33	0	41,43,55	0.44	0
3	PEE	D	901	-	50,50,50	0.30	0	53,55,55	0.38	0
3	PEE	B	902	-	12,12,50	0.44	0	12,12,55	0.31	0
3	PEE	C	902	-	12,12,50	0.43	0	12,12,55	0.31	0
3	PEE	A	902	-	38,38,50	0.33	0	41,43,55	0.45	0
3	PEE	B	903	-	38,38,50	0.33	0	41,43,55	0.36	0
3	PEE	D	902	-	13,13,50	0.41	0	13,13,55	0.30	0
3	PEE	A	904	-	12,12,50	0.43	0	12,12,55	0.32	0
3	PEE	C	903	-	38,38,50	0.33	0	41,43,55	0.40	0
3	PEE	F	901	-	50,50,50	0.30	0	53,55,55	0.35	0
3	PEE	F	902	-	10,10,50	0.45	0	10,10,55	0.28	0

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
3	PEE	A	903	-	-	2/11/11/54	-
3	PEE	F	903	-	-	4/42/42/54	-
3	PEE	A	901	-	-	7/54/54/54	-
3	PEE	C	901	-	-	0/11/11/54	-
3	PEE	E	901	-	-	3/11/11/54	-
3	PEE	B	901	-	-	4/11/11/54	-
3	PEE	E	902	-	-	4/42/42/54	-
3	PEE	D	903	-	-	3/42/42/54	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PEE	D	901	-	-	11/54/54/54	-
3	PEE	B	902	-	-	1/10/10/54	-
3	PEE	C	902	-	-	1/10/10/54	-
3	PEE	A	902	-	-	2/42/42/54	-
3	PEE	B	903	-	-	5/42/42/54	-
3	PEE	D	902	-	-	4/11/11/54	-
3	PEE	A	904	-	-	1/10/10/54	-
3	PEE	C	903	-	-	9/42/42/54	-
3	PEE	F	901	-	-	10/54/54/54	-
3	PEE	F	902	-	-	2/8/8/54	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (73) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	903	PEE	O5-C30-O3-C3
3	B	903	PEE	C31-C30-O3-C3
3	C	903	PEE	C4-O4P-P-O1P
3	C	903	PEE	C5-C4-O4P-P
3	C	903	PEE	O5-C30-O3-C3
3	C	903	PEE	C31-C30-O3-C3
3	D	901	PEE	C2-C1-O3P-P
3	D	901	PEE	C1-O3P-P-O2P
3	D	903	PEE	C1-O3P-P-O1P
3	F	901	PEE	C4-O4P-P-O1P
3	F	903	PEE	O5-C30-O3-C3
3	F	903	PEE	C31-C30-O3-C3
3	F	901	PEE	C2-C1-O3P-P
3	A	901	PEE	C32-C33-C34-C35
3	A	901	PEE	C10-C11-C12-C13
3	A	901	PEE	C30-C31-C32-C33
3	C	903	PEE	C10-C11-C12-C13
3	D	901	PEE	O2-C2-C3-O3
3	B	901	PEE	C18-C19-C20-C21
3	D	902	PEE	C18-C19-C20-C21
3	A	901	PEE	C5-C4-O4P-P
3	A	902	PEE	C5-C4-O4P-P

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Mol	Chain	Res	Type	Atoms
3	D	901	PEE	C5-C4-O4P-P
3	E	902	PEE	C5-C4-O4P-P
3	F	901	PEE	C5-C4-O4P-P
3	A	901	PEE	O3-C30-C31-C32
3	A	904	PEE	C16-C17-C18-C19
3	B	901	PEE	C16-C17-C18-C19
3	D	901	PEE	C36-C37-C38-C39
3	C	903	PEE	O2-C2-C3-O3
3	E	902	PEE	C36-C37-C38-C39
3	D	901	PEE	C4-O4P-P-O1P
3	C	903	PEE	C36-C37-C38-C39
3	D	901	PEE	O3P-C1-C2-C3
3	C	902	PEE	C16-C17-C18-C19
3	D	901	PEE	C18-C19-C20-C21
3	D	901	PEE	C16-C17-C18-C19
3	D	903	PEE	C36-C37-C38-C39
3	E	901	PEE	C16-C17-C18-C19
3	F	903	PEE	C16-C17-C18-C19
3	C	903	PEE	C30-C31-C32-C33
3	A	902	PEE	C18-C19-C20-C21
3	D	901	PEE	C38-C39-C40-C41
3	D	903	PEE	C16-C17-C18-C19
3	F	901	PEE	C33-C34-C35-C36
3	B	902	PEE	C16-C17-C18-C19
3	E	902	PEE	C18-C19-C20-C21
3	F	901	PEE	C18-C19-C20-C21
3	F	901	PEE	C36-C37-C38-C39
3	D	902	PEE	C16-C17-C18-C19
3	D	901	PEE	C1-C2-C3-O3
3	A	901	PEE	C18-C19-C20-C21
3	B	903	PEE	C16-C17-C18-C19
3	A	903	PEE	O2-C10-C11-C12
3	B	901	PEE	O2-C10-C11-C12
3	F	901	PEE	C31-C32-C33-C34
3	B	903	PEE	O2-C2-C3-O3
3	D	902	PEE	O2-C10-C11-C12
3	E	901	PEE	O2-C10-C11-C12
3	C	903	PEE	C16-C17-C18-C19
3	F	902	PEE	O2-C10-C11-C12
3	A	903	PEE	O4-C10-C11-C12
3	E	901	PEE	O4-C10-C11-C12
3	B	901	PEE	O4-C10-C11-C12

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Mol	Chain	Res	Type	Atoms
3	D	902	PEE	O4-C10-C11-C12
3	F	902	PEE	O4-C10-C11-C12
3	F	901	PEE	C16-C17-C18-C19
3	F	901	PEE	O3-C30-C31-C32
3	A	901	PEE	C13-C14-C15-C16
3	B	903	PEE	C1-C2-C3-O3
3	E	902	PEE	O3-C30-C31-C32
3	F	903	PEE	O3-C30-C31-C32
3	F	901	PEE	O5-C30-C31-C32

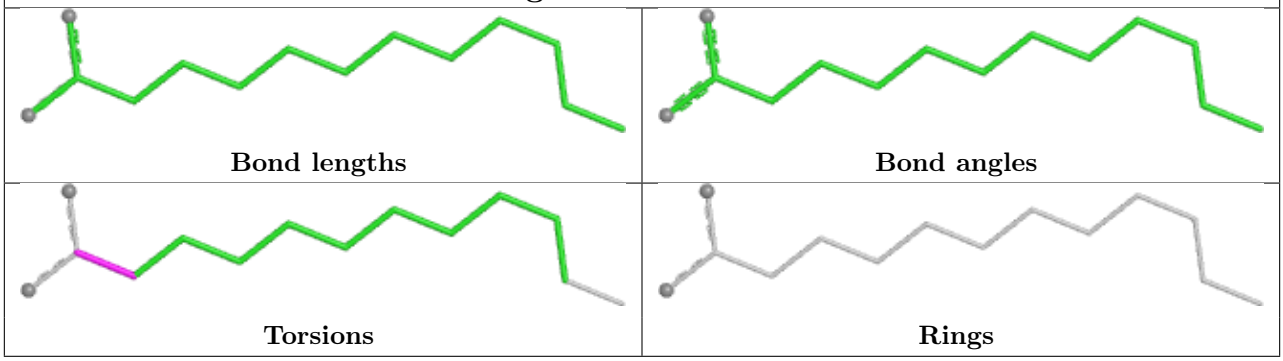
There are no ring outliers.

9 monomers are involved in 21 short contacts:

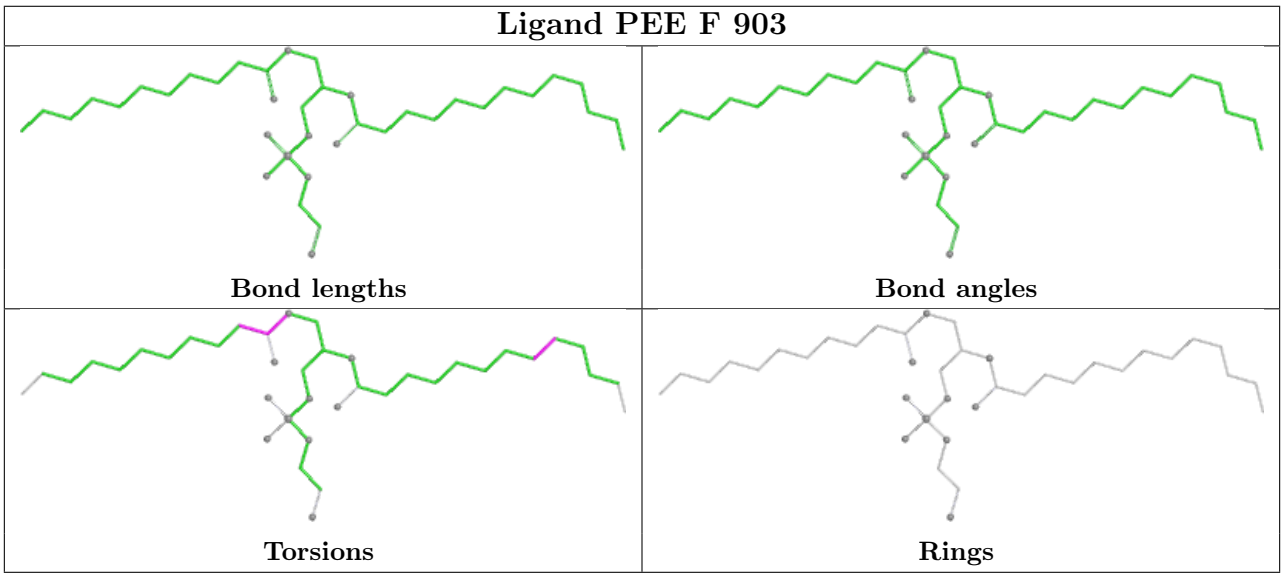
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	903	PEE	1	0
3	F	903	PEE	3	0
3	A	901	PEE	5	0
3	D	901	PEE	3	0
3	C	902	PEE	1	0
3	A	902	PEE	1	0
3	B	903	PEE	2	0
3	C	903	PEE	1	0
3	F	901	PEE	4	0

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 then 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.

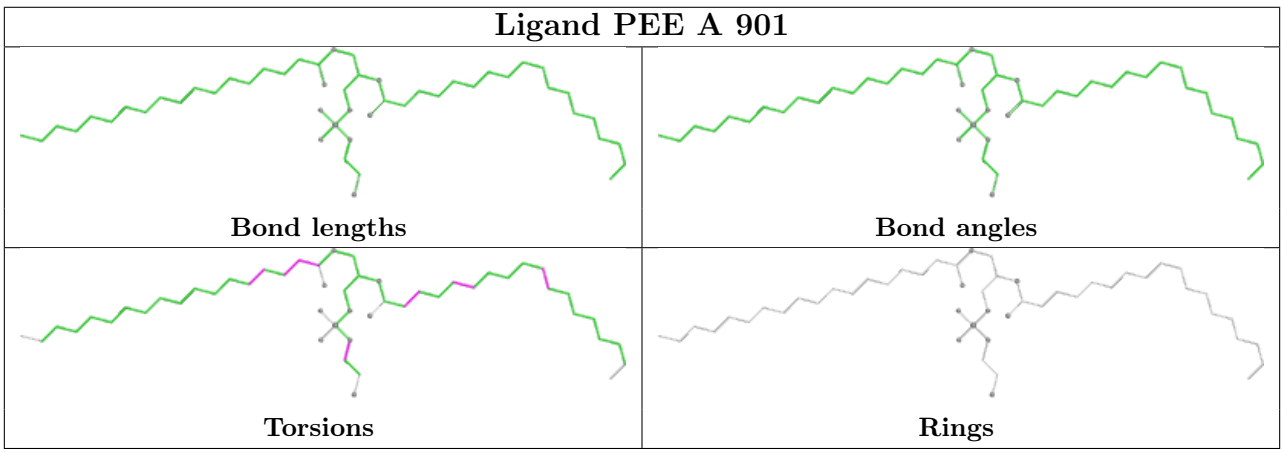
Ligand PEE A 903



Ligand PEE F 903



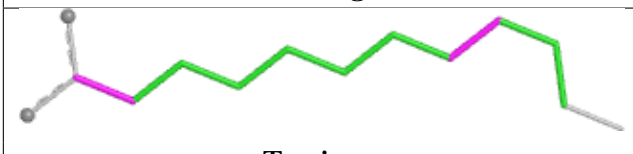
Ligand PEE A 901



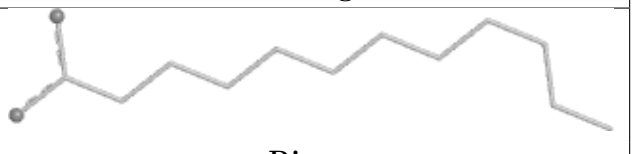
Ligand PEE E 901

Bond lengths

Bond angles



Torsions

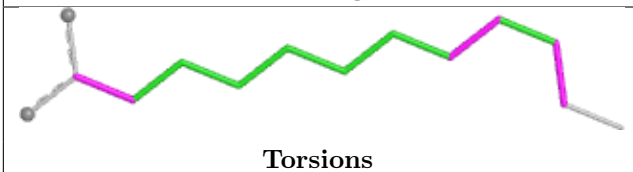


Rings

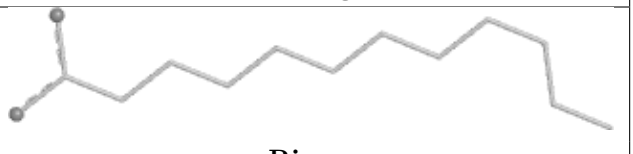
Ligand PEE B 901

Bond lengths

Bond angles

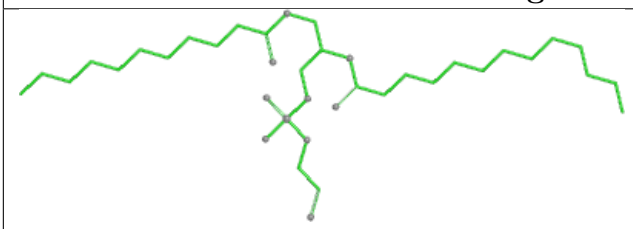


Torsions

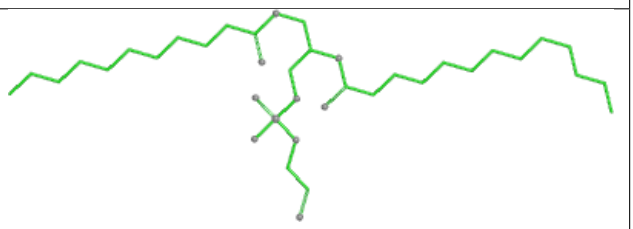


Rings

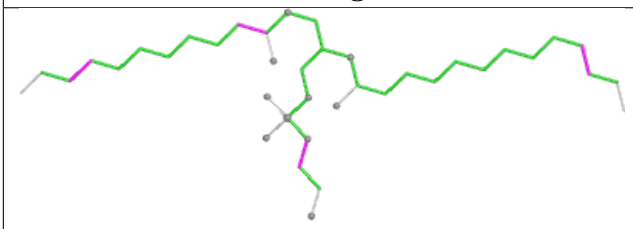
Ligand PEE E 902



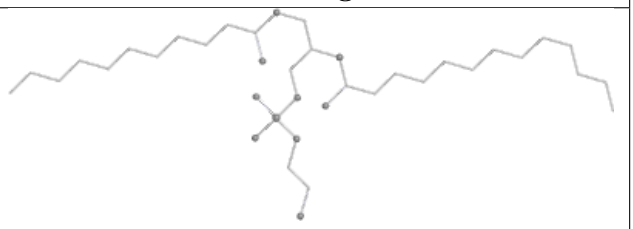
Bond lengths



Bond angles

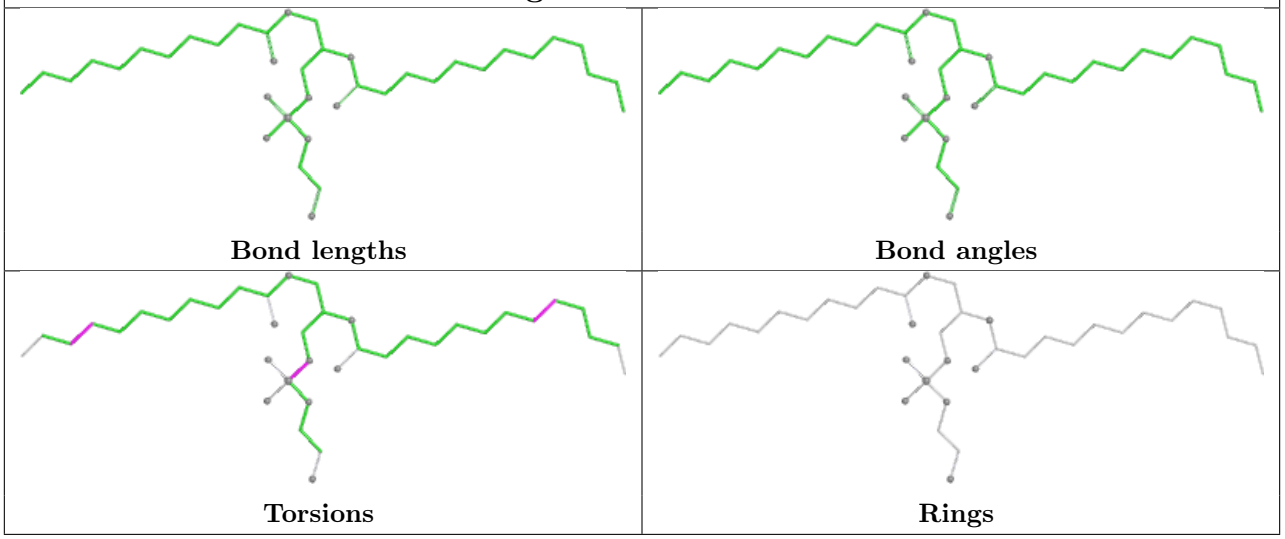


Torsions

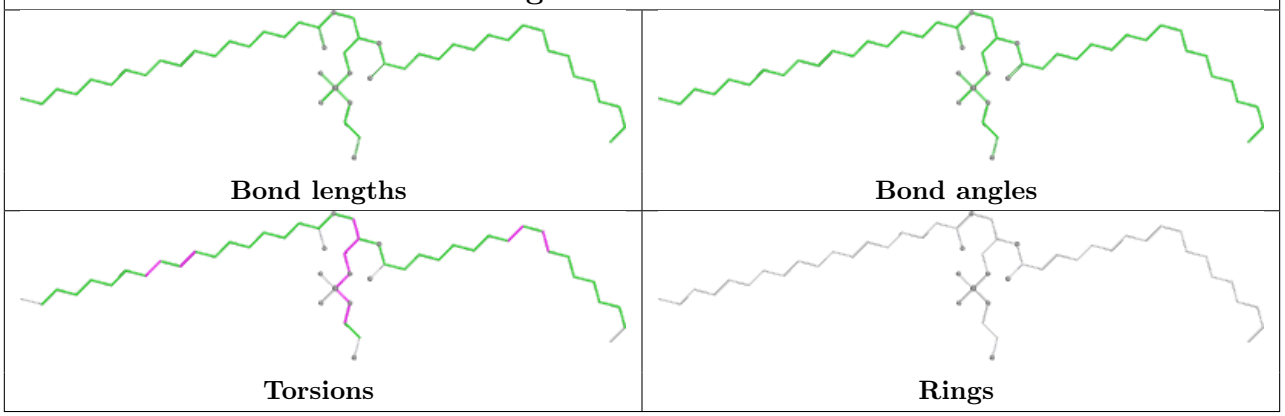


Rings

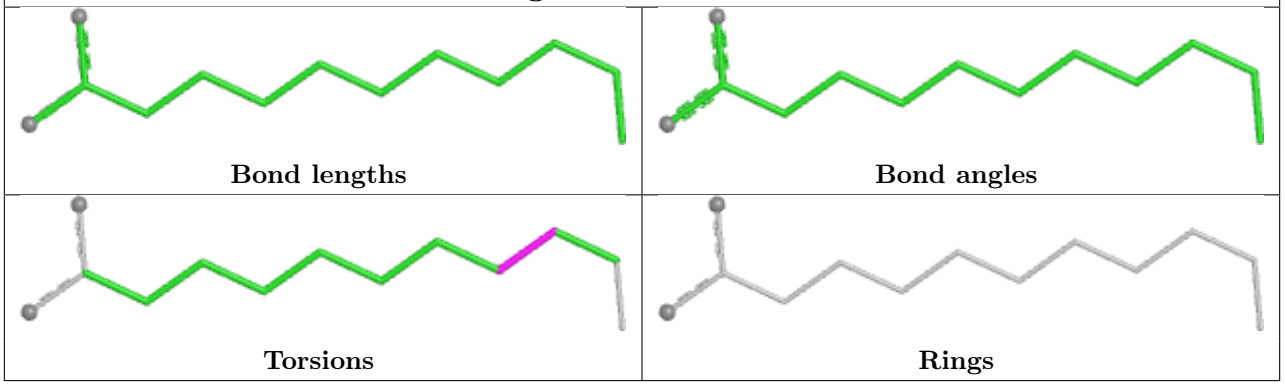
Ligand PEE D 903



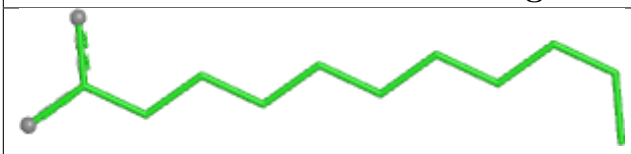
Ligand PEE D 901

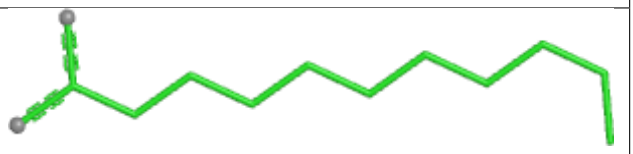


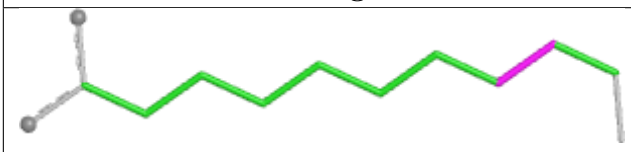
Ligand PEE B 902

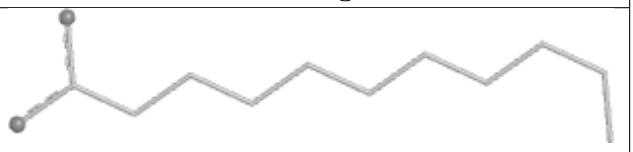


Ligand PEE C 902

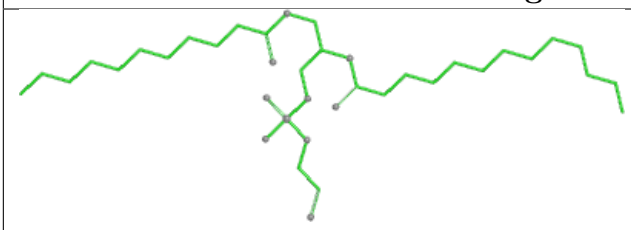

Bond lengths

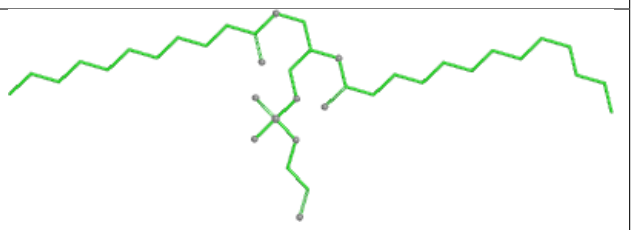

Bond angles

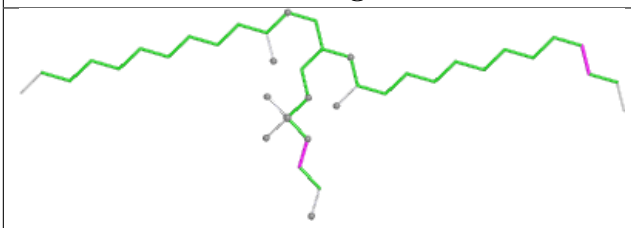

Torsions

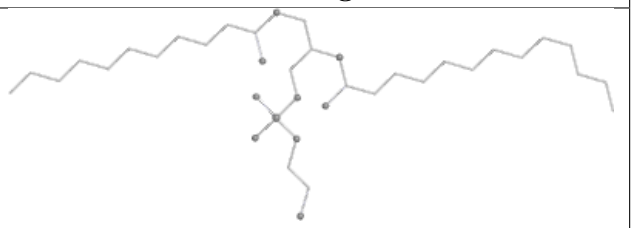

Rings

Ligand PEE A 902

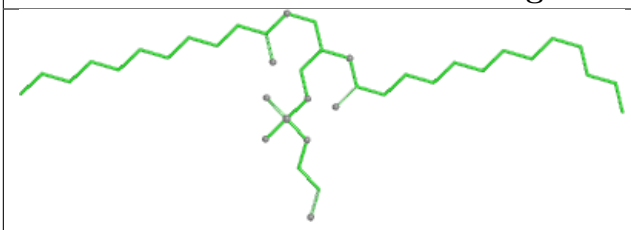

Bond lengths

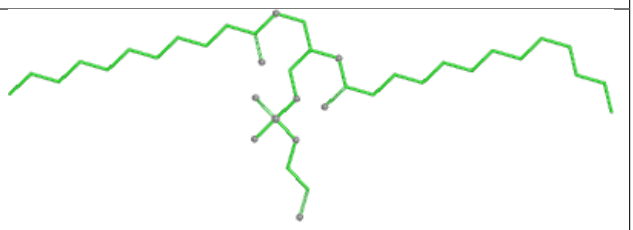

Bond angles

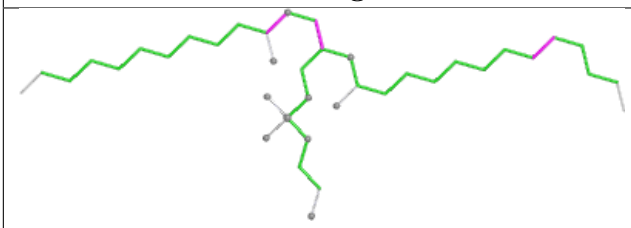

Torsions

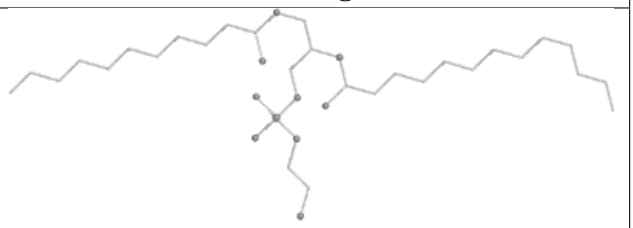

Rings

Ligand PEE B 903


Bond lengths


Bond angles


Torsions

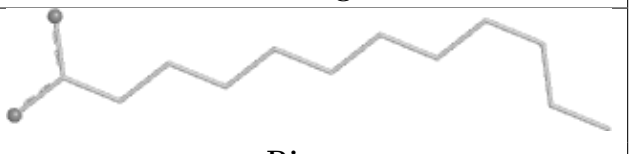

Rings

Ligand PEE D 902

Bond lengths

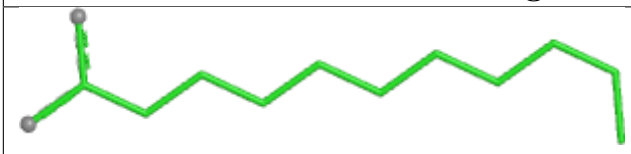
Bond angles

Torsions

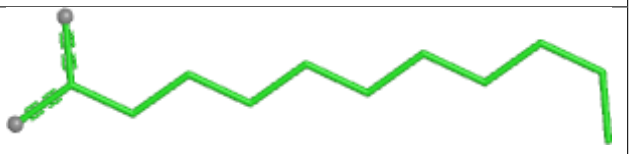


Rings

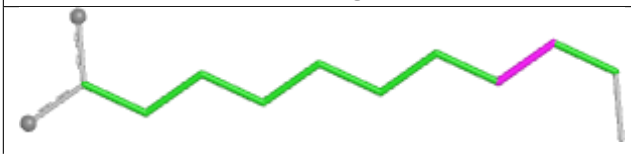
Ligand PEE A 904



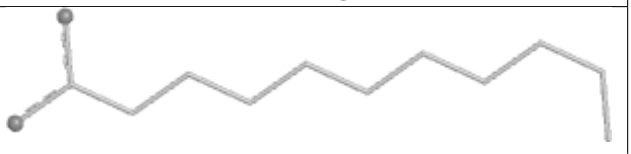
Bond lengths



Bond angles

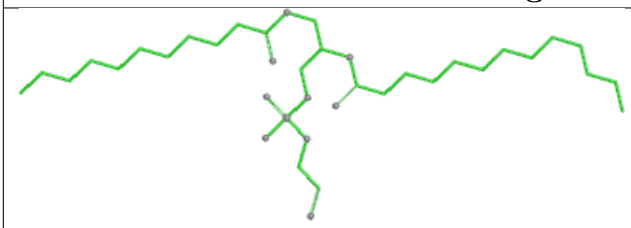


Torsions

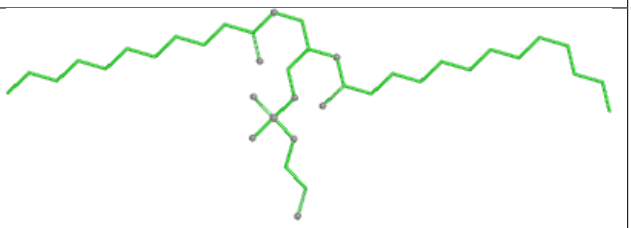


Rings

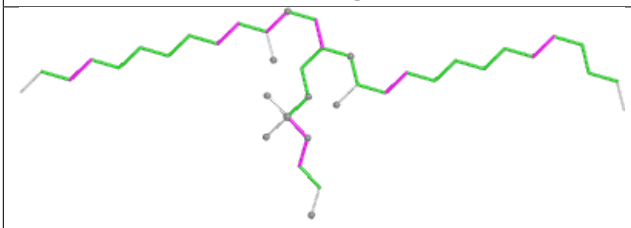
Ligand PEE C 903



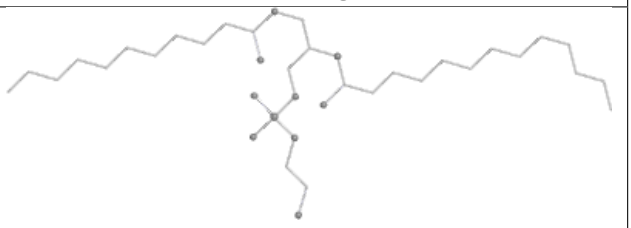
Bond lengths



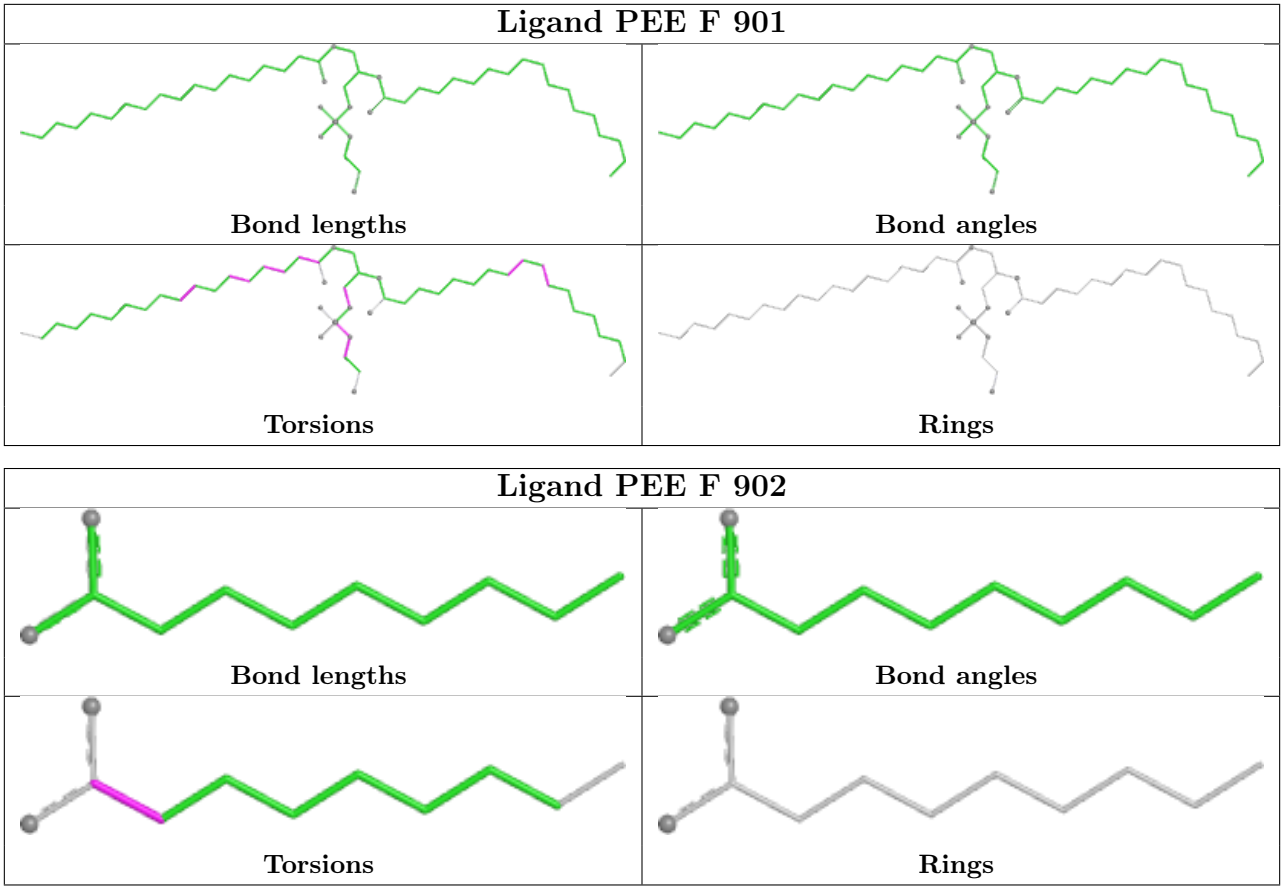
Bond angles



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.

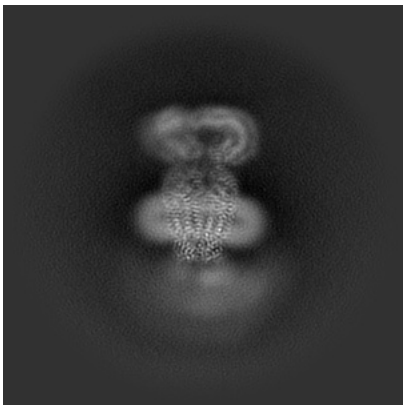
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-47283. These allow visual inspection of the internal detail of the map and identification of artifacts.

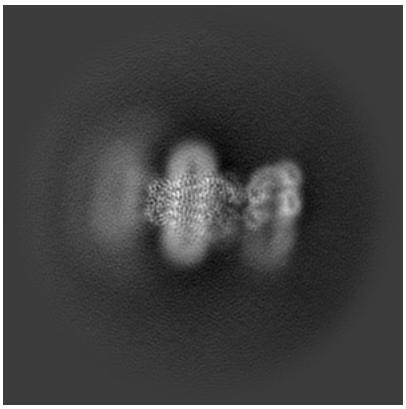
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

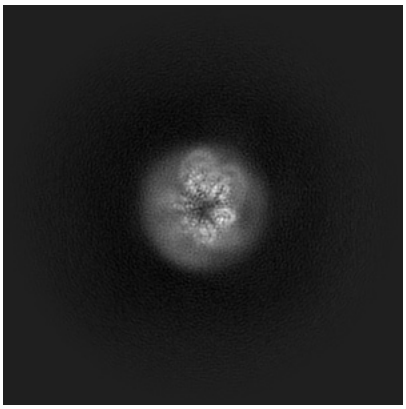
6.1.1 Primary map



X

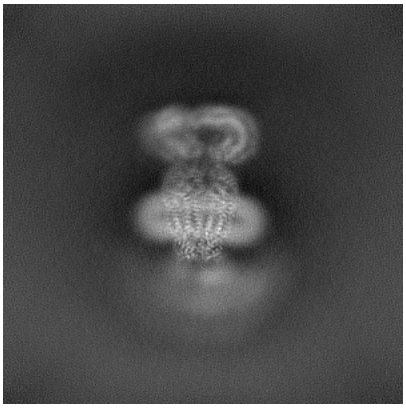


Y

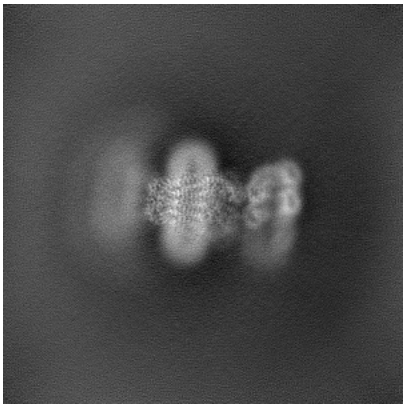


Z

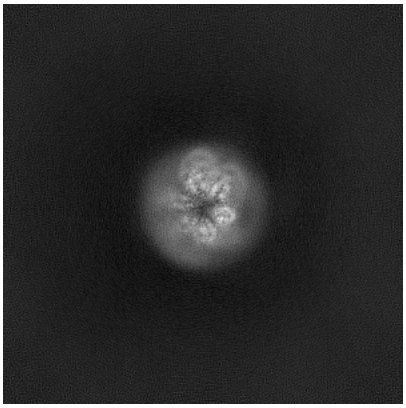
6.1.2 Raw map



X



Y

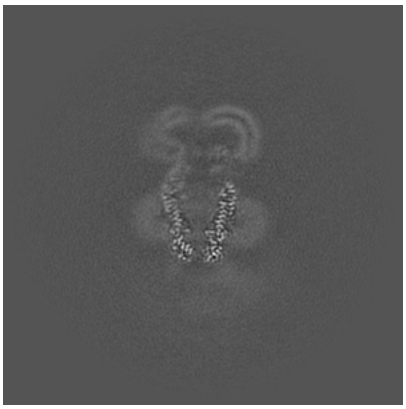


Z

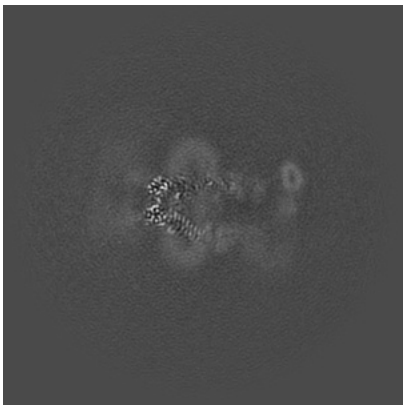
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

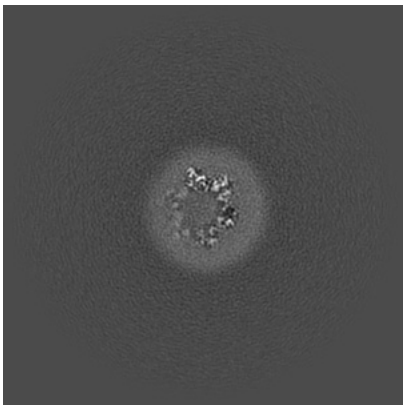
6.2.1 Primary map



X Index: 208



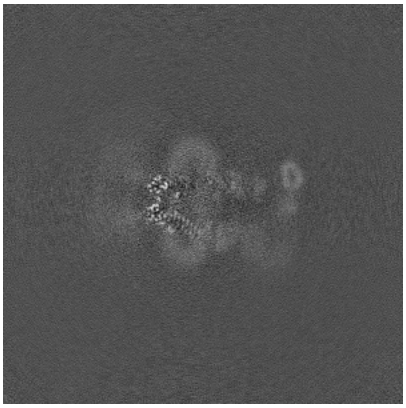
Y Index: 208



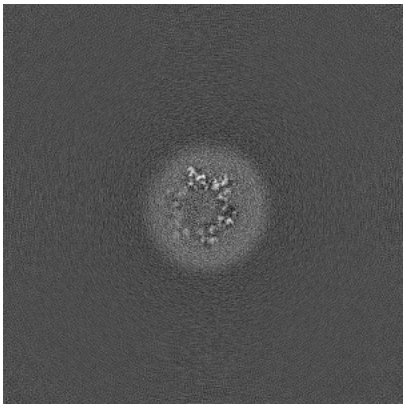
Z Index: 208

6.2.2 Raw map

X Index: 208



Y Index: 208

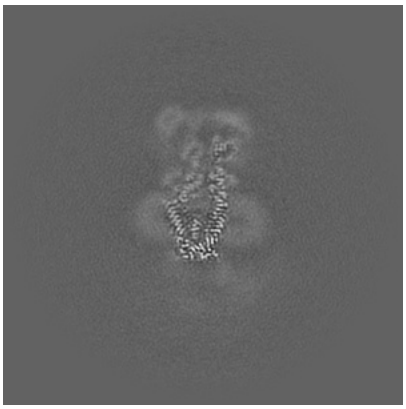


Z Index: 208

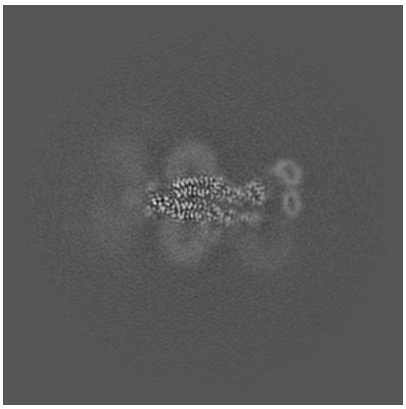
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

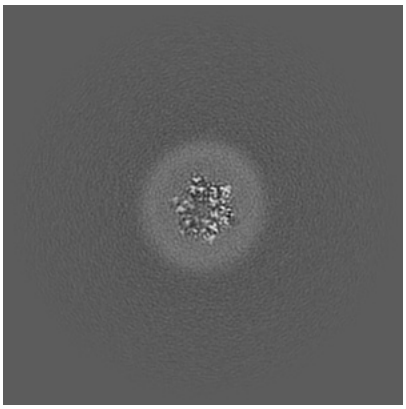
6.3.1 Primary map



X Index: 221

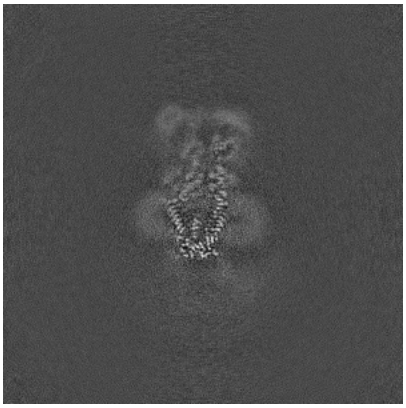


Y Index: 225

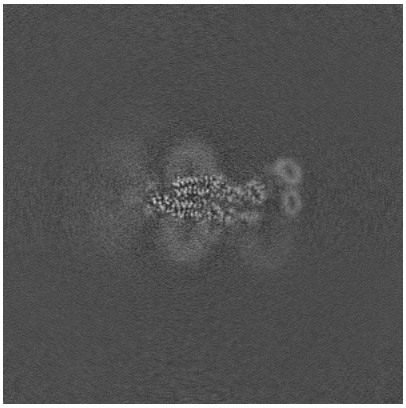


Z Index: 182

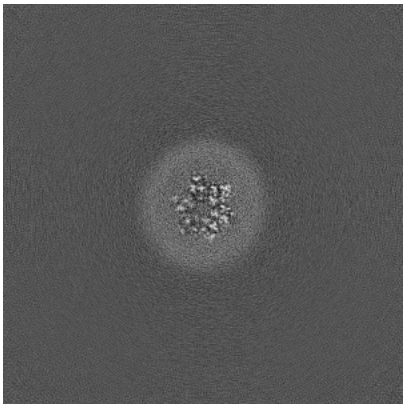
6.3.2 Raw map



X Index: 221



Y Index: 225



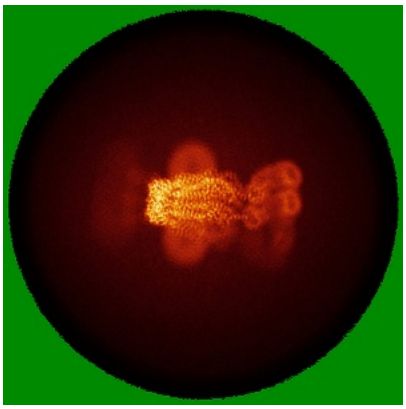
Z Index: 182

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

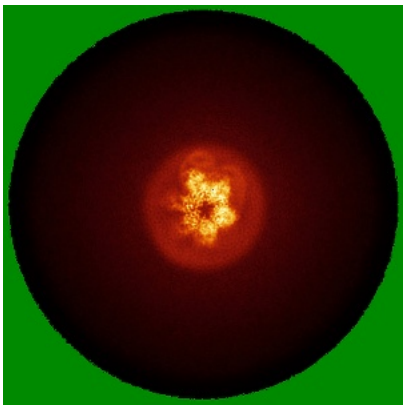
6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map

X

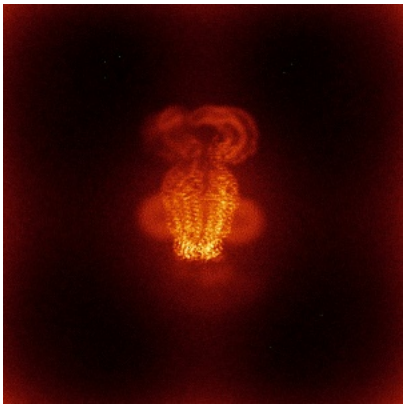


Y

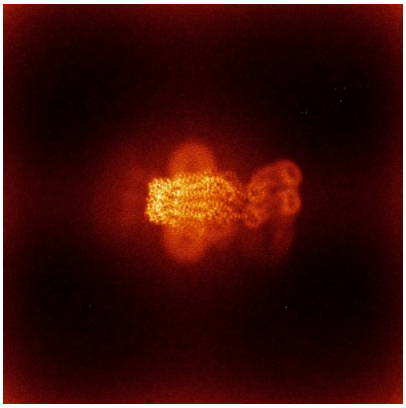


Z

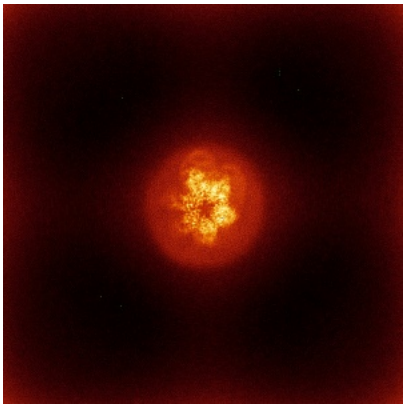
6.4.2 Raw map



X



Y

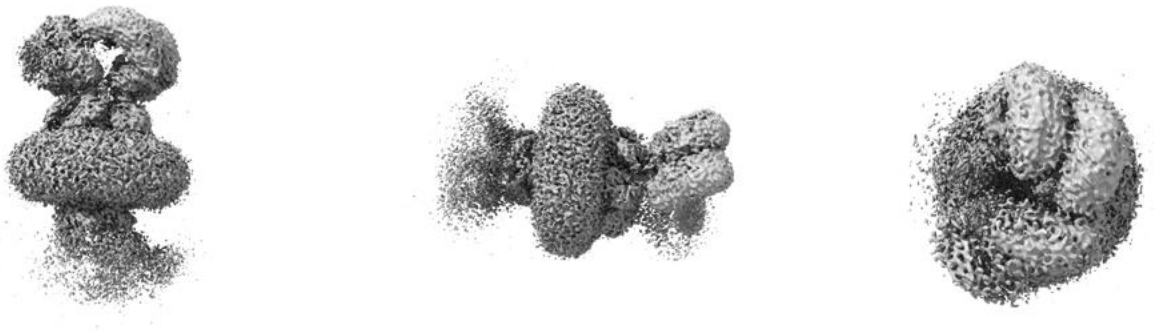


Z

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)

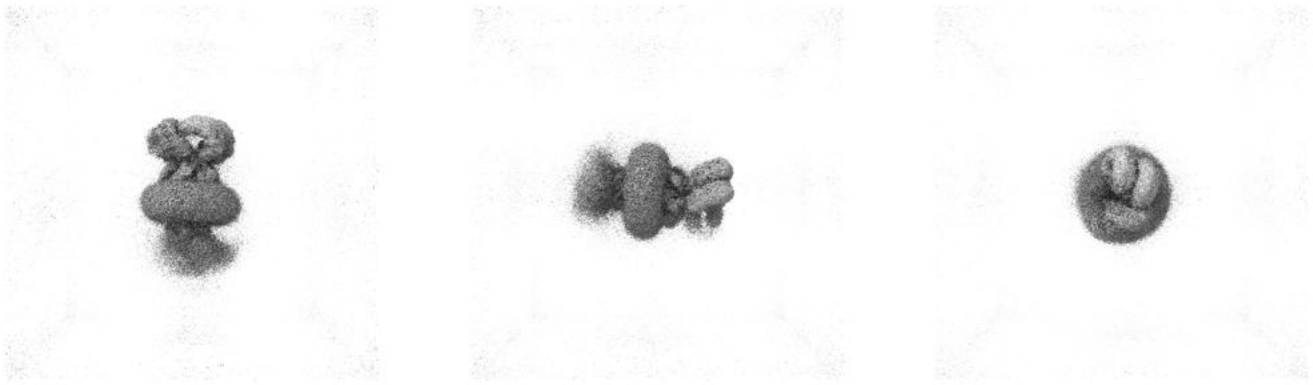
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.12. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



X Y Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

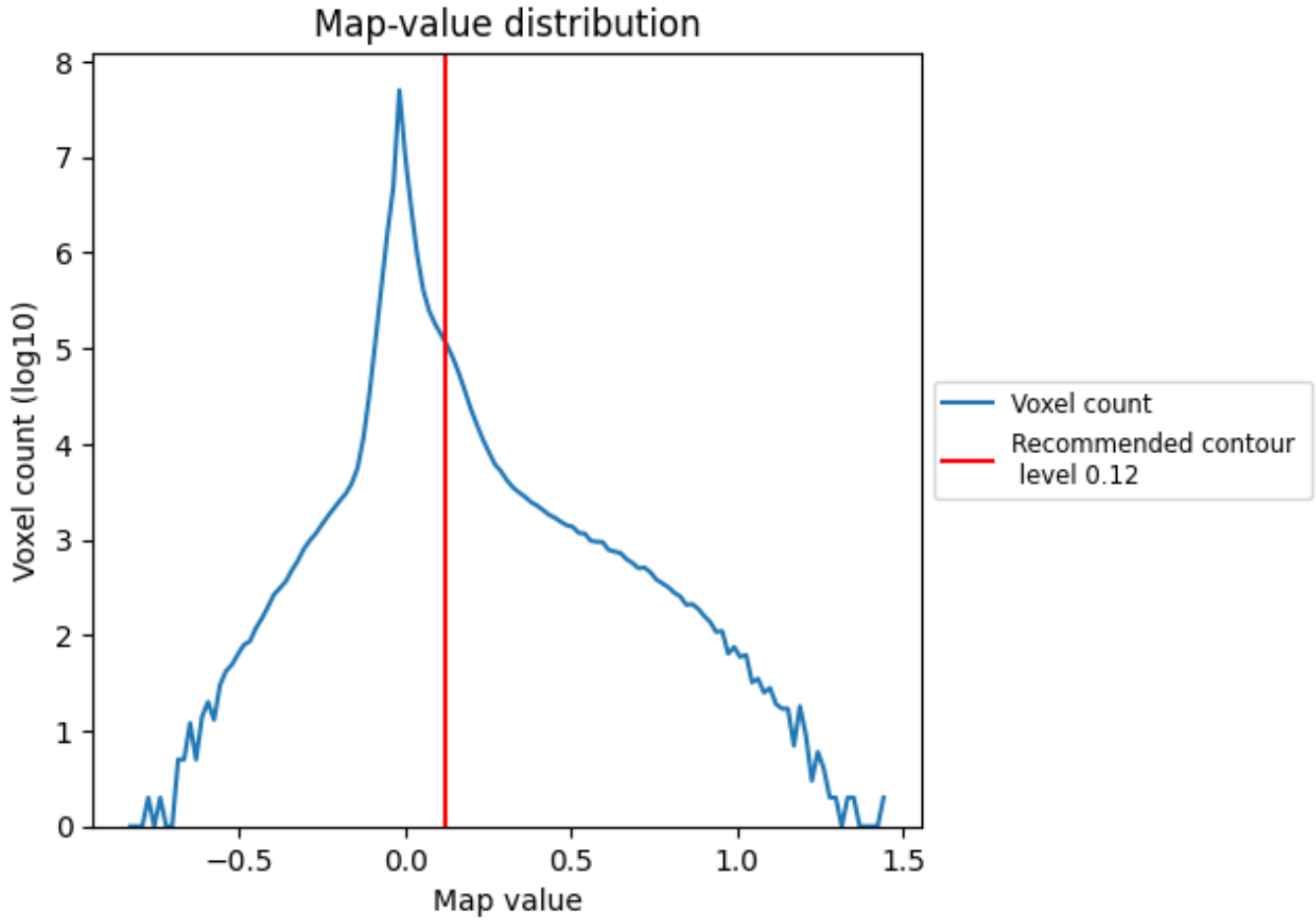
6.6 Mask visualisation (i)

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

7 Map analysis

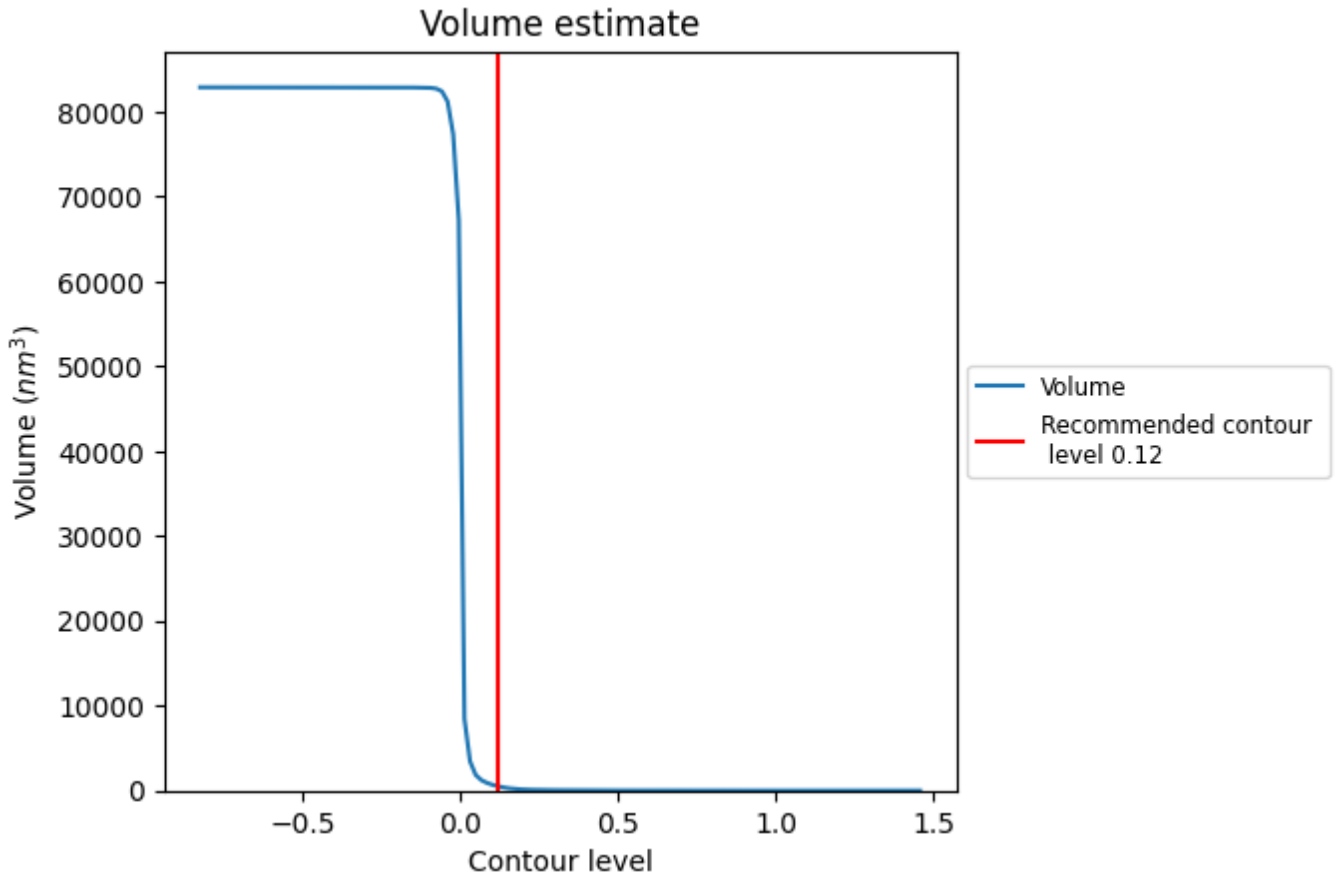
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

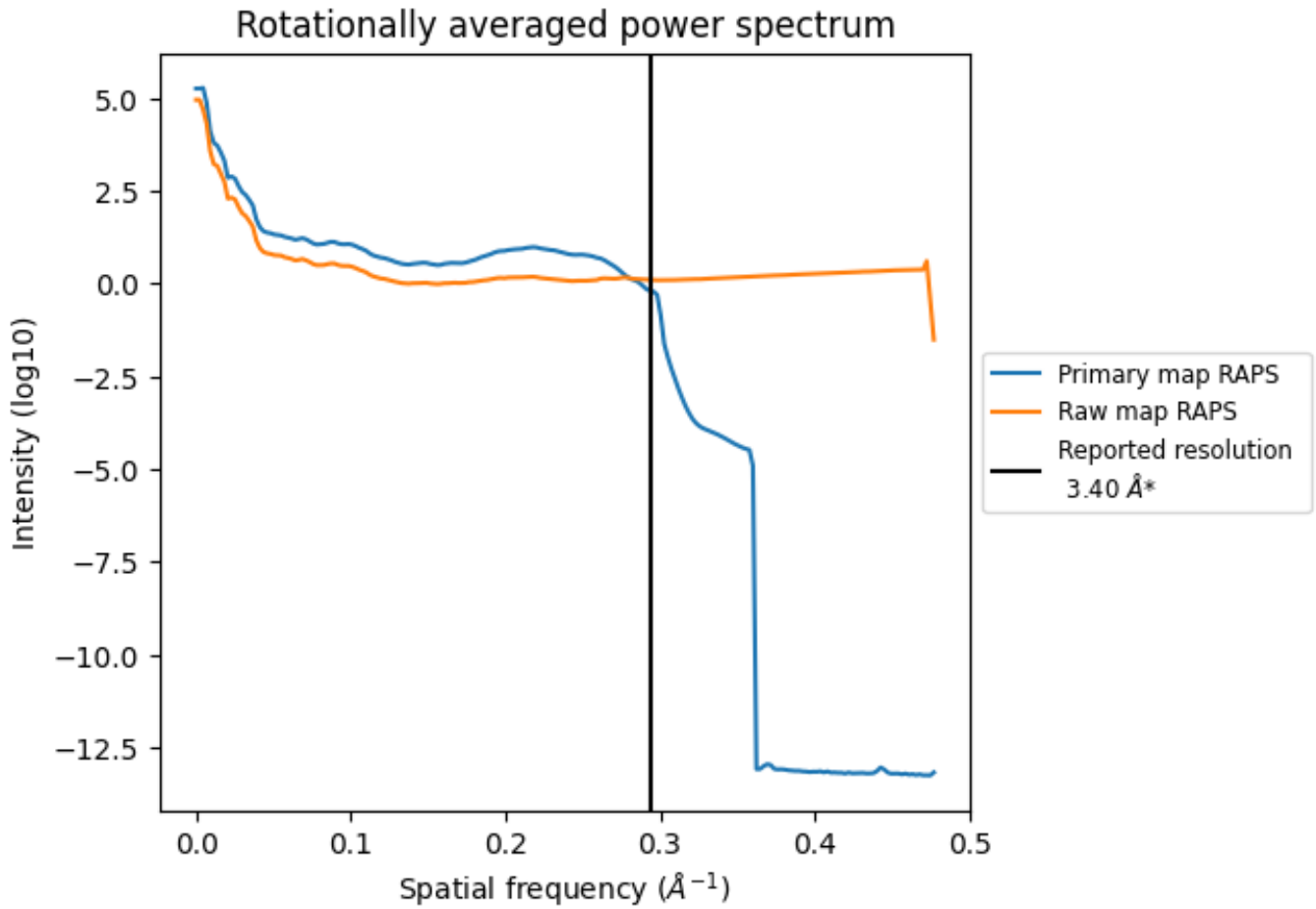
7.2 Volume estimate



The volume at the recommended contour level is 499 nm^3; this corresponds to an approximate mass of 450 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)

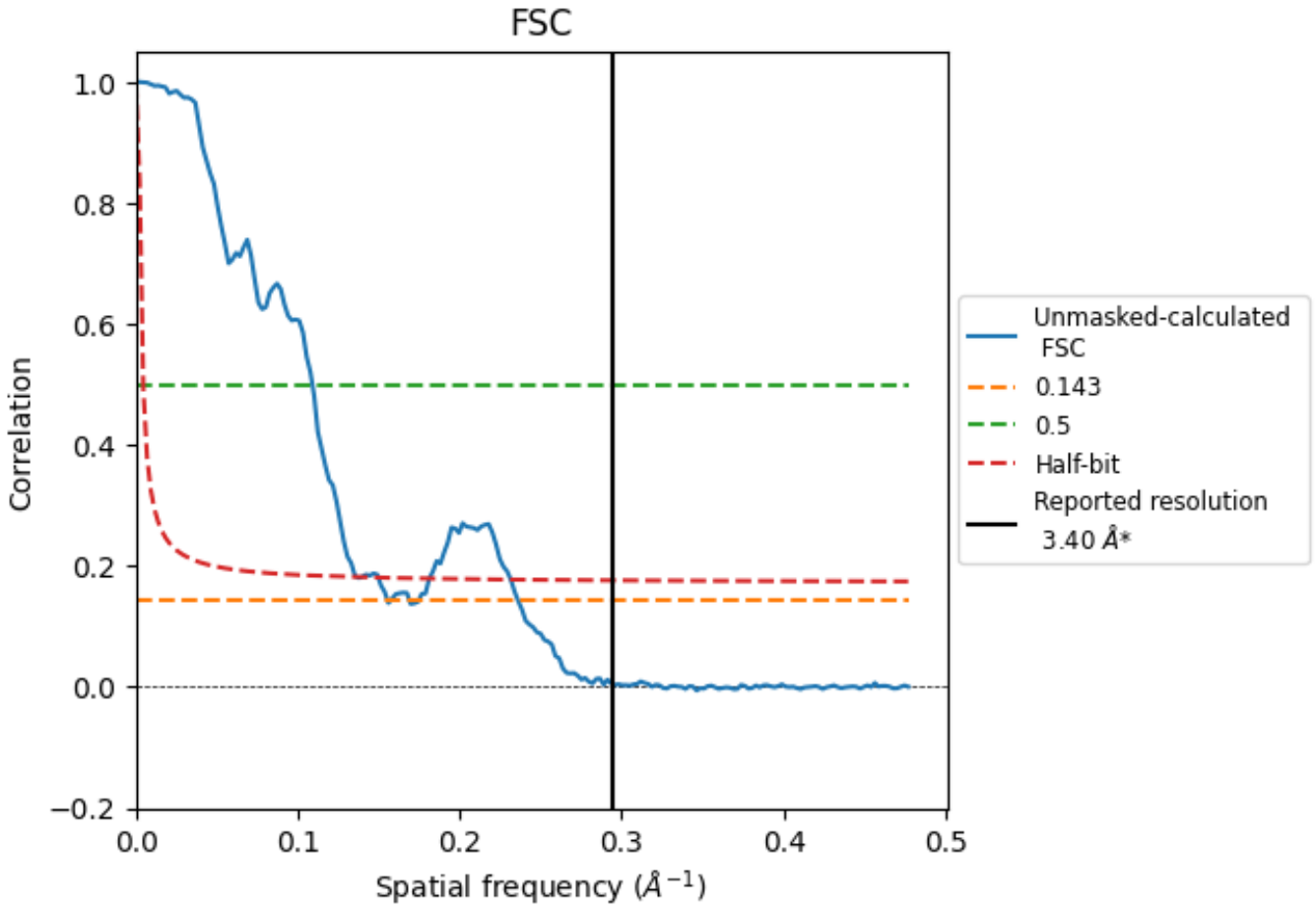


*Reported resolution corresponds to spatial frequency of 0.294 $Å^{-1}$

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.294 Å^{-1}

8.2 Resolution estimates (i)

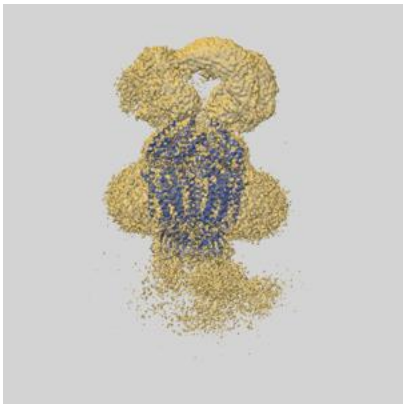
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	6.44	9.17	7.31

*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 6.44 differs from the reported value 3.4 by more than 10 %

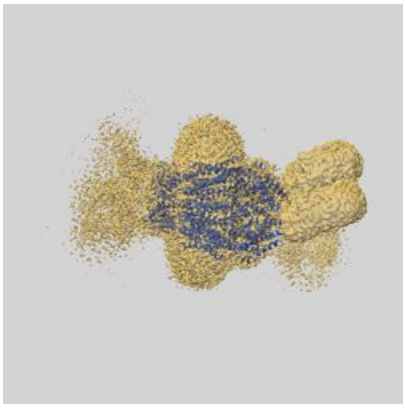
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-47283 and PDB model 9DXA. Per-residue inclusion information can be found in section 3 on page 8.

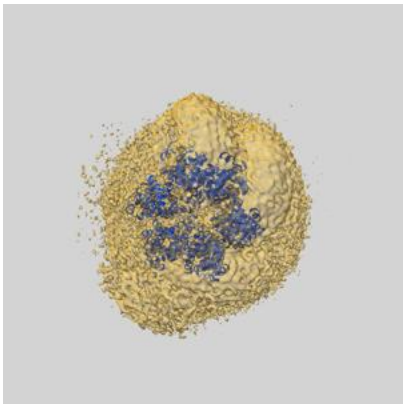
9.1 Map-model overlay



X



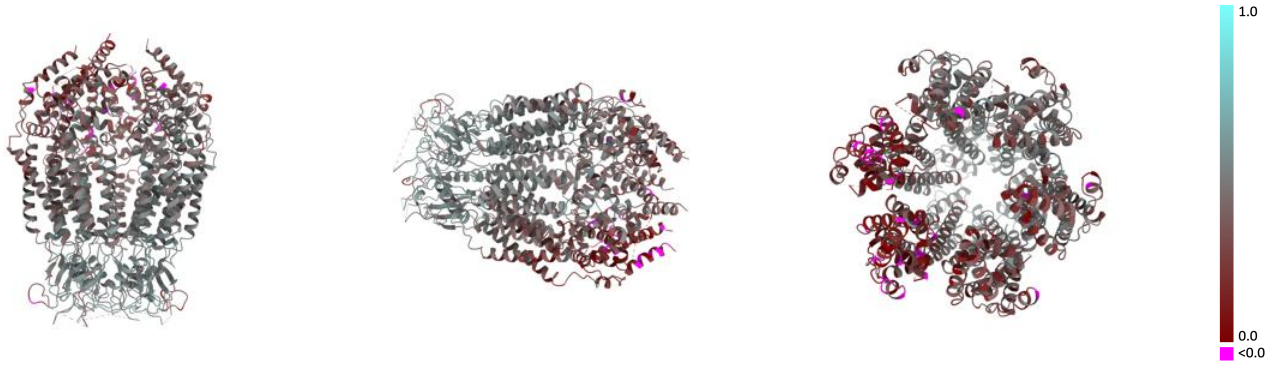
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.12 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.

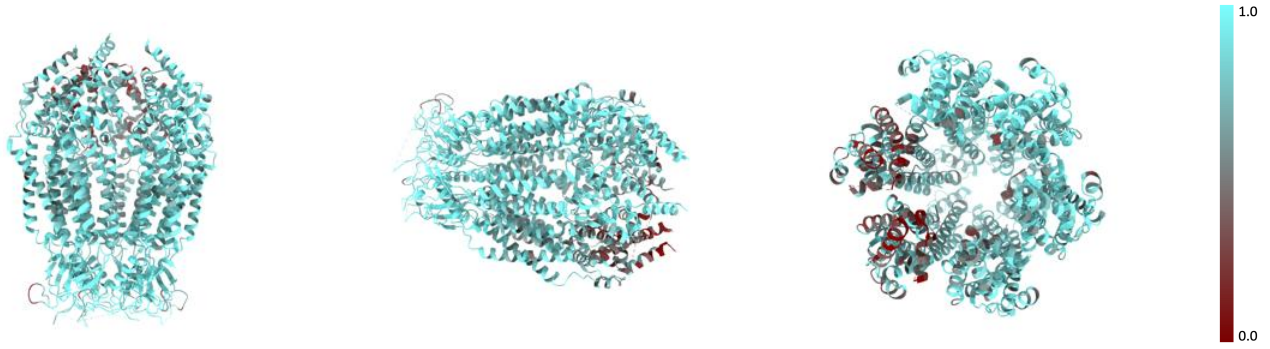
9.2 Q-score mapped to coordinate model (i)



X Y Z

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.

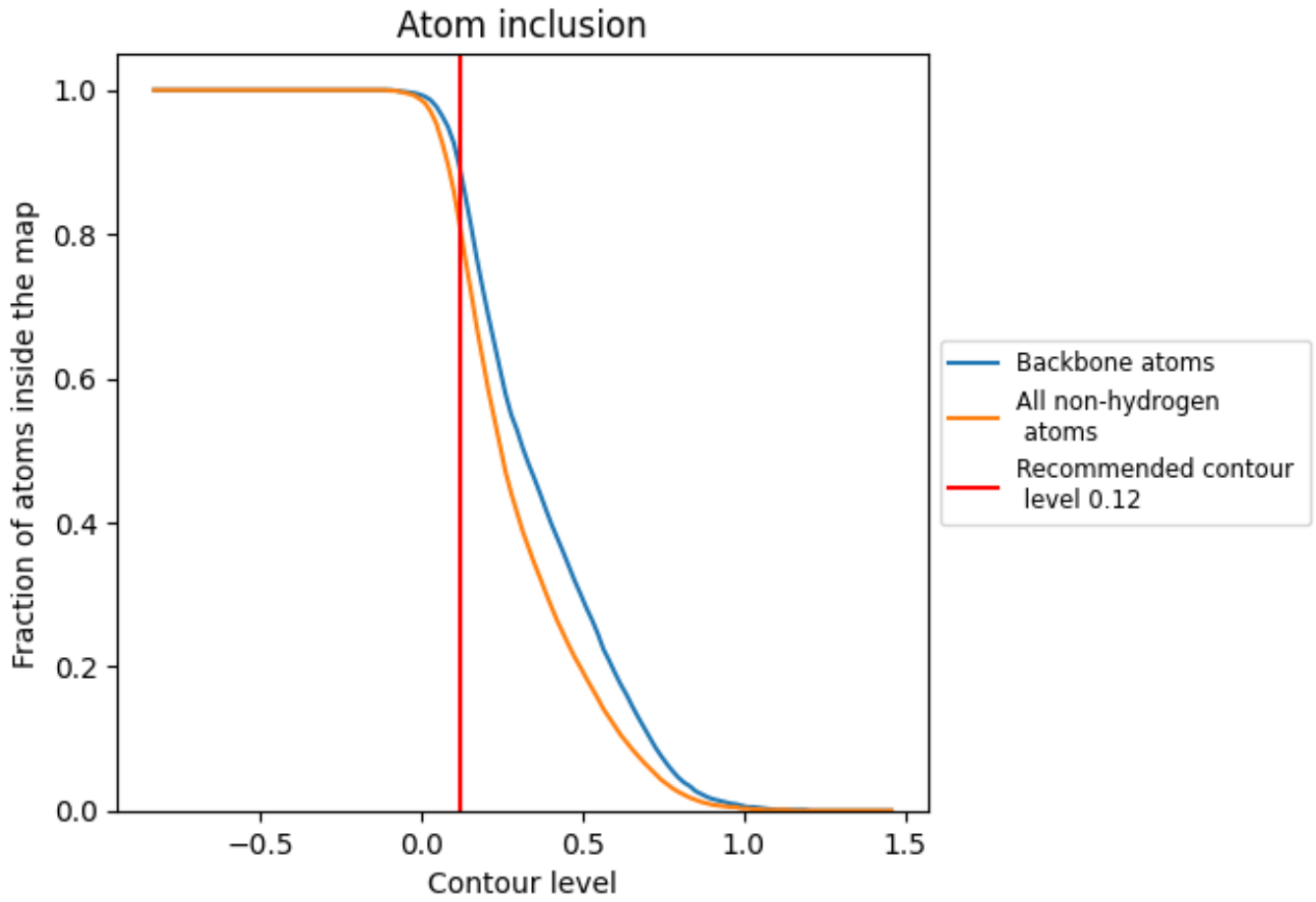
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.12).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 81% 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 (0.12) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8140	0.3930
A	0.8860	0.4580
B	0.8820	0.4580
C	0.8580	0.4280
D	0.8190	0.3850
E	0.7140	0.3070
F	0.7230	0.3160