Full wwPDB EM Validation Report ⓘ

Jun 9, 2025 – 01:44 PM JST

PDB ID	:	9KTL / pdb_00009ktl
EMDB ID	:	EMD-62562
Title	:	Cryo-EM structure of reduced form of formate dehydrogenase from Rhodobacter aestuarii (RaFDH) with NADH
Authors	:	Zhang, K.; Zhang, L.
Deposited on	:	2024-12-02
Resolution	:	3.09 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:

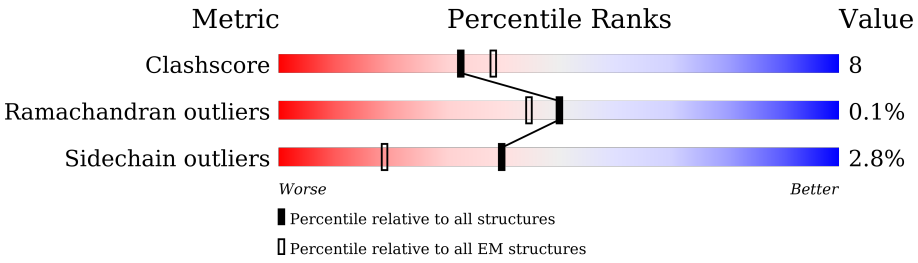
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0rc1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
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 3.09 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	958	79% 20%
1	B	958	79% 20%
2	G	70	71% 23% 6%
2	H	70	73% 20% 6%
3	E	150	77% 23%
3	F	150	79% 20%
4	C	502	79% 19%
4	D	502	77% 21%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
8	SF4	A	1005	-	-	X	-
8	SF4	A	1008	-	-	X	-
8	SF4	B	1005	-	-	X	-
8	SF4	B	1008	-	-	X	-

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 25368 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 formate dehydrogenase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	951	Total	C	N	O	S	0	0
			7222	4488	1303	1384	47		
1	B	951	Total	C	N	O	S	0	0
			7222	4488	1303	1384	47		

- Molecule 2 is a protein called Formate dehydrogenase delta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	G	66	Total	C	N	O	S	0	0
			477	302	90	83	2		
2	H	66	Total	C	N	O	S	0	0
			477	302	90	83	2		

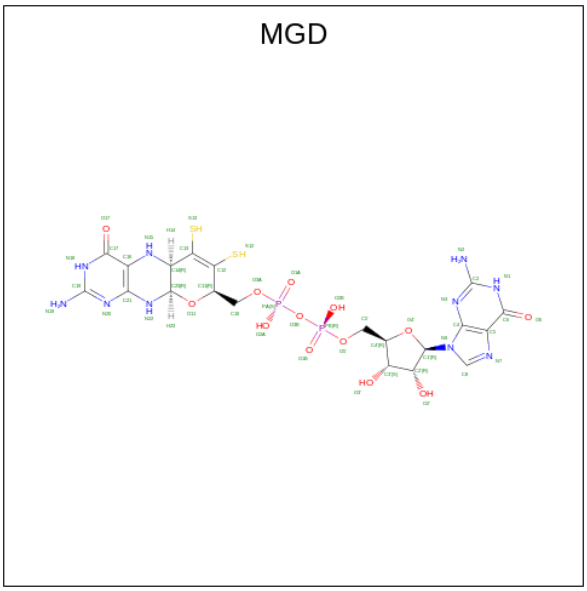
- Molecule 3 is a protein called Formate dehydrogenase gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	149	Total	C	N	O	S	0	0
			1096	683	203	203	7		
3	E	149	Total	C	N	O	S	0	0
			1096	683	203	203	7		

- Molecule 4 is a protein called Formate dehydrogenase beta subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	496	Total	C	N	O	S	0	0
			3671	2324	638	681	28		
4	D	496	Total	C	N	O	S	0	0
			3671	2324	638	681	28		

- Molecule 5 is 2-AMINO-5,6-DIMERCAPTO-7-METHYL-3,7,8A,9-TETRAHYDRO-8-OXA-1,3,9,10-TETRAAZA-ANTHRACEN-4-ONE GUANOSINE DINUCLEOTIDE (CCD ID: MGD) (formula: $C_{20}H_{26}N_{10}O_{13}P_2S_2$) (labeled as "Ligand of Interest" by depositor).

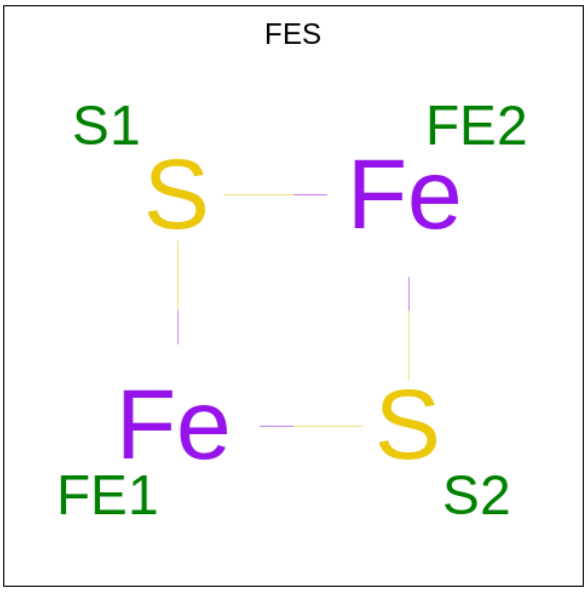


Mol	Chain	Residues	Atoms						AltConf
5	A	1	Total	C	N	O	P	S	0
			47	20	10	13	2	2	
5	A	1	Total	C	N	O	P	S	0
			47	20	10	13	2	2	
5	B	1	Total	C	N	O	P	S	0
			47	20	10	13	2	2	
5	B	1	Total	C	N	O	P	S	0
			47	20	10	13	2	2	

- Molecule 6 is MOLYBDENUM(VI) ION (CCD ID: 6MO) (formula: Mo) (labeled as "Ligand of Interest" by depositor).

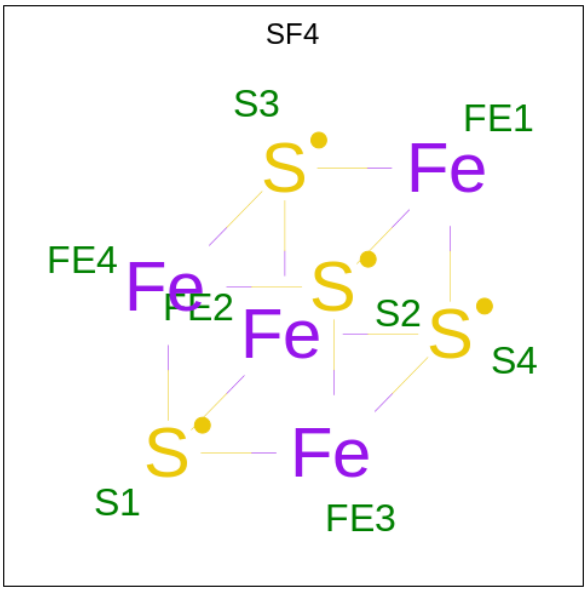
Mol	Chain	Residues	Atoms		AltConf
6	A	1	Total	Mo	0
			1	1	
6	B	1	Total	Mo	0
			1	1	

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (CCD ID: FES) (formula: Fe_2S_2) (labeled as "Ligand of Interest" by depositor).



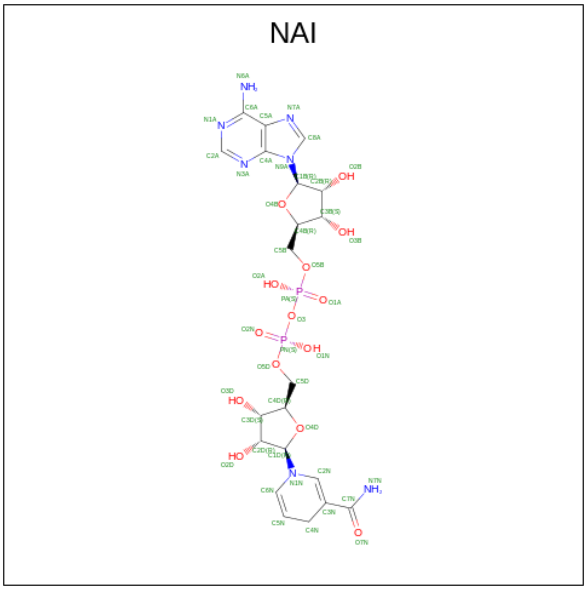
Mol	Chain	Residues	Atoms	AltConf
7	A	1	Total Fe S 4 2 2	0
7	F	1	Total Fe S 4 2 2	0
7	E	1	Total Fe S 4 2 2	0
7	B	1	Total Fe S 4 2 2	0

- Molecule 8 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe_4S_4) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
8	A	1	Total Fe S 8 4 4	0
8	A	1	Total Fe S 8 4 4	0
8	A	1	Total Fe S 8 4 4	0
8	A	1	Total Fe S 8 4 4	0
8	C	1	Total Fe S 8 4 4	0
8	B	1	Total Fe S 8 4 4	0
8	B	1	Total Fe S 8 4 4	0
8	B	1	Total Fe S 8 4 4	0
8	B	1	Total Fe S 8 4 4	0
8	D	1	Total Fe S 8 4 4	0

- Molecule 9 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (CCD ID: NAI) (formula: $C_{21}H_{29}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	AltConf
9	C	1	Total C N O P 44 21 7 14 2	0

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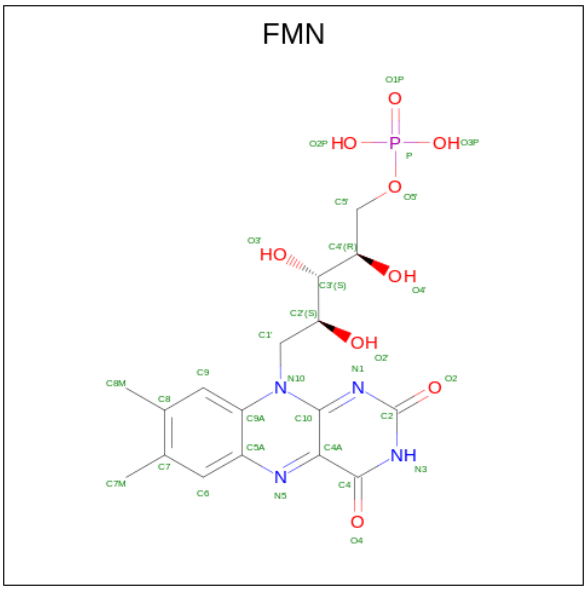
Mol	Chain	Residues	Atoms					AltConf
9	D	1	Total	C	N	O	P	0
			44	21	7	14	2	

- Molecule 10 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$) (labeled as "Ligand of Interest" by depositor).



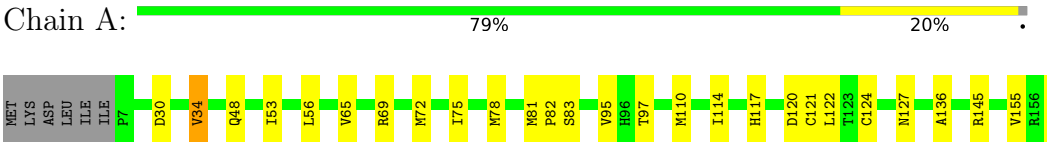
Mol	Chain	Residues	Atoms					AltConf
10	C	1	Total	C	N	O	P	0
			31	17	4	9	1	
10	D	1	Total	C	N	O	P	0
			31	17	4	9	1	

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.

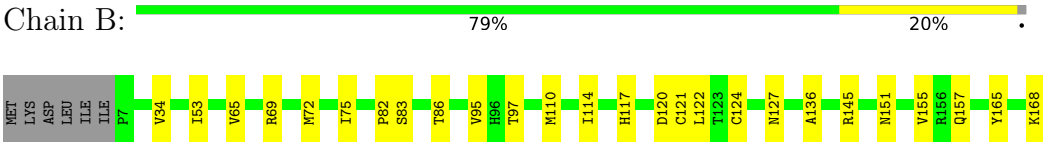
- Molecule 1: formate dehydrogenase

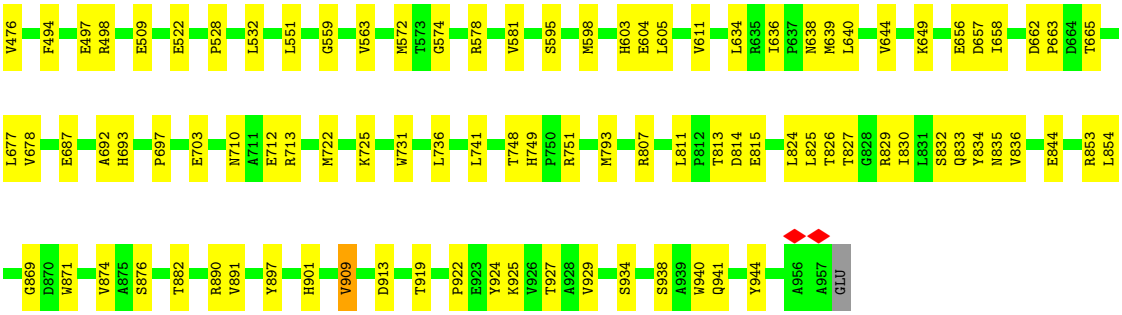
Chain A:



- Molecule 1: formate dehydrogenase

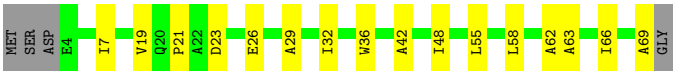
Chain B:





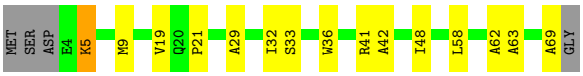
• Molecule 2: Formate dehydrogenase delta subunit

Chain G:



• Molecule 2: Formate dehydrogenase delta subunit

Chain H:

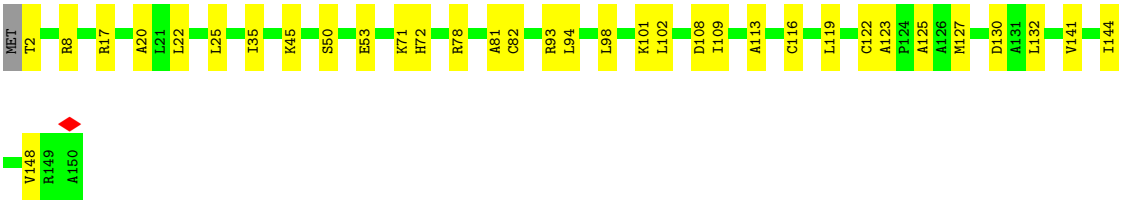


• Molecule 3: Formate dehydrogenase gamma subunit

Chain F:

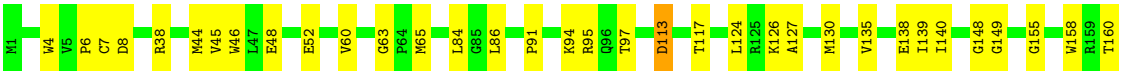
• Molecule 3: Formate dehydrogenase gamma subunit

Chain E:



• Molecule 4: Formate dehydrogenase beta subunit

Chain C:



• Molecule 4: Formate dehydrogenase beta subunit

Chain D:

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	294386	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)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	1.776	Depositor
Minimum map value	-0.431	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.133	Depositor
Map size (Å)	279.0, 279.0, 279.0	wwPDB
Map dimensions	300, 300, 300	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.93, 0.93, 0.93	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, 6MO, MGD, FES, NAI, FMN

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	0.32	0/7382	0.38	0/10060
1	B	0.31	0/7382	0.38	0/10060
2	G	0.18	0/487	0.30	0/664
2	H	0.19	0/487	0.28	0/664
3	E	0.26	0/1111	0.35	0/1505
3	F	0.26	0/1111	0.41	0/1505
4	C	0.29	0/3749	0.38	0/5089
4	D	0.29	0/3749	0.39	0/5089
All	All	0.30	0/25458	0.38	0/34636

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	7222	0	7000	130	0
1	B	7222	0	7000	118	0
2	G	477	0	478	9	0
2	H	477	0	478	8	0
3	E	1096	0	1106	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1096	0	1106	18	0
4	C	3671	0	3646	60	0
4	D	3671	0	3646	64	0
5	A	94	0	48	10	0
5	B	94	0	48	9	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	4	0	0	0	0
7	B	4	0	0	0	0
7	E	4	0	0	1	0
7	F	4	0	0	1	0
8	A	32	0	0	5	0
8	B	32	0	0	4	0
8	C	8	0	0	1	0
8	D	8	0	0	1	0
9	C	44	0	27	4	0
9	D	44	0	27	5	0
10	C	31	0	19	0	0
10	D	31	0	19	2	0
All	All	25368	0	24648	416	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 8.

All (416) 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)
4:D:160:THR:HG21	9:D:601:NAI:H2A	1.56	0.86
1:B:826:THR:HG21	5:B:1002:MGD:H8	1.57	0.86
1:A:826:THR:HG21	5:A:1002:MGD:H8	1.59	0.85
1:B:829:ARG:HH22	5:B:1001:MGD:H15	1.25	0.84
1:A:829:ARG:HH11	5:A:1002:MGD:H15	1.25	0.82
1:B:362:GLU:HG2	1:B:731:TRP:HB3	1.62	0.82
4:C:149:GLY:HA3	9:C:601:NAI:H1D	1.61	0.81
1:A:362:GLU:HG2	1:A:731:TRP:HB3	1.63	0.80
1:A:497:GLU:HG3	1:A:498:ARG:HG2	1.66	0.77
1:B:363:THR:HG21	1:B:595:SER:HA	1.66	0.77
1:B:391:GLY:HA2	1:B:401:SER:HB2	1.67	0.76
1:A:363:THR:HG21	1:A:595:SER:HA	1.66	0.76
4:D:185:ASP:HA	4:D:297:LEU:HD22	1.69	0.75
1:B:406:ASP:HA	1:B:712:GLU:HG3	1.70	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:391:GLY:HA2	1:A:401:SER:HB2	1.69	0.73
4:C:185:ASP:HA	4:C:297:LEU:HD22	1.69	0.73
3:E:102:LEU:HD21	3:E:113:ALA:HB2	1.70	0.73
1:B:415:LEU:HD12	1:B:443:LYS:HB2	1.70	0.73
4:D:435:CYS:HB2	8:D:603:SF4:S1	2.29	0.73
1:A:415:LEU:HD12	1:A:443:LYS:HB2	1.70	0.73
1:A:168:LYS:HD3	1:A:178:ASP:HB2	1.71	0.73
1:B:168:LYS:HD3	1:B:178:ASP:HB2	1.71	0.72
4:C:435:CYS:HB2	8:C:603:SF4:S1	2.30	0.72
3:E:127:MET:HE3	3:E:130:ASP:HA	1.71	0.71
1:B:938:SER:HB3	1:B:941:GLN:HG3	1.73	0.71
3:F:102:LEU:HD21	3:F:113:ALA:HB2	1.74	0.70
1:A:114:ILE:HD12	1:B:122:LEU:HD13	1.74	0.70
4:C:127:ALA:HB2	4:C:307:LEU:HD22	1.74	0.70
1:A:938:SER:HB3	1:A:941:GLN:HG3	1.74	0.70
1:A:406:ASP:HA	1:A:712:GLU:HG3	1.72	0.70
4:C:148:GLY:O	9:C:601:NAI:N7N	2.23	0.70
1:A:122:LEU:HD13	1:B:114:ILE:HD12	1.74	0.69
4:D:127:ALA:HB2	4:D:307:LEU:HD22	1.74	0.69
3:F:93:ARG:HB3	3:F:141:VAL:HG11	1.73	0.69
4:C:124:LEU:HB2	4:C:198:GLU:HG3	1.74	0.68
4:D:124:LEU:HB2	4:D:198:GLU:HG3	1.74	0.68
4:C:470:GLY:O	1:B:69:ARG:HD3	1.93	0.68
1:B:829:ARG:NH2	5:B:1001:MGD:H15	1.91	0.68
4:D:149:GLY:HA2	4:D:400:GLY:HA2	1.75	0.68
4:D:386:PRO:HG2	4:D:391:LEU:HD23	1.75	0.68
3:F:127:MET:HE3	3:F:130:ASP:HA	1.76	0.68
1:A:69:ARG:HD3	4:D:470:GLY:O	1.93	0.67
1:A:656:GLU:HG2	1:A:658:ILE:HG23	1.77	0.67
3:E:93:ARG:HB3	3:E:141:VAL:HG11	1.76	0.67
1:A:192:CYS:HA	1:A:196:GLN:HB3	1.78	0.66
1:B:829:ARG:HH11	5:B:1002:MGD:H15	1.44	0.66
1:B:853:ARG:HH12	1:B:869:GLY:HA2	1.61	0.66
1:A:117:HIS:CE1	8:A:1005:SF4:S2	2.89	0.66
4:C:160:THR:HG21	9:C:601:NAI:H2A	1.76	0.66
1:B:117:HIS:CE1	8:B:1005:SF4:S2	2.89	0.66
4:D:148:GLY:O	9:D:601:NAI:N7N	2.29	0.65
1:A:853:ARG:HH12	1:A:869:GLY:HA2	1.60	0.65
4:C:202:VAL:HG11	4:C:307:LEU:HD13	1.79	0.65
4:D:150:ALA:HB2	9:D:601:NAI:H4D	1.78	0.65
4:D:202:VAL:HG11	4:D:307:LEU:HD13	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:656:GLU:HG2	1:B:658:ILE:HG23	1.79	0.64
1:A:304:THR:HG22	1:A:725:LYS:HE2	1.79	0.64
1:A:331:LEU:HD11	1:A:736:LEU:HB3	1.80	0.64
4:C:386:PRO:HG2	4:C:391:LEU:HD23	1.78	0.64
1:A:337:ARG:HB2	1:A:677:LEU:HD22	1.79	0.64
3:F:42:PRO:HA	3:F:45:LYS:HE3	1.79	0.64
4:D:474:ALA:HB3	10:D:602:FMN:HM82	1.80	0.62
4:D:200:MET:HG2	4:D:300:LEU:HD13	1.82	0.62
4:C:113:ASP:O	4:C:117:THR:HG23	1.99	0.62
4:D:113:ASP:O	4:D:117:THR:HG23	1.99	0.62
1:A:400:THR:HG22	1:A:402:ALA:H	1.63	0.62
4:C:200:MET:HG2	4:C:300:LEU:HD13	1.82	0.61
1:B:815:GLU:HG2	1:B:927:THR:HA	1.83	0.61
1:B:400:THR:HG22	1:B:402:ALA:H	1.65	0.61
4:D:330:VAL:HG12	4:D:334:VAL:HG11	1.83	0.61
3:F:98:LEU:HD22	3:F:109:ILE:HD13	1.83	0.61
1:A:815:GLU:HG2	1:A:927:THR:HA	1.83	0.60
1:B:117:HIS:HE1	8:B:1005:SF4:S2	2.21	0.60
1:A:117:HIS:HE1	8:A:1005:SF4:S2	2.19	0.60
4:C:7:CYS:HB3	4:C:38:ARG:HB3	1.83	0.59
1:B:829:ARG:NH1	5:B:1002:MGD:H15	2.00	0.59
1:B:640:LEU:O	1:B:644:VAL:HG23	2.03	0.59
1:A:829:ARG:HH22	5:A:1001:MGD:H15	1.50	0.59
1:A:640:LEU:O	1:A:644:VAL:HG23	2.03	0.58
4:D:366:LYS:HB2	4:D:409:ASP:HA	1.85	0.58
4:D:60:VAL:HG12	4:D:86:LEU:HD12	1.85	0.58
1:A:188:CYS:SG	1:A:230:CYS:HB3	2.43	0.58
4:D:44:MET:HB3	4:D:46:TRP:CZ3	2.39	0.58
4:C:366:LYS:HB2	4:C:409:ASP:HA	1.85	0.57
1:B:497:GLU:HG3	1:B:498:ARG:HG2	1.86	0.57
1:A:145:ARG:HB2	4:D:459:LEU:HD13	1.86	0.57
4:C:459:LEU:HD13	1:B:145:ARG:HB2	1.86	0.57
4:C:140:ILE:HG13	4:C:155:GLY:HA3	1.86	0.57
4:D:140:ILE:HG13	4:D:155:GLY:HA3	1.87	0.57
1:B:354:THR:HG21	1:B:363:THR:HG23	1.86	0.57
1:A:354:THR:HG21	1:A:363:THR:HG23	1.86	0.57
1:A:829:ARG:HD3	5:A:1002:MGD:C16	2.35	0.57
1:B:927:THR:HG23	1:B:929:VAL:HG13	1.87	0.57
9:D:601:NAI:H52N	10:D:602:FMN:H9	1.86	0.57
1:A:768:THR:H	1:A:771:MET:HG2	1.70	0.56
4:C:44:MET:HB3	4:C:46:TRP:CZ3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:457:THR:HG23	1:A:460:ILE:HB	1.87	0.56
1:A:927:THR:HG23	1:A:929:VAL:HG13	1.87	0.56
2:G:42:ALA:HB2	2:G:69:ALA:HB2	1.88	0.56
1:B:457:THR:HG23	1:B:460:ILE:HB	1.88	0.56
1:A:244:VAL:HG21	1:A:278:ARG:HH11	1.70	0.56
1:B:244:VAL:HG21	1:B:278:ARG:HH11	1.71	0.56
1:B:827:THR:HG21	5:B:1001:MGD:H191	1.71	0.56
4:C:60:VAL:HG12	4:C:86:LEU:HD12	1.87	0.55
2:H:42:ALA:HB2	2:H:69:ALA:HB2	1.89	0.55
1:A:854:LEU:HD13	1:A:874:VAL:HG21	1.89	0.55
3:F:41:GLU:O	3:F:45:LYS:HG3	2.07	0.55
1:A:262:GLY:O	1:A:710:ASN:HB2	2.08	0.54
1:A:388:SER:C	1:A:919:THR:HG21	2.33	0.54
4:D:235:GLU:HG3	4:D:240:LEU:HD12	1.90	0.54
3:F:17:ARG:HB3	3:F:20:ALA:HB2	1.89	0.54
4:C:235:GLU:HG3	4:C:240:LEU:HD12	1.90	0.54
4:D:171:ILE:HD13	4:D:293:VAL:HB	1.90	0.53
4:D:363:ARG:HH21	4:D:410:ARG:HG3	1.74	0.53
4:C:171:ILE:HD13	4:C:293:VAL:HB	1.89	0.53
1:B:262:GLY:O	1:B:710:ASN:HB2	2.07	0.53
1:B:388:SER:C	1:B:919:THR:HG21	2.33	0.53
3:F:94:LEU:HD13	3:F:141:VAL:HG13	1.90	0.53
1:B:854:LEU:HD13	1:B:874:VAL:HG21	1.91	0.53
4:C:347:THR:HA	4:C:386:PRO:HA	1.91	0.53
3:F:25:LEU:HD22	3:F:35:ILE:HD12	1.90	0.52
1:A:665:THR:HB	1:A:909:VAL:HG12	1.90	0.52
1:A:829:ARG:NH1	5:A:1002:MGD:H15	2.00	0.52
4:C:197:ILE:HG13	4:C:227:MET:HE1	1.91	0.52
3:E:25:LEU:HD22	3:E:35:ILE:HD12	1.91	0.52
1:A:408:ASP:O	1:A:411:GLU:HG3	2.09	0.52
1:B:281:PRO:HG3	1:B:292:SER:HB3	1.91	0.52
4:C:363:ARG:HH21	4:C:410:ARG:HG3	1.75	0.52
4:D:347:THR:HA	4:D:386:PRO:HA	1.91	0.52
2:G:23:ASP:HB2	2:G:26:GLU:HB2	1.90	0.52
1:B:390:THR:HA	1:B:563:VAL:HG11	1.92	0.52
1:B:665:THR:HB	1:B:909:VAL:HG12	1.91	0.52
1:B:410:VAL:O	1:B:437:ARG:HG2	2.10	0.51
1:A:386:CYS:HG	5:A:1001:MGD:H13	1.59	0.51
4:D:399:VAL:HG12	4:D:399:VAL:O	2.08	0.51
4:C:97:THR:HG21	4:C:317:TYR:CE1	2.46	0.51
3:E:144:ILE:O	3:E:148:VAL:HG12	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:GLU:HG3	1:B:722:MET:HG3	1.92	0.51
4:C:399:VAL:HG12	4:C:399:VAL:O	2.10	0.51
1:A:390:THR:HA	1:A:563:VAL:HG11	1.91	0.51
1:A:827:THR:HG21	5:A:1001:MGD:H191	1.75	0.51
3:E:17:ARG:HB3	3:E:20:ALA:HB2	1.91	0.51
1:A:281:PRO:HG3	1:A:292:SER:HB3	1.92	0.50
1:A:826:THR:CG2	5:A:1002:MGD:H8	2.37	0.50
1:B:331:LEU:HD11	1:B:736:LEU:HB3	1.93	0.50
4:D:4:TRP:HB2	4:D:52:GLU:HB2	1.93	0.50
1:B:304:THR:HG22	1:B:725:LYS:HE3	1.93	0.50
4:D:100:THR:HG22	4:D:188:LEU:HD13	1.94	0.50
4:D:126:LYS:O	4:D:130:MET:HG3	2.12	0.50
1:A:410:VAL:O	1:A:437:ARG:HG2	2.11	0.49
4:D:197:ILE:HG13	4:D:227:MET:HE1	1.94	0.49
4:C:275:VAL:HG11	4:C:473:CYS:HB3	1.94	0.49
4:C:297:LEU:HD23	4:C:298:LEU:HD23	1.94	0.49
4:D:97:THR:HG21	4:D:317:TYR:CE1	2.47	0.49
1:B:265:CYS:SG	1:B:288:ASN:HB3	2.52	0.49
4:D:63:GLY:O	4:D:65:MET:HG2	2.12	0.49
3:E:98:LEU:HD22	3:E:109:ILE:HD13	1.95	0.49
3:F:81:ALA:HB3	7:F:201:FES:S1	2.53	0.49
4:D:297:LEU:HD23	4:D:298:LEU:HD23	1.93	0.49
1:A:434:LEU:O	1:A:438:LEU:HG	2.12	0.49
1:B:75:ILE:HG12	1:B:95:VAL:HG22	1.95	0.49
4:C:220:TYR:HB3	4:C:223:CYS:HB2	1.95	0.49
1:B:434:LEU:O	1:B:438:LEU:HG	2.12	0.49
2:G:48:ILE:HD13	2:G:63:ALA:HB2	1.94	0.48
4:C:45:VAL:HA	4:C:48:GLU:HG2	1.95	0.48
1:B:678:VAL:HB	1:B:692:ALA:HA	1.95	0.48
1:B:826:THR:CG2	5:B:1002:MGD:H8	2.37	0.48
4:D:275:VAL:HG11	4:D:473:CYS:HB3	1.93	0.48
2:H:5:LYS:O	2:H:9:MET:HG3	2.13	0.48
4:C:126:LYS:O	4:C:130:MET:HG3	2.13	0.48
4:D:218:SER:HB3	4:D:252:GLY:O	2.12	0.48
3:E:94:LEU:HD13	3:E:141:VAL:HG13	1.93	0.48
1:A:265:CYS:SG	1:A:288:ASN:HB3	2.52	0.48
1:B:381:THR:HG23	1:B:383:ALA:H	1.78	0.48
4:C:188:LEU:HD22	4:C:297:LEU:HD21	1.96	0.48
2:H:48:ILE:HD13	2:H:63:ALA:HB2	1.96	0.48
1:B:295:LYS:HD2	1:B:834:TYR:HB2	1.95	0.48
1:A:381:THR:HG23	1:A:383:ALA:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:78:ARG:HD3	3:F:102:LEU:HD22	1.94	0.48
4:D:45:VAL:HA	4:D:48:GLU:HG2	1.96	0.48
1:A:75:ILE:HG12	1:A:95:VAL:HG22	1.96	0.48
1:A:476:VAL:HG13	1:A:532:LEU:HD21	1.96	0.48
4:C:63:GLY:O	4:C:65:MET:HG2	2.14	0.48
1:B:309:ILE:HG22	1:B:697:PRO:HB3	1.95	0.48
1:B:439:ARG:HG2	1:B:459:HIS:HB2	1.96	0.47
1:B:853:ARG:NH1	1:B:869:GLY:HA2	2.29	0.47
1:A:876:SER:HB3	1:A:929:VAL:HG12	1.96	0.47
3:E:81:ALA:HB3	7:E:201:FES:S1	2.54	0.47
4:D:220:TYR:HB3	4:D:223:CYS:HB2	1.96	0.47
1:B:344:THR:HB	1:B:345:HIS:CD2	2.49	0.47
1:B:634:LEU:HD22	1:B:638:ASN:HB3	1.97	0.47
1:A:295:LYS:HD2	1:A:834:TYR:HB2	1.96	0.47
1:A:703:GLU:HG3	1:A:722:MET:HG3	1.95	0.47
3:E:119:LEU:HD12	3:E:125:ALA:HB1	1.97	0.47
1:B:380:ASP:HB3	1:B:636:ILE:HG13	1.96	0.47
1:A:345:HIS:CD2	1:A:649:LYS:HG3	2.50	0.47
1:A:380:ASP:HB3	1:A:636:ILE:HG13	1.97	0.47
1:B:658:ILE:O	1:B:662:ASP:HB2	2.15	0.47
4:D:375:GLY:HA2	4:D:398:LEU:HD21	1.97	0.47
4:C:374:LEU:HD12	9:C:601:NAI:H5N	1.94	0.47
1:A:193:GLU:HG2	1:A:199:PHE:CE2	2.50	0.47
1:A:658:ILE:O	1:A:662:ASP:HB2	2.15	0.47
1:A:853:ARG:NH1	1:A:869:GLY:HA2	2.29	0.47
4:C:375:GLY:HA2	4:C:398:LEU:HD21	1.96	0.47
4:C:388:CYS:HB3	4:C:391:LEU:HB2	1.97	0.47
1:B:186:MET:HE2	1:B:186:MET:HB2	1.84	0.47
1:B:316:GLU:HG3	1:B:337:ARG:HH21	1.80	0.47
1:B:476:VAL:HG13	1:B:532:LEU:HD21	1.96	0.47
1:A:678:VAL:HB	1:A:692:ALA:HA	1.97	0.47
1:B:559:GLY:O	1:B:563:VAL:HG23	2.16	0.47
1:A:657:ASP:HB3	1:A:836:VAL:HG11	1.96	0.46
1:B:825:LEU:HB3	1:B:927:THR:HG22	1.98	0.46
4:D:388:CYS:HB3	4:D:391:LEU:HB2	1.97	0.46
1:A:439:ARG:HG2	1:A:459:HIS:HB2	1.96	0.46
1:B:110:MET:HG2	1:B:136:ALA:HA	1.98	0.46
4:D:54:GLU:HG2	4:D:59:ARG:HG3	1.97	0.46
1:A:829:ARG:HD3	5:A:1002:MGD:N15	2.30	0.46
3:E:71:LYS:HD2	3:E:72:HIS:NE2	2.30	0.46
3:F:74:ILE:HD11	3:F:148:VAL:HG21	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:LEU:HD22	1:A:638:ASN:HB3	1.97	0.46
1:A:559:GLY:O	1:A:563:VAL:HG23	2.16	0.46
3:F:41:GLU:HG3	3:F:51:ARG:HG3	1.98	0.46
1:B:75:ILE:HD12	1:B:82:PRO:HG2	1.97	0.46
1:A:309:ILE:HG22	1:A:697:PRO:HB3	1.97	0.45
4:C:4:TRP:HB2	4:C:52:GLU:HB2	1.98	0.45
1:B:657:ASP:HB3	1:B:836:VAL:HG11	1.97	0.45
1:B:876:SER:HB3	1:B:929:VAL:HG12	1.97	0.45
1:A:825:LEU:HB3	1:A:927:THR:HG22	1.98	0.45
1:B:363:THR:HG22	1:B:598:MET:HB2	1.98	0.45
1:A:428:PRO:HD2	8:A:1008:SF4:S1	2.56	0.45
1:A:807:ARG:HE	2:H:21:PRO:HG3	1.82	0.45
2:G:21:PRO:HG3	1:B:807:ARG:HE	1.81	0.45
4:D:261:GLU:O	4:D:265:LEU:HG	2.17	0.45
1:A:78:MET:HE2	1:A:78:MET:HB3	1.84	0.45
1:A:327:TRP:O	1:A:331:LEU:HG	2.17	0.45
2:H:33:SER:HA	2:H:41:ARG:HD3	1.98	0.45
4:C:138:GLU:HG2	4:C:307:LEU:HG	1.98	0.45
4:D:39:ASN:HA	4:D:109:PRO:HD3	1.98	0.45
4:D:175:VAL:HG13	4:D:185:ASP:HB3	1.98	0.45
1:B:345:HIS:CD2	1:B:649:LYS:HG3	2.52	0.45
1:B:551:LEU:HB2	1:B:925:LYS:HE2	1.99	0.45
4:D:138:GLU:HG2	4:D:307:LEU:HG	1.98	0.45
1:A:200:ALA:HB3	8:A:1007:SF4:S1	2.57	0.45
1:B:178:ASP:O	1:B:238:THR:HG23	2.17	0.45
1:A:110:MET:HG2	1:A:136:ALA:HA	1.98	0.44
1:A:363:THR:HG22	1:A:598:MET:HB2	1.98	0.44
4:C:175:VAL:HG22	4:C:297:LEU:HB2	1.98	0.44
4:C:247:LEU:HA	4:C:247:LEU:HD23	1.70	0.44
4:C:261:GLU:O	4:C:265:LEU:HG	2.17	0.44
4:C:325:THR:HA	4:C:343:GLY:HA2	1.99	0.44
1:A:270:HIS:HB2	1:A:278:ARG:HG2	2.00	0.44
1:B:263:VAL:HA	1:B:407:PHE:HE2	1.82	0.44
3:E:119:LEU:HD11	3:E:132:LEU:HD22	1.98	0.44
1:B:72:MET:HA	1:B:83:SER:HA	1.98	0.44
4:C:139:ILE:HG13	4:C:158:TRP:CZ3	2.53	0.44
1:B:429:VAL:O	1:B:433:ARG:HG3	2.17	0.44
1:B:826:THR:O	1:B:897:TYR:HA	2.17	0.44
1:A:313:MET:HG2	1:A:324:GLU:HG2	1.99	0.44
1:B:420:GLY:HA2	5:B:1002:MGD:N3	2.33	0.44
4:D:257:VAL:HG11	4:D:429:CYS:HB3	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:CYS:HB2	1:A:267:PHE:CE1	2.53	0.44
1:B:909:VAL:HG11	1:B:940:TRP:CD1	2.53	0.44
1:A:230:CYS:HB2	1:A:239:LEU:HD13	1.99	0.44
1:A:404:THR:HA	1:A:793:MET:HB2	1.99	0.44
2:G:7:ILE:HG23	2:G:55:LEU:HG	2.00	0.44
4:C:378:HIS:HB3	4:C:382:ASP:HB2	2.00	0.44
1:B:240:VAL:HG13	1:B:245:GLU:OE2	2.18	0.44
1:B:258:CYS:HB2	1:B:267:PHE:CE1	2.52	0.44
1:B:270:HIS:HB2	1:B:278:ARG:HG2	1.99	0.44
1:B:687:GLU:HB3	1:B:944:TYR:OH	2.18	0.44
4:D:247:LEU:HD23	4:D:247:LEU:HA	1.76	0.44
4:D:374:LEU:HD12	9:D:601:NAI:H5N	2.00	0.44
1:A:72:MET:HA	1:A:83:SER:HA	1.99	0.43
1:A:178:ASP:O	1:A:238:THR:HG23	2.17	0.43
1:A:186:MET:HE2	1:A:186:MET:HB2	1.90	0.43
1:A:263:VAL:HA	1:A:407:PHE:HE2	1.82	0.43
2:G:32:ILE:O	2:G:36:TRP:HB2	2.18	0.43
2:H:32:ILE:O	2:H:36:TRP:HB2	2.18	0.43
1:B:193:GLU:HG2	1:B:199:PHE:CD2	2.53	0.43
4:D:325:THR:HA	4:D:343:GLY:HA2	2.00	0.43
4:C:7:CYS:HA	4:C:38:ARG:HH21	1.83	0.43
1:B:121:CYS:O	1:B:127:ASN:HB2	2.18	0.43
1:A:605:LEU:HG	1:A:611:VAL:HG12	2.00	0.43
2:G:63:ALA:HA	2:G:66:ILE:HD12	1.99	0.43
1:A:75:ILE:HD12	1:A:82:PRO:HG2	1.99	0.43
1:A:121:CYS:O	1:A:127:ASN:HB2	2.18	0.43
1:A:169:ASP:HB3	1:A:177:TYR:HB3	2.00	0.43
1:A:909:VAL:HG11	1:A:940:TRP:CD1	2.53	0.43
4:C:257:VAL:HG11	4:C:429:CYS:HB3	1.99	0.43
1:A:155:VAL:HG22	1:A:165:TYR:CZ	2.53	0.43
4:C:414:LEU:HG	4:C:494:PHE:CD2	2.54	0.43
1:B:338:LEU:HD13	1:B:741:LEU:HD11	2.00	0.43
4:D:139:ILE:HG13	4:D:158:TRP:CZ3	2.54	0.43
3:F:101:LYS:HA	3:F:101:LYS:HD2	1.90	0.43
1:B:824:LEU:HD23	1:B:824:LEU:HA	1.88	0.43
1:A:871:TRP:HE3	1:A:882:THR:HG22	1.83	0.43
4:C:218:SER:HB3	4:C:252:GLY:O	2.19	0.43
4:C:231:ILE:HD12	4:C:249:VAL:HG23	2.01	0.43
4:D:47:LEU:HA	4:D:64:PRO:HD3	2.01	0.43
4:D:63:GLY:HA2	4:D:84:LEU:HD11	2.00	0.43
4:D:418:ARG:HA	4:D:446:LEU:HD13	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:457:LEU:HD12	4:D:496:VAL:HB	2.00	0.43
1:A:193:GLU:HG2	1:A:199:PHE:CD2	2.54	0.43
4:C:63:GLY:HA2	4:C:84:LEU:HD11	2.00	0.43
1:B:155:VAL:HG22	1:B:165:TYR:CZ	2.54	0.43
4:D:378:HIS:HB3	4:D:382:ASP:HB2	2.01	0.43
1:A:56:LEU:HA	1:A:56:LEU:HD23	1.80	0.43
1:A:420:GLY:HA2	5:A:1002:MGD:N3	2.33	0.43
2:G:29:ALA:HB2	2:G:62:ALA:HB1	2.01	0.43
4:C:6:PRO:HG2	4:C:48:GLU:OE1	2.19	0.43
4:C:418:ARG:HA	4:C:446:LEU:HD13	2.00	0.43
4:D:186:ARG:HG3	4:D:223:CYS:SG	2.58	0.43
1:A:338:LEU:HD13	1:A:741:LEU:HD11	2.01	0.43
1:B:428:PRO:HD2	8:B:1008:SF4:S1	2.59	0.43
4:D:264:MET:HE2	4:D:264:MET:HB3	1.84	0.43
1:A:157:GLN:OE1	1:A:157:GLN:HA	2.18	0.42
1:A:177:TYR:HA	1:A:238:THR:O	2.19	0.42
1:A:402:ALA:HB1	1:A:713:ARG:HD3	2.01	0.42
1:A:578:ARG:O	1:A:581:VAL:HG22	2.19	0.42
1:B:385:VAL:HB	1:B:924:TYR:HE2	1.84	0.42
1:B:749:HIS:ND1	1:B:751:ARG:HB2	2.34	0.42
1:A:522:GLU:HG3	1:A:528:PRO:HA	2.01	0.42
3:E:101:LYS:HA	3:E:101:LYS:HD2	1.89	0.42
1:B:169:ASP:HB3	1:B:177:TYR:HB3	2.00	0.42
1:B:634:LEU:O	1:B:639:MET:HE3	2.19	0.42
1:A:634:LEU:O	1:A:639:MET:HE3	2.18	0.42
1:A:835:ASN:O	1:A:901:HIS:HA	2.20	0.42
3:E:72:HIS:CB	3:E:148:VAL:HG23	2.49	0.42
3:E:119:LEU:HB3	3:E:122:CYS:SG	2.59	0.42
1:B:295:LYS:HE2	8:B:1008:SF4:S4	2.60	0.42
2:G:58:LEU:HD12	2:G:58:LEU:HA	1.83	0.42
4:C:264:MET:HE2	4:C:264:MET:HB3	1.83	0.42
2:H:29:ALA:HB2	2:H:62:ALA:HB1	2.01	0.42
4:D:135:VAL:HG13	4:D:307:LEU:HD21	2.02	0.42
1:A:188:CYS:SG	1:A:188:CYS:O	2.78	0.42
1:A:313:MET:HE3	1:A:313:MET:HB2	1.84	0.42
1:A:331:LEU:CD1	1:A:736:LEU:HB3	2.48	0.42
1:A:551:LEU:HB2	1:A:925:LYS:HE2	2.02	0.42
4:C:457:LEU:HD12	4:C:496:VAL:HB	2.02	0.42
1:B:522:GLU:HG3	1:B:528:PRO:HA	2.01	0.42
1:B:603:HIS:NE2	1:B:604:GLU:HG3	2.35	0.42
1:A:174:TYR:CZ	1:A:844:GLU:HB2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:749:HIS:ND1	1:A:751:ARG:HB2	2.34	0.42
3:E:78:ARG:HD3	3:E:102:LEU:HD22	2.02	0.42
1:B:53:ILE:HG23	1:B:97:THR:HG23	2.02	0.42
1:B:177:TYR:HA	1:B:238:THR:O	2.20	0.42
1:B:316:GLU:HG3	1:B:337:ARG:NH2	2.34	0.42
1:B:578:ARG:O	1:B:581:VAL:HG22	2.19	0.42
1:A:53:ILE:HG23	1:A:97:THR:HG23	2.02	0.42
1:B:871:TRP:HE3	1:B:882:THR:HG22	1.85	0.42
1:A:720:ARG:HE	1:A:720:ARG:HB3	1.73	0.42
1:A:826:THR:O	1:A:897:TYR:HA	2.20	0.42
2:H:58:LEU:HD12	2:H:58:LEU:HA	1.83	0.42
3:F:7:LEU:HD21	3:F:42:PRO:HB2	2.02	0.41
4:C:175:VAL:HG13	4:C:185:ASP:HB3	2.01	0.41
4:D:414:LEU:HG	4:D:494:PHE:CD2	2.55	0.41
1:A:295:LYS:HE2	8:A:1008:SF4:S4	2.60	0.41
1:A:419:ILE:HG23	1:A:447:VAL:HB	2.02	0.41
1:B:605:LEU:HG	1:B:611:VAL:HG12	2.01	0.41
1:A:344:THR:HB	1:A:345:HIS:CD2	2.55	0.41
4:C:91:PRO:O	4:C:95:ARG:HG3	2.20	0.41
1:A:168:LYS:HG2	1:A:170:THR:HG23	2.01	0.41
1:B:415:LEU:HD21	1:B:445:ILE:HD12	2.03	0.41
1:B:663:PRO:HG3	1:B:922:PRO:HB3	2.02	0.41
1:B:677:LEU:HD12	1:B:693:HIS:HB2	2.02	0.41
4:D:91:PRO:O	4:D:95:ARG:HG3	2.20	0.41
4:D:392:PHE:HB2	4:D:399:VAL:HG23	2.03	0.41
1:A:663:PRO:HG3	1:A:922:PRO:HB3	2.03	0.41
1:A:722:MET:HE2	1:A:722:MET:HB3	1.89	0.41
3:F:119:LEU:HD11	3:F:132:LEU:HD13	2.02	0.41
1:B:435:ARG:NE	1:B:457:THR:HB	2.36	0.41
3:F:94:LEU:HD12	3:F:94:LEU:HA	1.88	0.41
4:C:265:LEU:HD11	4:C:282:PRO:HB3	2.03	0.41
1:B:168:LYS:HG2	1:B:170:THR:HG23	2.01	0.41
1:B:386:CYS:SG	5:B:1002:MGD:S12	3.18	0.41
4:D:231:ILE:HD12	4:D:249:VAL:HG23	2.02	0.41
4:D:335:LYS:HD3	4:D:336:TYR:CE1	2.56	0.41
1:A:81:MET:HE3	1:A:81:MET:HB2	1.97	0.41
1:A:919:THR:H	1:A:919:THR:HG23	1.69	0.41
4:C:265:LEU:HD22	4:C:287:LEU:HB2	2.02	0.41
1:B:174:TYR:CZ	1:B:844:GLU:HB2	2.55	0.41
1:B:271:MET:HE3	1:B:271:MET:HB3	1.97	0.41
1:B:402:ALA:HB1	1:B:713:ARG:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:240:VAL:HG13	1:A:245:GLU:OE2	2.19	0.41
1:A:677:LEU:HD12	1:A:693:HIS:HB2	2.01	0.41
1:B:404:THR:HA	1:B:793:MET:HB2	2.01	0.41
1:A:30:ASP:HB3	1:B:274:GLU:HB3	2.03	0.41
1:A:345:HIS:CE1	1:A:649:LYS:HE3	2.56	0.41
1:A:378:ASN:HB3	1:A:639:MET:HE2	2.03	0.41
1:A:415:LEU:HD22	1:A:539:TYR:HA	2.03	0.41
3:F:76:LEU:HD12	3:F:126:ALA:HB2	2.02	0.41
1:B:120:ASP:O	1:B:124:CYS:HB2	2.21	0.41
1:B:494:PHE:CD1	1:B:574:GLY:HA2	2.56	0.41
1:A:245:GLU:H	1:A:245:GLU:HG3	1.71	0.41
4:C:135:VAL:HG13	4:C:307:LEU:HD21	2.02	0.41
4:C:279:PRO:HG2	1:B:86:THR:O	2.21	0.41
4:D:265:LEU:HD11	4:D:282:PRO:HB3	2.03	0.41
1:A:824:LEU:HD23	1:A:824:LEU:HA	1.88	0.40
1:A:854:LEU:HB2	1:A:883:LEU:HD21	2.02	0.40
3:E:50:SER:HB3	3:E:53:GLU:HG3	2.03	0.40
1:B:830:ILE:CD1	1:B:833:GLN:H	2.34	0.40
1:B:835:ASN:O	1:B:901:HIS:HA	2.21	0.40
4:D:182:SER:HA	4:D:329:GLN:OE1	2.21	0.40
4:C:182:SER:HA	4:C:329:GLN:OE1	2.21	0.40
1:B:313:MET:HE3	1:B:313:MET:HB2	1.90	0.40
1:A:188:CYS:O	1:A:189:VAL:C	2.64	0.40
1:B:151:ASN:ND2	1:B:157:GLN:HE22	2.19	0.40
1:B:419:ILE:HG23	1:B:447:VAL:HB	2.03	0.40
1:A:494:PHE:CD1	1:A:574:GLY:HA2	2.56	0.40
1:B:263:VAL:HA	1:B:407:PHE:CE2	2.57	0.40
1:B:331:LEU:CD1	1:B:736:LEU:HB3	2.51	0.40
4:D:171:ILE:O	4:D:212:GLY:HA2	2.22	0.40
1:A:34:VAL:HG23	1:A:48:GLN:OE1	2.22	0.40
1:A:120:ASP:O	1:A:124:CYS:HB2	2.21	0.40
3:E:82:CYS:HA	3:E:123:ALA:HB1	2.04	0.40
1:B:345:HIS:CE1	1:B:649:LYS:HE3	2.56	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	949/958 (99%)	921 (97%)	28 (3%)	0	100	100
1	B	949/958 (99%)	921 (97%)	28 (3%)	0	100	100
2	G	64/70 (91%)	62 (97%)	2 (3%)	0	100	100
2	H	64/70 (91%)	61 (95%)	3 (5%)	0	100	100
3	E	147/150 (98%)	144 (98%)	2 (1%)	1 (1%)	19	51
3	F	147/150 (98%)	142 (97%)	4 (3%)	1 (1%)	19	51
4	C	494/502 (98%)	475 (96%)	19 (4%)	0	100	100
4	D	494/502 (98%)	476 (96%)	17 (3%)	1 (0%)	44	74
All	All	3308/3360 (98%)	3202 (97%)	103 (3%)	3 (0%)	50	79

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	116	CYS
3	E	116	CYS
4	D	400	GLY

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	756/763 (99%)	739 (98%)	17 (2%)	47	71
1	B	756/763 (99%)	734 (97%)	22 (3%)	37	65

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	G	42/45 (93%)	41 (98%)	1 (2%)	44 70
2	H	42/45 (93%)	40 (95%)	2 (5%)	21 51
3	E	106/107 (99%)	101 (95%)	5 (5%)	22 52
3	F	106/107 (99%)	102 (96%)	4 (4%)	28 59
4	C	371/375 (99%)	360 (97%)	11 (3%)	36 64
4	D	371/375 (99%)	361 (97%)	10 (3%)	40 67
All	All	2550/2580 (99%)	2478 (97%)	72 (3%)	40 66

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	VAL
1	A	65	VAL
1	A	246	GLU
1	A	311	LYS
1	A	363	THR
1	A	365	LEU
1	A	457	THR
1	A	509	GLU
1	A	572	MET
1	A	748	THR
1	A	813	THR
1	A	814	ASP
1	A	832	SER
1	A	890	ARG
1	A	891	VAL
1	A	909	VAL
1	A	913	ASP
2	G	19	VAL
3	F	8	ARG
3	F	22	LEU
3	F	102	LEU
3	F	108	ASP
2	H	5	LYS
2	H	19	VAL
4	C	8	ASP
4	C	94	LYS
4	C	113	ASP
4	C	222	ASP
4	C	242	GLU

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Mol	Chain	Res	Type
4	C	307	LEU
4	C	316	SER
4	C	339	LEU
4	C	398	LEU
4	C	414	LEU
4	C	462	ASP
3	E	2	THR
3	E	8	ARG
3	E	22	LEU
3	E	45	LYS
3	E	108	ASP
1	B	34	VAL
1	B	65	VAL
1	B	246	GLU
1	B	311	LYS
1	B	363	THR
1	B	379	THR
1	B	388	SER
1	B	456	GLU
1	B	457	THR
1	B	474	VAL
1	B	509	GLU
1	B	572	MET
1	B	748	THR
1	B	811	LEU
1	B	813	THR
1	B	814	ASP
1	B	832	SER
1	B	890	ARG
1	B	891	VAL
1	B	909	VAL
1	B	913	ASP
1	B	934	SER
4	D	94	LYS
4	D	113	ASP
4	D	114	GLN
4	D	222	ASP
4	D	307	LEU
4	D	316	SER
4	D	334	VAL
4	D	339	LEU
4	D	398	LEU

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Mol	Chain	Res	Type
4	D	418	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	117	HIS
1	A	218	ASN
1	A	339	ASN
1	A	345	HIS
1	A	482	HIS
1	A	575	ASN
1	A	716	ASN
1	A	835	ASN
1	A	908	ASN
1	A	914	ASN
3	F	83	GLN
2	H	31	HIS
4	C	174	ASN
4	C	296	ASN
4	C	309	HIS
1	B	117	HIS
1	B	218	ASN
1	B	345	HIS
1	B	482	HIS
1	B	575	ASN
1	B	638	ASN
1	B	716	ASN
1	B	908	ASN
1	B	914	ASN
4	D	174	ASN
4	D	309	HIS
4	D	380	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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)

Of 24 ligands modelled in this entry, 2 are monoatomic - leaving 22 for Mogul analysis.

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	$\#\|Z\| > 2$
10	FMN	D	602	-	33,33,33	0.63	0	48,50,50	0.67	1 (2%)
10	FMN	C	602	-	33,33,33	1.17	3 (9%)	48,50,50	1.30	7 (14%)
5	MGD	A	1002	-	41,52,52	1.46	6 (14%)	40,81,81	1.73	3 (7%)
5	MGD	B	1001	-	41,52,52	1.33	5 (12%)	40,81,81	1.26	5 (12%)
7	FES	F	201	3	0,4,4	-	-	-		
8	SF4	D	603	4	0,12,12	-	-	-		
8	SF4	A	1005	1	0,12,12	-	-	-		
7	FES	A	1004	1	0,4,4	-	-	-		
8	SF4	A	1008	1	0,12,12	-	-	-		
7	FES	B	1004	1	0,4,4	-	-	-		
9	NAI	D	601	-	42,48,48	0.58	0	47,73,73	0.72	2 (4%)
8	SF4	A	1006	1	0,12,12	-	-	-		
8	SF4	A	1007	1	0,12,12	-	-	-		
5	MGD	B	1002	-	41,52,52	1.46	6 (14%)	40,81,81	1.67	3 (7%)
7	FES	E	201	3	0,4,4	-	-	-		
8	SF4	B	1005	1	0,12,12	-	-	-		
8	SF4	B	1006	1	0,12,12	-	-	-		
8	SF4	B	1008	1	0,12,12	-	-	-		
8	SF4	C	603	4	0,12,12	-	-	-		
5	MGD	A	1001	-	41,52,52	1.30	5 (12%)	40,81,81	1.34	6 (15%)
8	SF4	B	1007	1	0,12,12	-	-	-		
9	NAI	C	601	-	42,48,48	0.59	0	47,73,73	0.70	2 (4%)

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
10	FMN	D	602	-	-	3/18/18/18	0/3/3/3
10	FMN	C	602	-	-	4/18/18/18	0/3/3/3
5	MGD	A	1002	-	-	7/18/66/66	0/6/6/6
5	MGD	B	1001	-	-	7/18/66/66	0/6/6/6
7	FES	F	201	3	-	-	0/1/1/1
8	SF4	D	603	4	-	-	0/6/5/5
8	SF4	A	1005	1	-	-	0/6/5/5
7	FES	A	1004	1	-	-	0/1/1/1
8	SF4	A	1008	1	-	-	0/6/5/5
7	FES	B	1004	1	-	-	0/1/1/1
9	NAI	D	601	-	-	12/25/72/72	0/5/5/5
8	SF4	A	1006	1	-	-	0/6/5/5
8	SF4	A	1007	1	-	-	0/6/5/5
5	MGD	B	1002	-	-	7/18/66/66	0/6/6/6
7	FES	E	201	3	-	-	0/1/1/1
8	SF4	B	1005	1	-	-	0/6/5/5
8	SF4	B	1006	1	-	-	0/6/5/5
8	SF4	B	1008	1	-	-	0/6/5/5
8	SF4	C	603	4	-	-	0/6/5/5
5	MGD	A	1001	-	-	8/18/66/66	0/6/6/6
8	SF4	B	1007	1	-	-	0/6/5/5
9	NAI	C	601	-	-	7/25/72/72	0/5/5/5

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	C	602	FMN	C4A-N5	3.64	1.37	1.30
5	B	1002	MGD	O11-C11	-3.60	1.38	1.43
5	A	1002	MGD	O11-C11	-3.53	1.39	1.43
5	B	1001	MGD	C8-N7	-3.30	1.29	1.35
5	A	1001	MGD	C8-N7	-3.22	1.29	1.35
5	B	1002	MGD	C8-N7	-3.17	1.29	1.35
5	A	1002	MGD	C8-N7	-3.16	1.29	1.35
5	B	1002	MGD	C23-N22	-3.08	1.40	1.45
5	A	1002	MGD	C23-N22	-3.05	1.40	1.45
5	A	1002	MGD	C5-C6	-2.80	1.41	1.47
5	B	1002	MGD	C5-C6	-2.78	1.41	1.47
5	A	1001	MGD	O11-C11	-2.72	1.40	1.43
5	B	1001	MGD	O11-C11	-2.71	1.40	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1001	MGD	C5-C6	-2.65	1.42	1.47
5	A	1001	MGD	C5-C6	-2.52	1.42	1.47
5	A	1001	MGD	C23-N22	-2.20	1.41	1.45
5	B	1001	MGD	C23-N22	-2.17	1.41	1.45
10	C	602	FMN	C4A-C10	-2.10	1.37	1.44
5	B	1002	MGD	O11-C23	-2.09	1.40	1.43
5	A	1002	MGD	C5-C4	-2.07	1.37	1.43
5	B	1001	MGD	C5-C4	-2.06	1.37	1.43
10	C	602	FMN	C10-N1	2.04	1.37	1.33
5	A	1001	MGD	C5-C4	-2.03	1.37	1.43
5	B	1002	MGD	C5-C4	-2.03	1.37	1.43
5	A	1002	MGD	O11-C23	-2.01	1.40	1.43

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1002	MGD	O11-C23-N22	-8.99	99.33	108.57
5	B	1002	MGD	O11-C23-N22	-8.56	99.77	108.57
5	A	1001	MGD	O11-C23-N22	4.80	113.50	108.57
5	B	1001	MGD	O11-C23-N22	4.43	113.12	108.57
10	C	602	FMN	C4-N3-C2	-3.58	119.03	125.64
5	A	1001	MGD	O11-C23-C14	3.01	110.97	108.96
10	C	602	FMN	C4A-C4-N3	2.95	120.69	113.19
10	C	602	FMN	O4-C4-C4A	-2.87	118.97	126.60
10	C	602	FMN	C4A-C10-N10	2.56	120.22	116.48
5	B	1002	MGD	O6-C6-C5	2.50	129.25	124.37
5	A	1002	MGD	O6-C6-C5	2.49	129.24	124.37
9	C	601	NAI	C3D-C2D-C1D	2.48	106.15	101.43
5	A	1001	MGD	PA-O3B-PB	-2.47	124.35	132.83
5	B	1001	MGD	PA-O3B-PB	-2.47	124.36	132.83
9	D	601	NAI	C3D-C2D-C1D	2.43	106.05	101.43
5	A	1001	MGD	O6-C6-C5	2.33	128.92	124.37
10	C	602	FMN	C4A-C10-N1	-2.31	119.38	124.73
10	C	602	FMN	C9A-C5A-N5	-2.28	119.95	122.43
9	C	601	NAI	C5A-C6A-N6A	2.25	123.77	120.35
9	D	601	NAI	C5A-C6A-N6A	2.23	123.74	120.35
5	B	1001	MGD	O11-C23-C14	2.23	110.45	108.96
5	B	1001	MGD	C19-N20-C21	2.11	117.24	113.43
5	B	1001	MGD	O6-C6-C5	2.10	128.47	124.37
5	A	1001	MGD	C19-N20-C21	2.09	117.20	113.43
10	D	602	FMN	C4-N3-C2	-2.09	121.78	125.64
10	C	602	FMN	C10-C4A-N5	-2.08	120.44	124.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	A	1001	MGD	C5-C6-N1	-2.07	110.30	113.95
5	A	1002	MGD	PA-O3A-C10	-2.04	109.70	121.68
5	B	1002	MGD	PA-O3A-C10	-2.03	109.77	121.68

There are no chirality outliers.

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	1001	MGD	C5'-O5'-PB-O1B
5	A	1001	MGD	C10-O3A-PA-O1A
5	A	1001	MGD	C10-O3A-PA-O2A
5	A	1002	MGD	C5'-O5'-PB-O3B
5	A	1002	MGD	C10-O3A-PA-O3B
5	A	1002	MGD	O4'-C4'-C5'-O5'
5	B	1001	MGD	C5'-O5'-PB-O1B
5	B	1001	MGD	C10-O3A-PA-O1A
5	B	1001	MGD	C10-O3A-PA-O2A
5	B	1002	MGD	C5'-O5'-PB-O3B
5	B	1002	MGD	C10-O3A-PA-O3B
5	B	1002	MGD	C10-O3A-PA-O2A
5	B	1002	MGD	O4'-C4'-C5'-O5'
9	C	601	NAI	O4B-C4B-C5B-O5B
9	D	601	NAI	C5B-O5B-PA-O2A
9	D	601	NAI	C5B-O5B-PA-O3
9	D	601	NAI	O4B-C4B-C5B-O5B
9	D	601	NAI	C5D-O5D-PN-O1N
9	D	601	NAI	C5D-O5D-PN-O2N
5	A	1002	MGD	C3'-C4'-C5'-O5'
5	B	1002	MGD	C3'-C4'-C5'-O5'
9	C	601	NAI	C3B-C4B-C5B-O5B
9	D	601	NAI	C3D-C4D-C5D-O5D
9	D	601	NAI	PA-O3-PN-O2N
10	C	602	FMN	O2'-C2'-C3'-C4'
10	C	602	FMN	C4'-C5'-O5'-P
9	C	601	NAI	PN-O3-PA-O5B
9	C	601	NAI	PA-O3-PN-O5D
9	D	601	NAI	PA-O3-PN-O5D
5	A	1002	MGD	C5'-O5'-PB-O1B
5	A	1002	MGD	C5'-O5'-PB-O2B
5	A	1002	MGD	C10-O3A-PA-O2A
5	B	1002	MGD	C5'-O5'-PB-O1B
5	B	1002	MGD	C5'-O5'-PB-O2B

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Mol	Chain	Res	Type	Atoms
10	D	602	FMN	N10-C1'-C2'-O2'
9	D	601	NAI	O4D-C1D-N1N-C2N
5	A	1001	MGD	PB-O3B-PA-O1A
10	D	602	FMN	C4'-C5'-O5'-P
10	C	602	FMN	O2'-C2'-C3'-O3'
5	A	1001	MGD	O4'-C4'-C5'-O5'
5	B	1001	MGD	O4'-C4'-C5'-O5'
9	C	601	NAI	O4D-C1D-N1N-C2N
9	D	601	NAI	C2D-C1D-N1N-C2N
5	B	1001	MGD	PB-O3B-PA-O1A
9	C	601	NAI	PN-O3-PA-O1A
9	C	601	NAI	C2D-C1D-N1N-C2N
9	D	601	NAI	O4D-C4D-C5D-O5D
5	A	1001	MGD	C10-O3A-PA-O3B
5	B	1001	MGD	C10-O3A-PA-O3B
9	D	601	NAI	C5D-O5D-PN-O3
5	A	1001	MGD	C3'-C4'-C5'-O5'
5	A	1001	MGD	PB-O3B-PA-O2A
5	B	1001	MGD	C3'-C4'-C5'-O5'
10	C	602	FMN	N10-C1'-C2'-O2'
10	D	602	FMN	N10-C1'-C2'-C3'

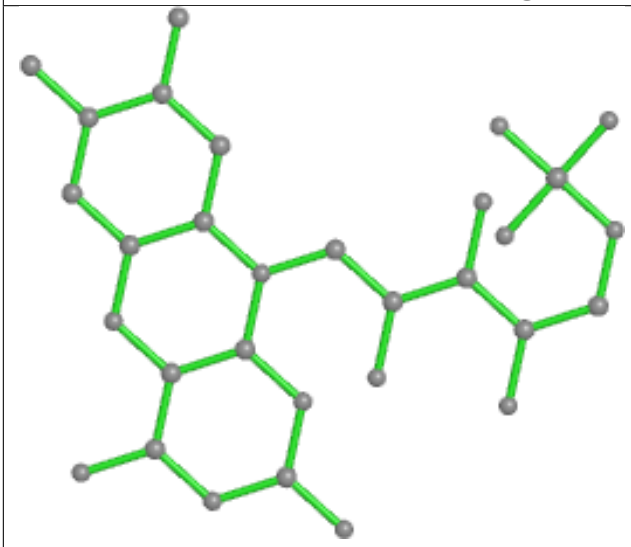
There are no ring outliers.

16 monomers are involved in 42 short contacts:

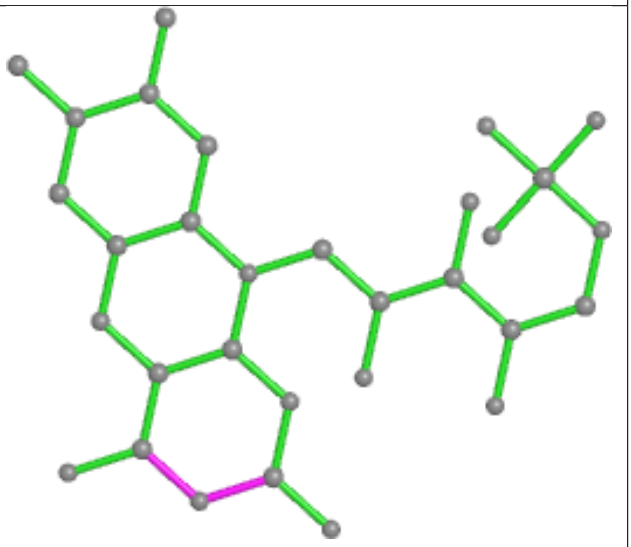
Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	D	602	FMN	2	0
5	A	1002	MGD	7	0
5	B	1001	MGD	3	0
7	F	201	FES	1	0
8	D	603	SF4	1	0
8	A	1005	SF4	2	0
8	A	1008	SF4	2	0
9	D	601	NAI	5	0
8	A	1007	SF4	1	0
5	B	1002	MGD	6	0
7	E	201	FES	1	0
8	B	1005	SF4	2	0
8	B	1008	SF4	2	0
8	C	603	SF4	1	0
5	A	1001	MGD	3	0
9	C	601	NAI	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.

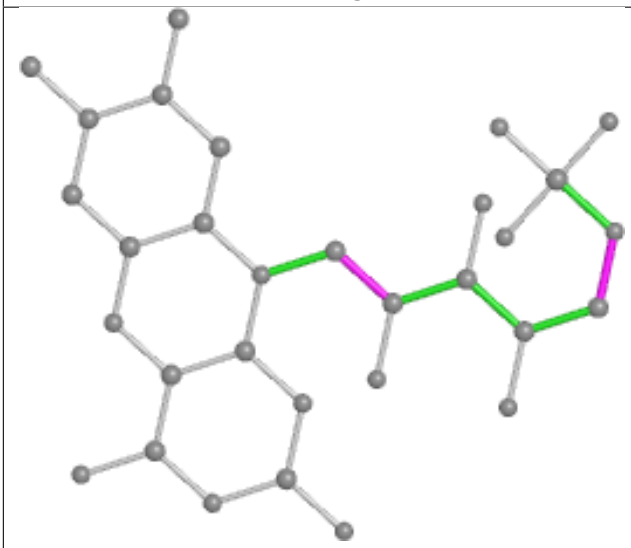
Ligand FMN D 602



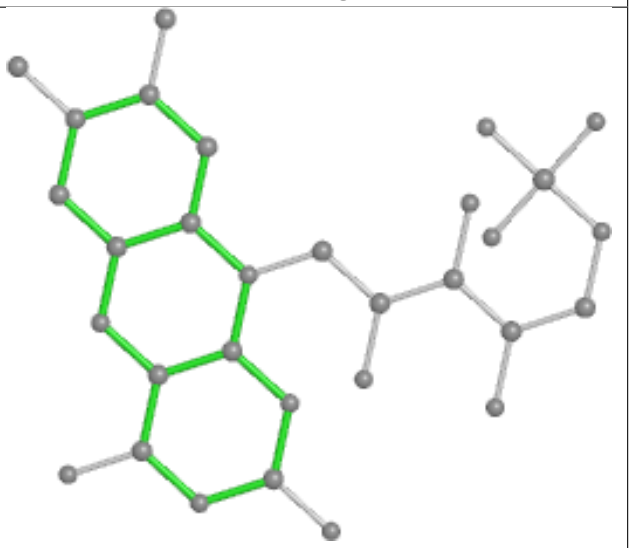
Bond lengths



Bond angles

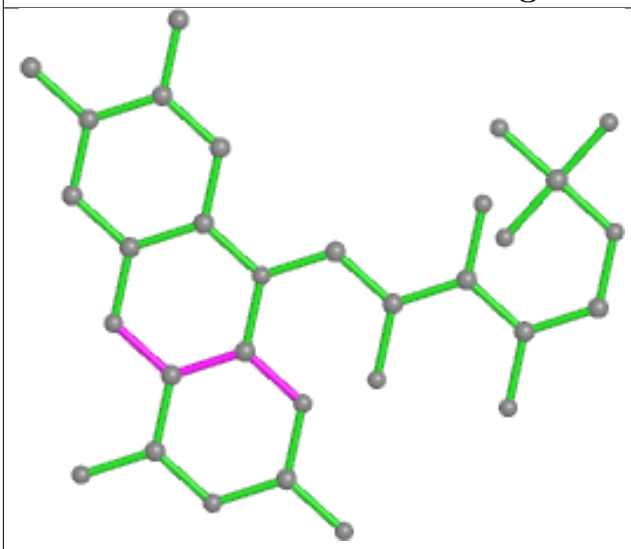


Torsions



Rings

Ligand FMN C 602



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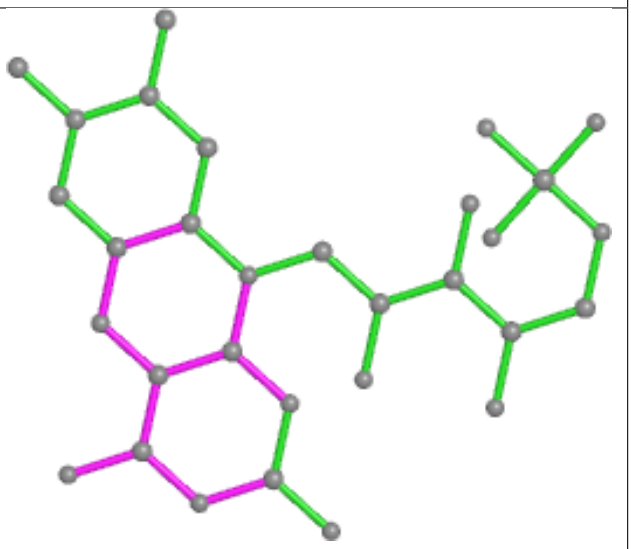
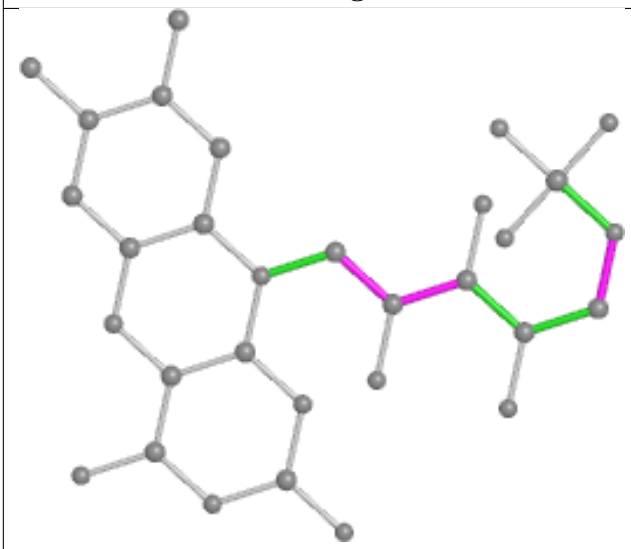


Bond angles



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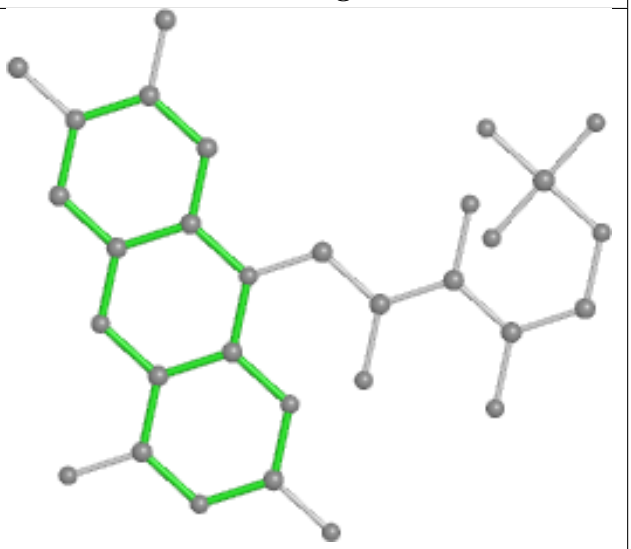
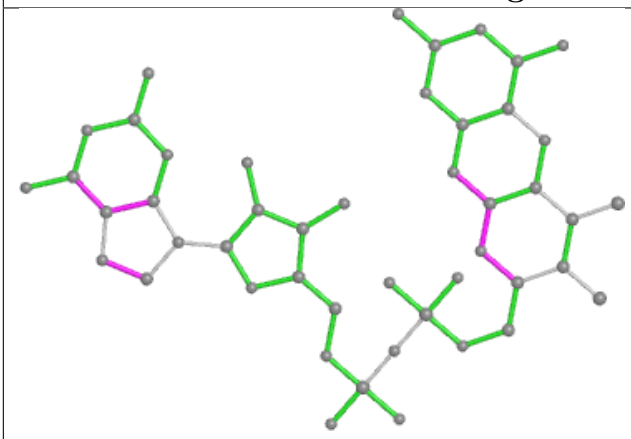


Rings

Ligand MGD A 1002



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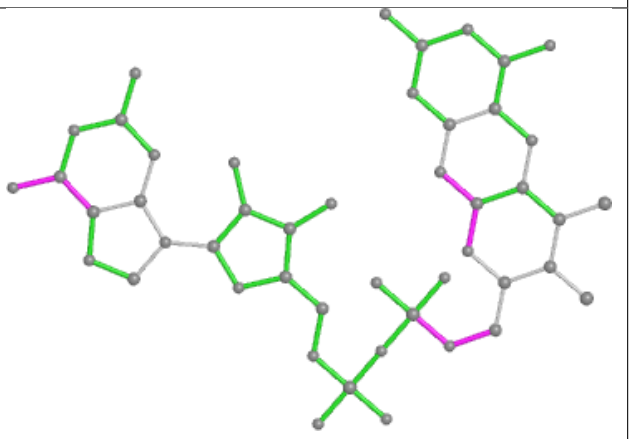

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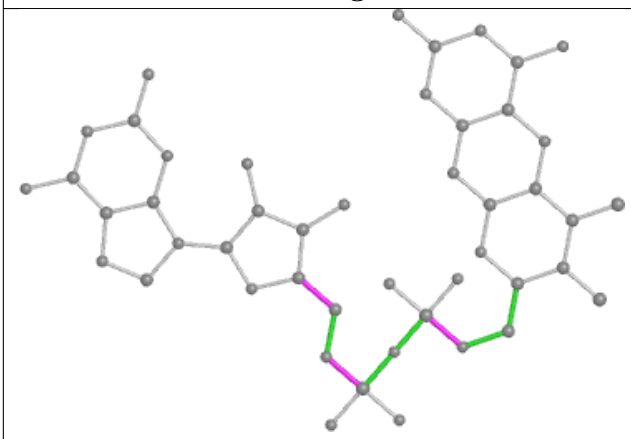

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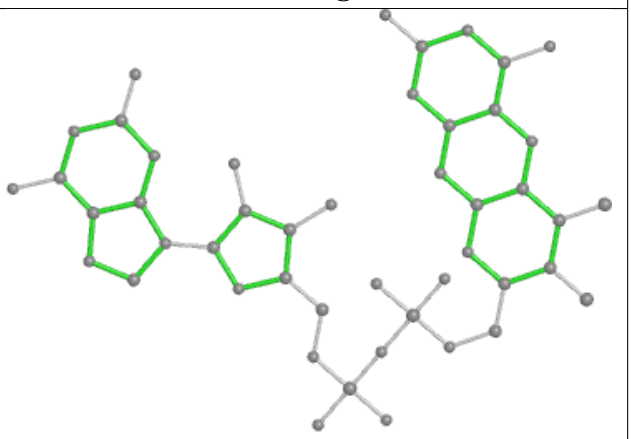
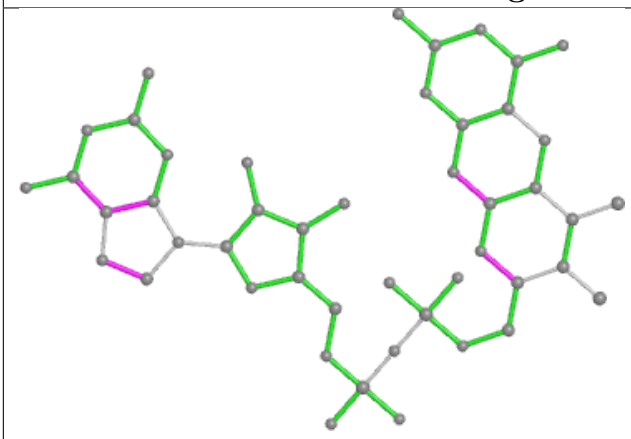


Rings

Ligand MGD B 1001



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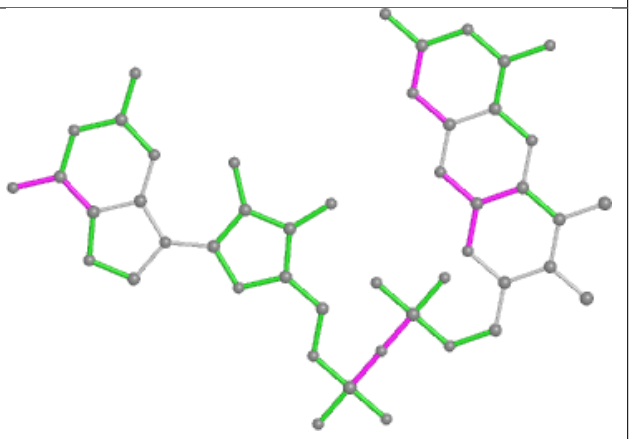

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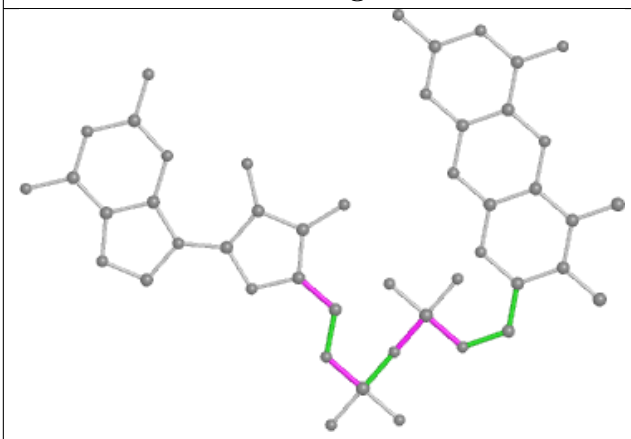

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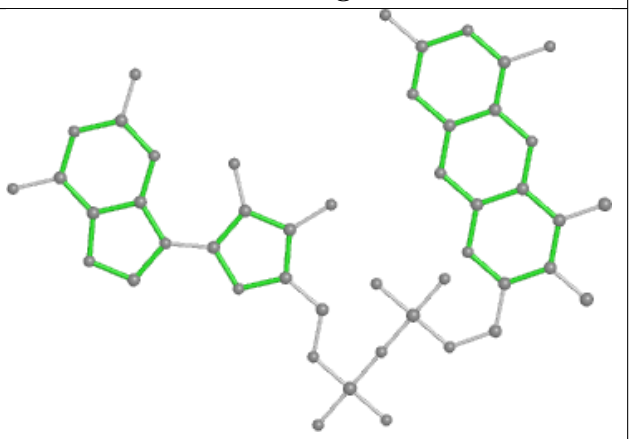
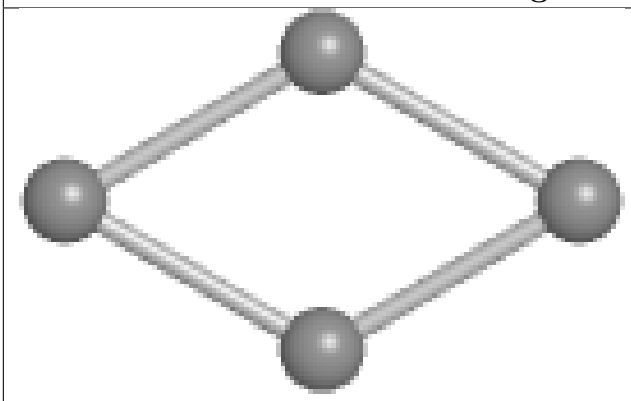


Rings

Ligand FES F 201



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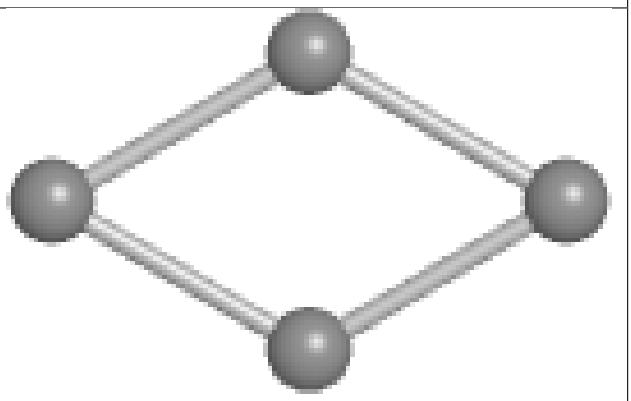

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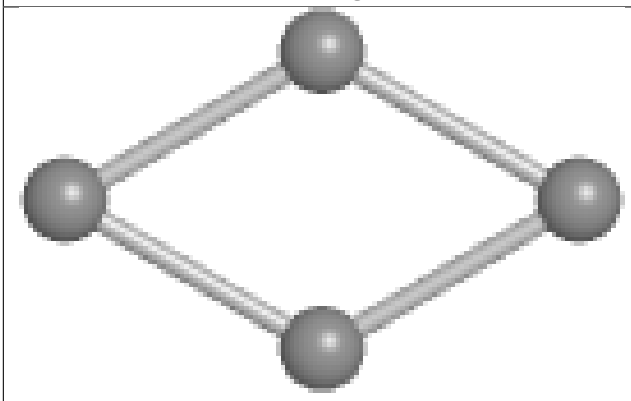

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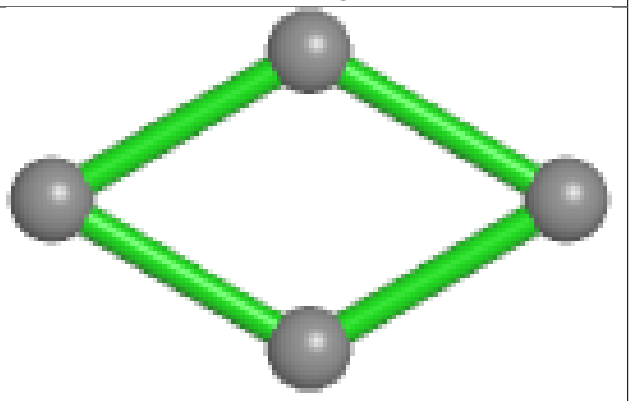
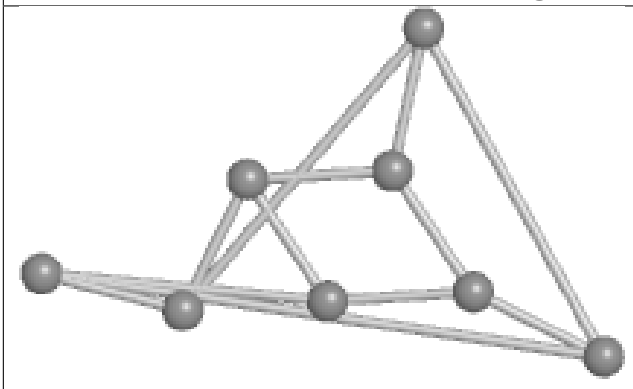


Rings

Ligand SF4 D 603



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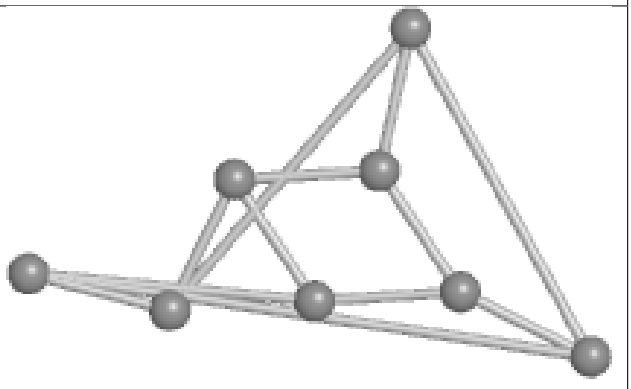

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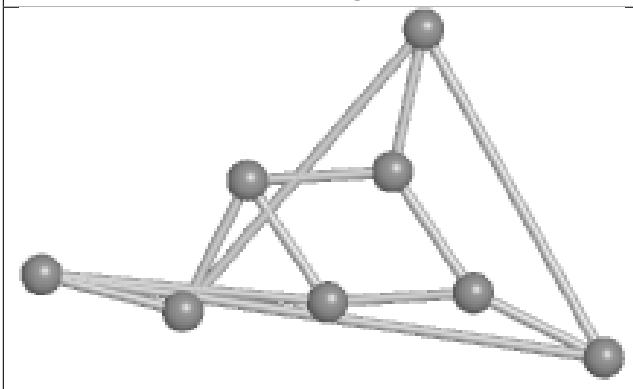

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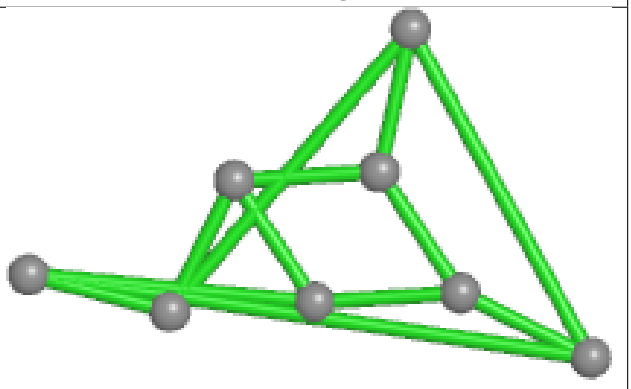
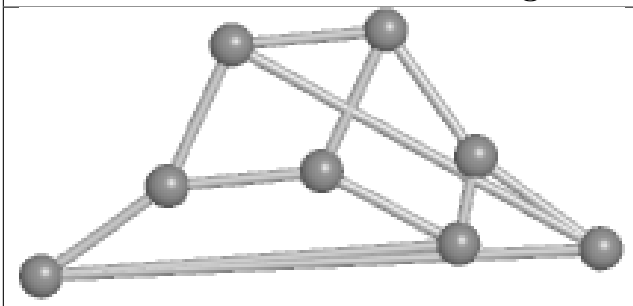


Rings

Ligand SF4 A 1005



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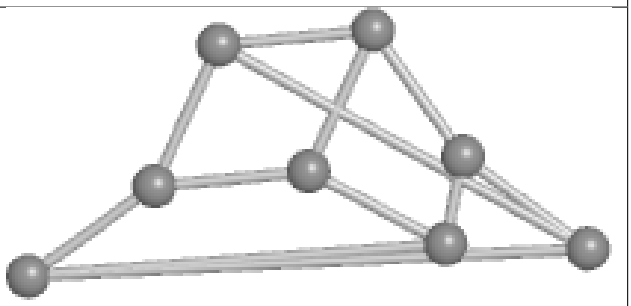

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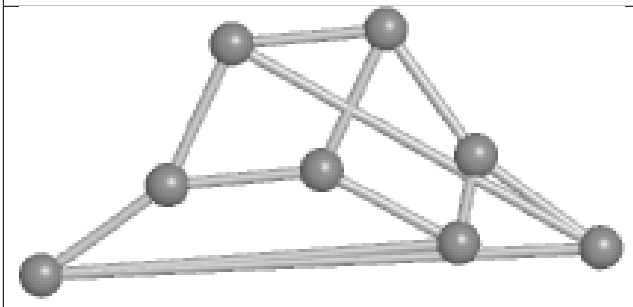

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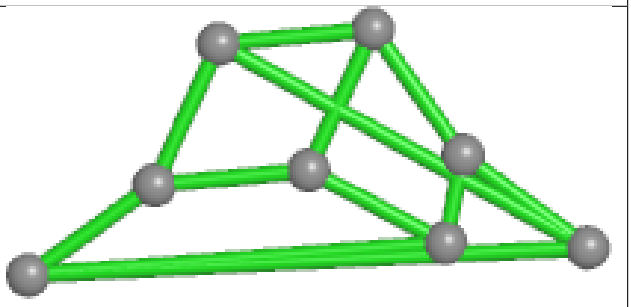
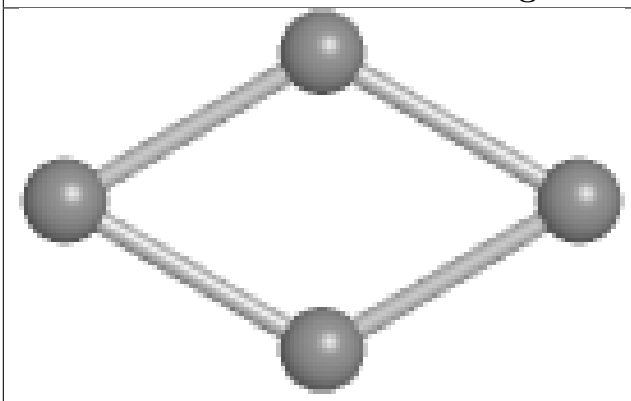


Rings

Ligand FES A 1004



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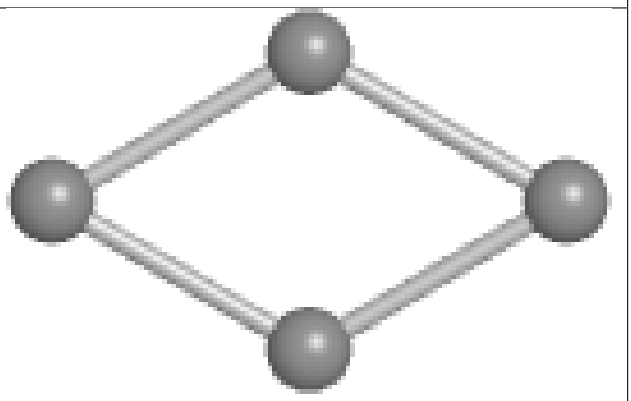

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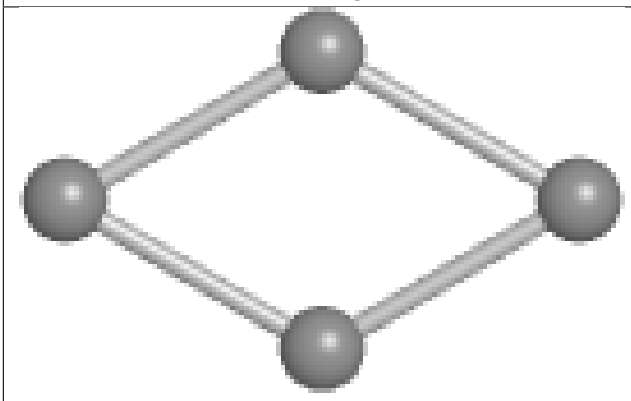

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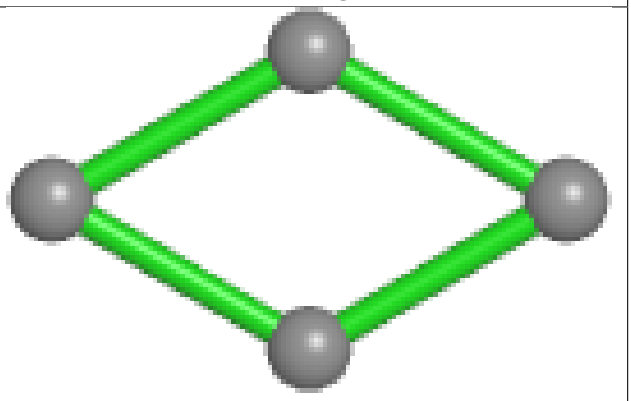
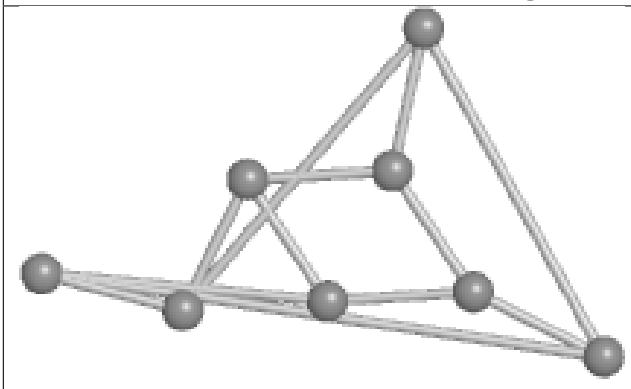


Rings

Ligand SF4 A 1008



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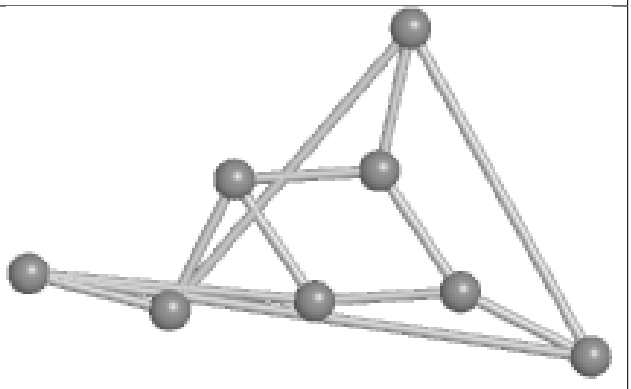

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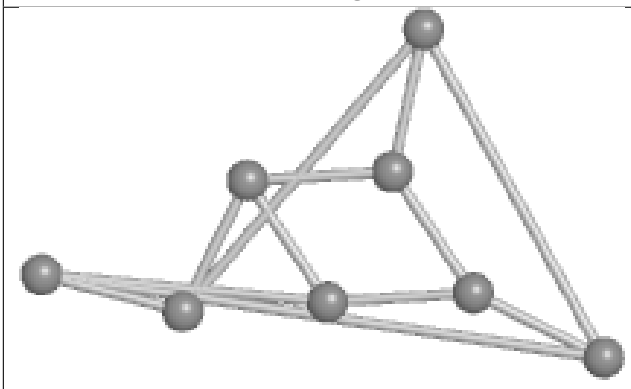

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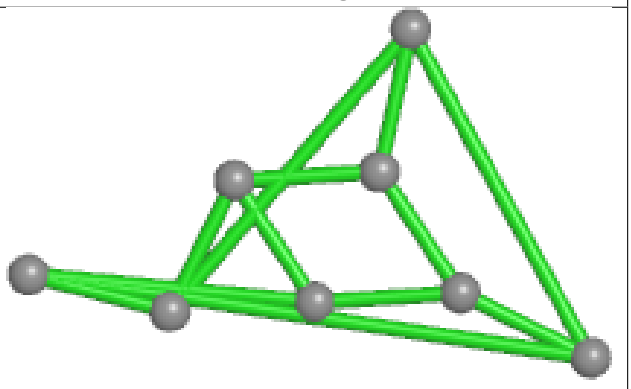
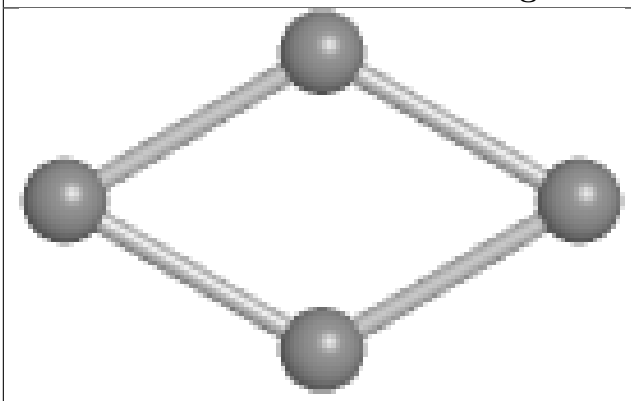


Rings

Ligand FES B 1004



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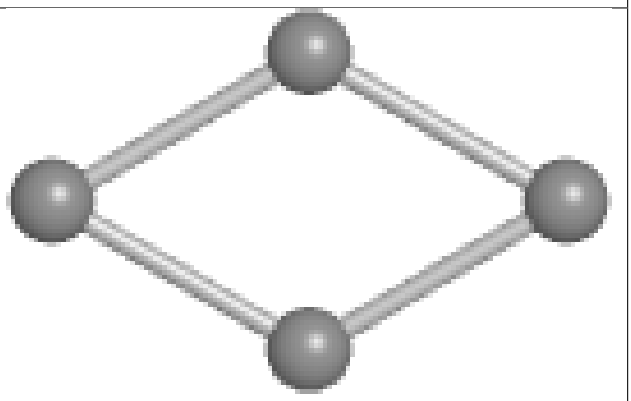

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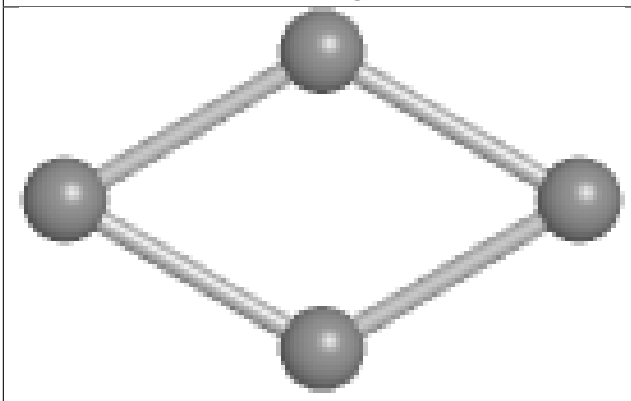

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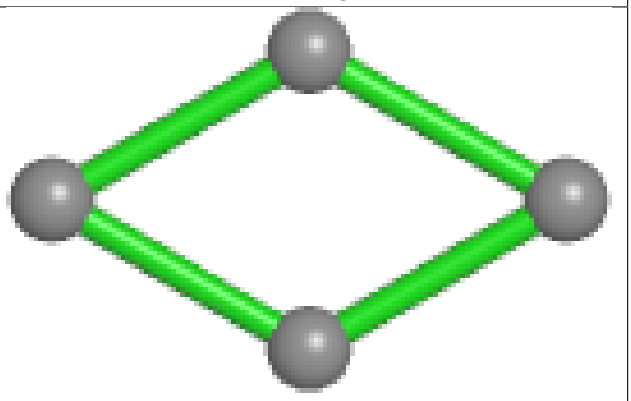
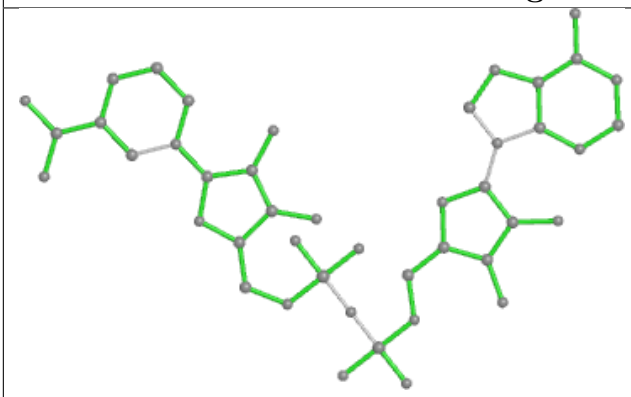
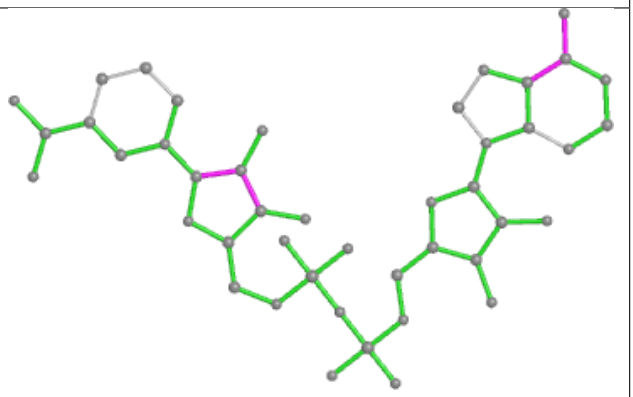


Rings

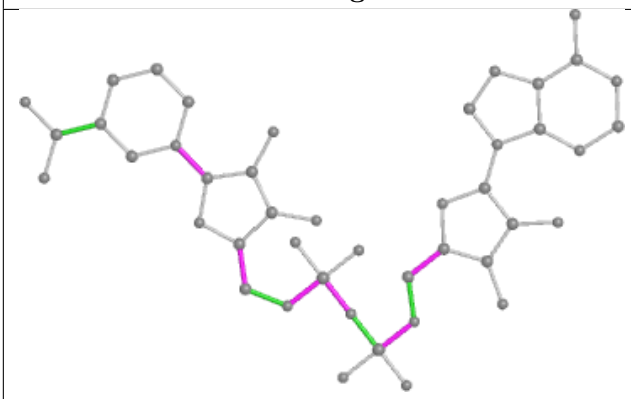
Ligand NAI D 601



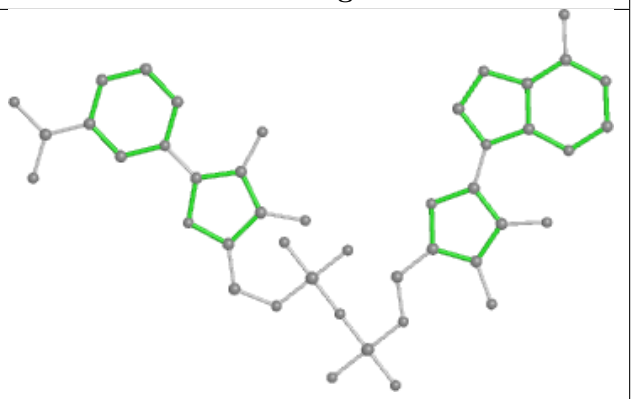
Bond lengths



Bond angles

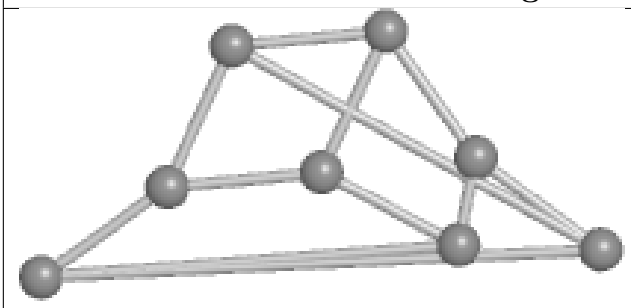


Torsions



Rings

Ligand SF4 A 1006



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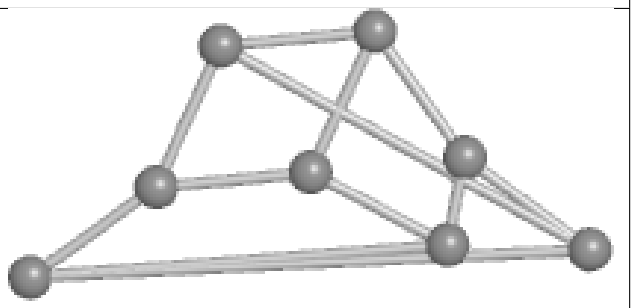
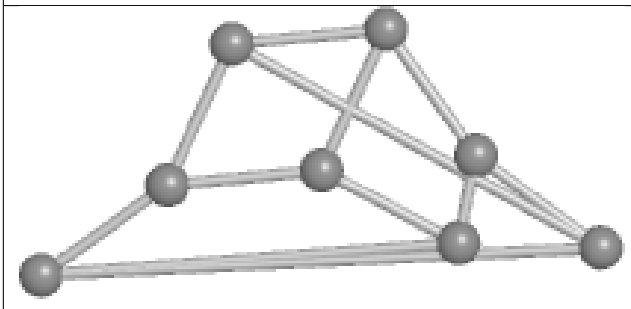


Bond angles



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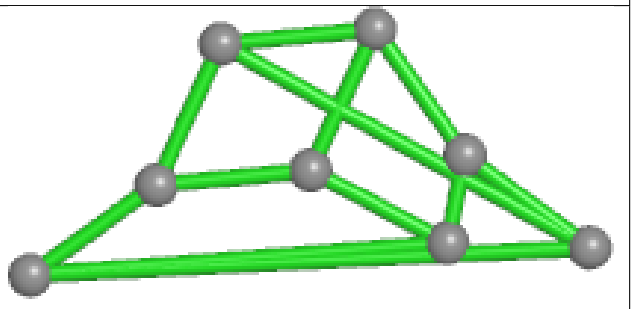
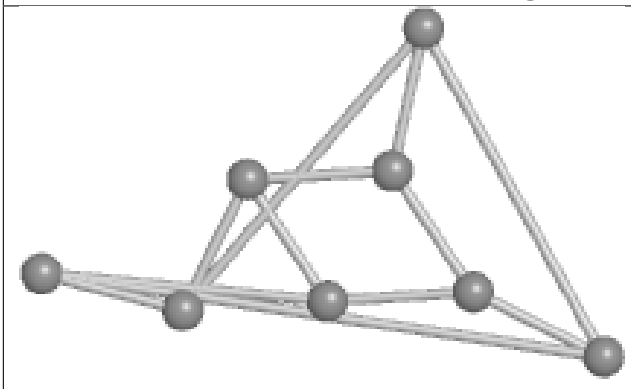


Rings

Ligand SF4 A 1007



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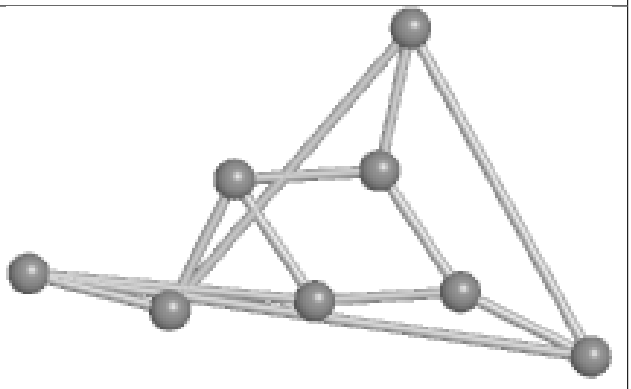
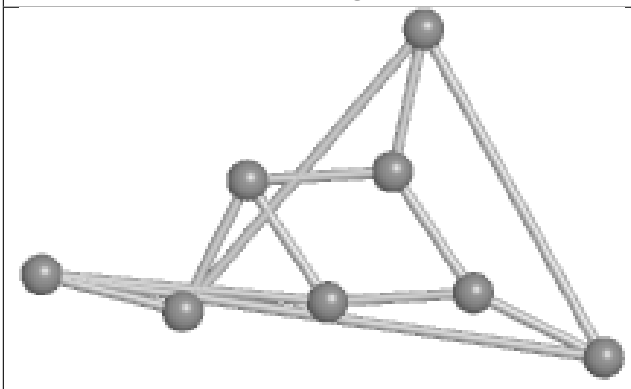
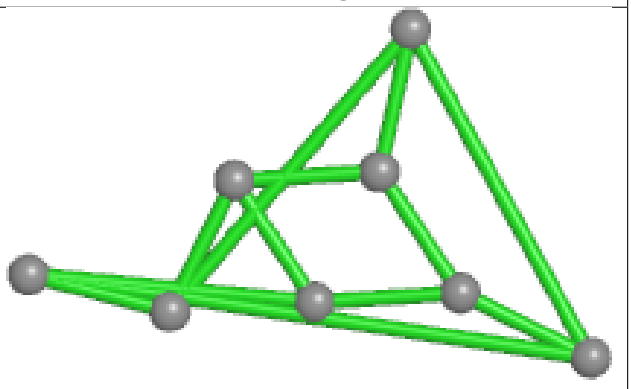


Bond angles

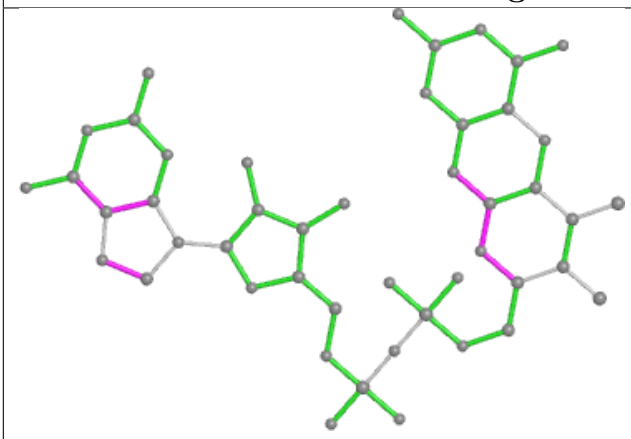


Torsions

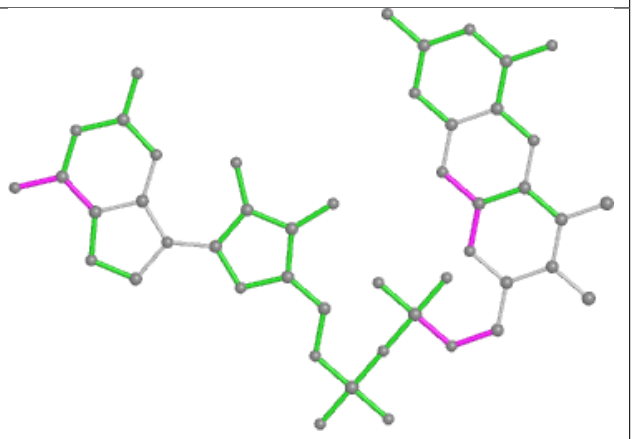


Rings

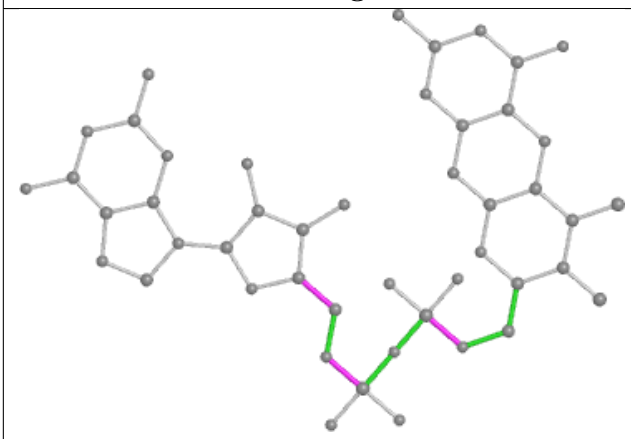
Ligand MGD B 1002



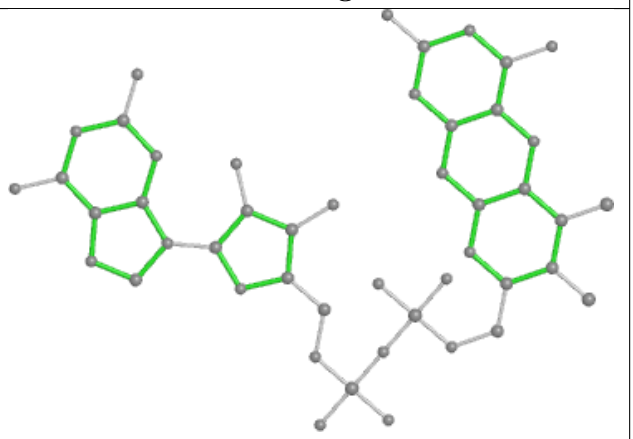
Bond lengths



Bond angles

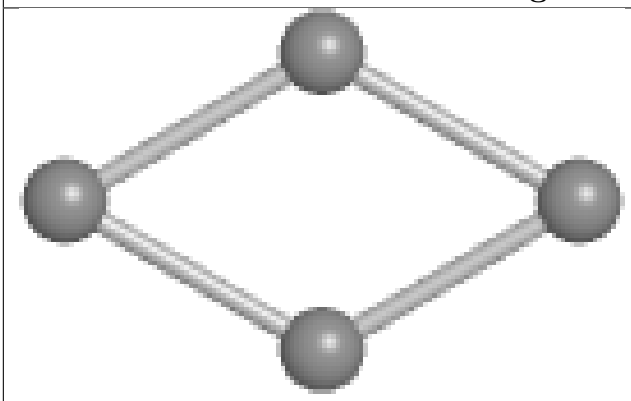


Torsions

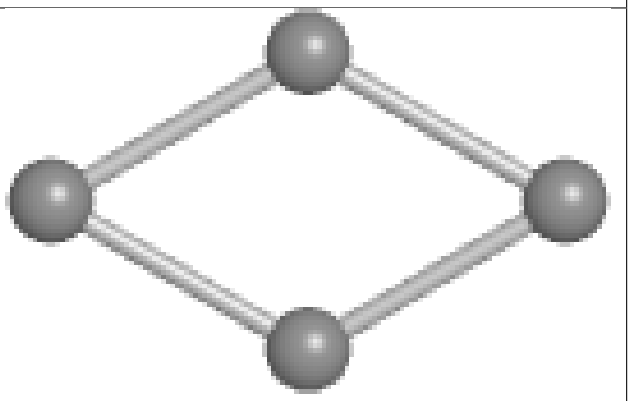


Rings

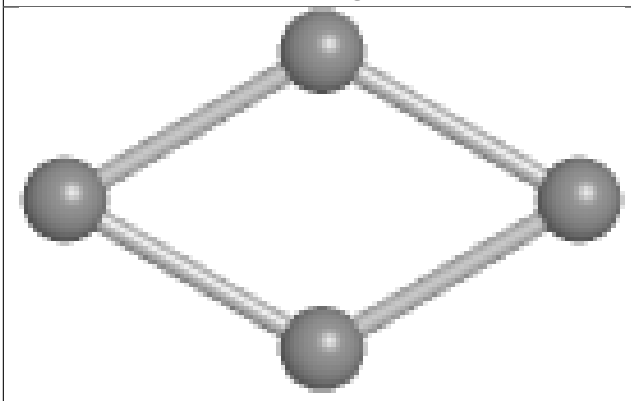
Ligand FES E 201



Bond lengths



Bond angles



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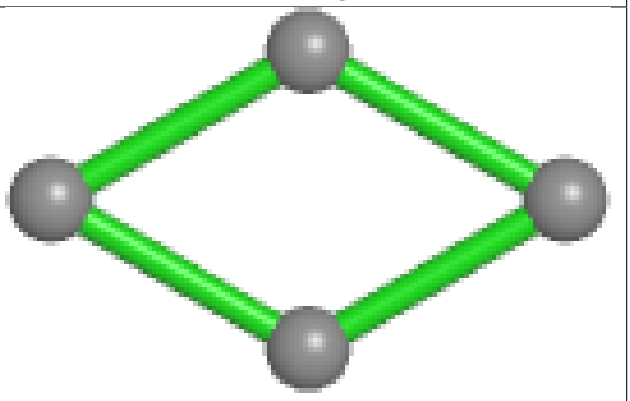
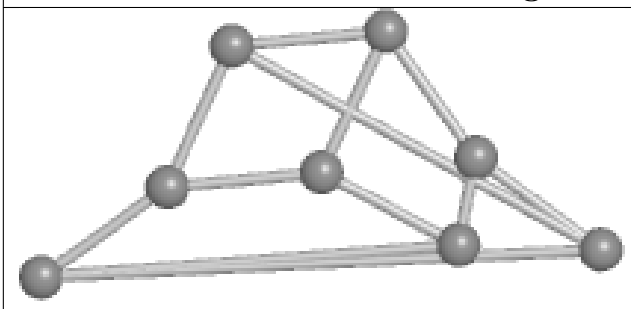
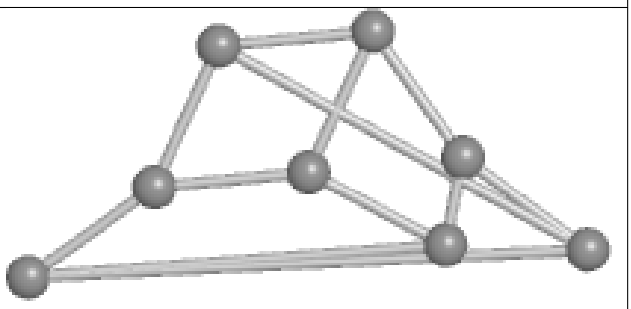


Rings

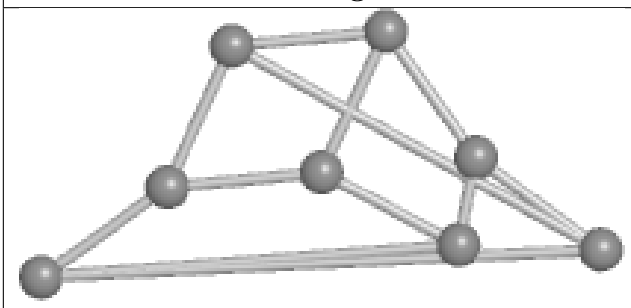
Ligand SF4 B 1005



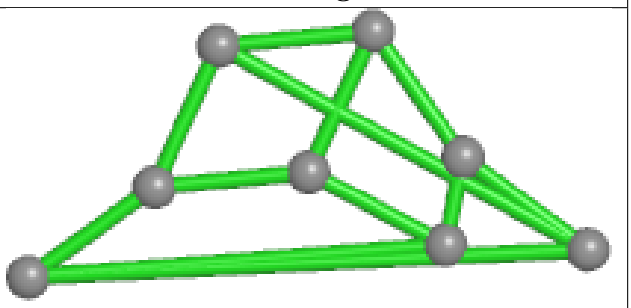
Bond lengths



Bond angles

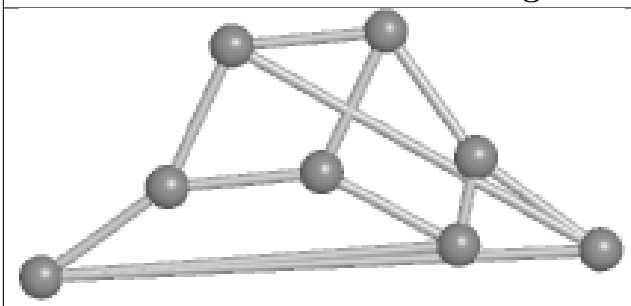


Torsions



Rings

Ligand SF4 B 1006



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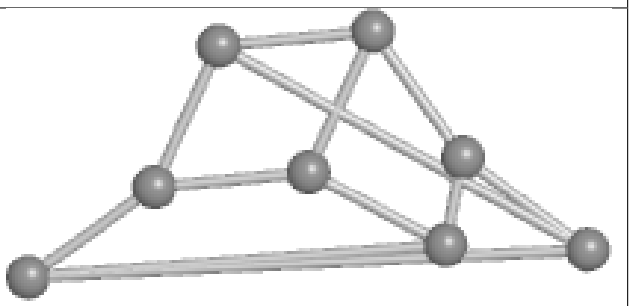
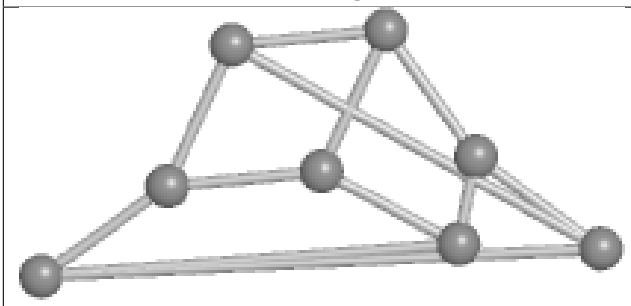


Bond angles



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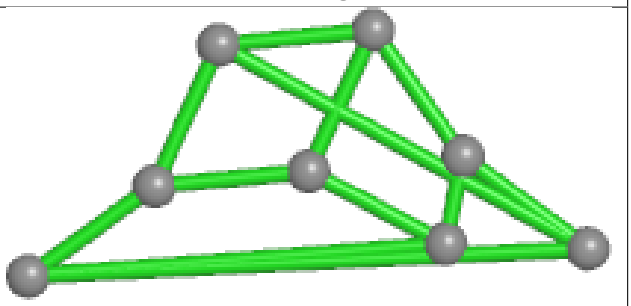
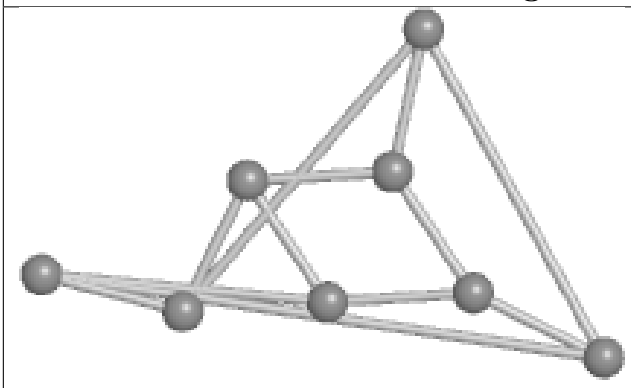
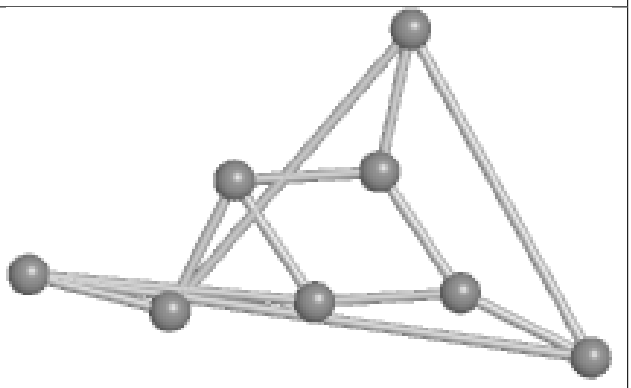


Rings

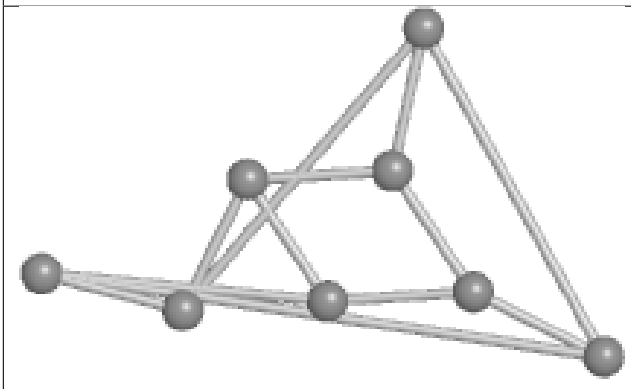
Ligand SF4 B 1008



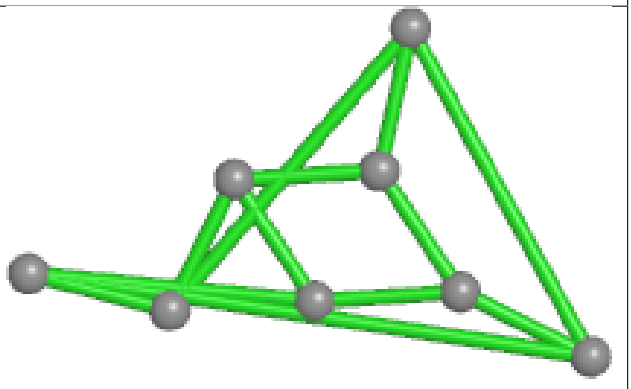
Bond lengths



Bond angles

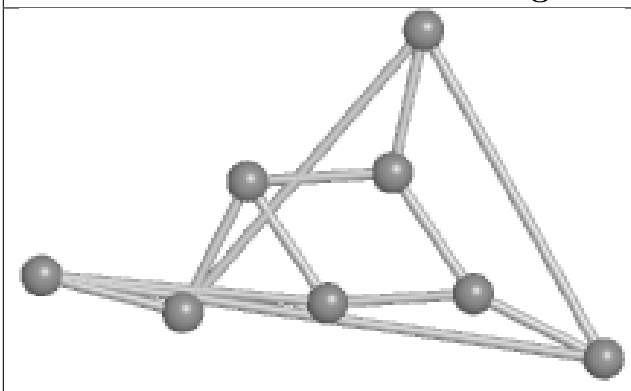


Torsions

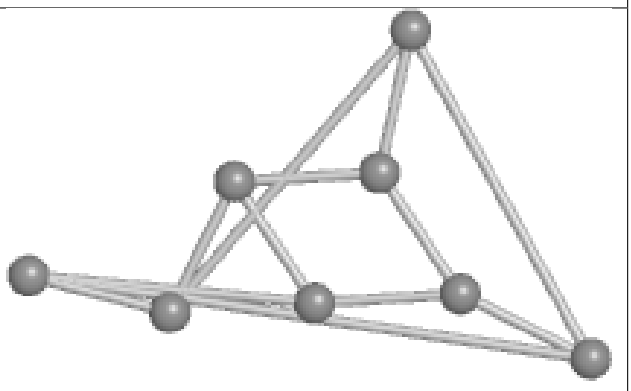


Rings

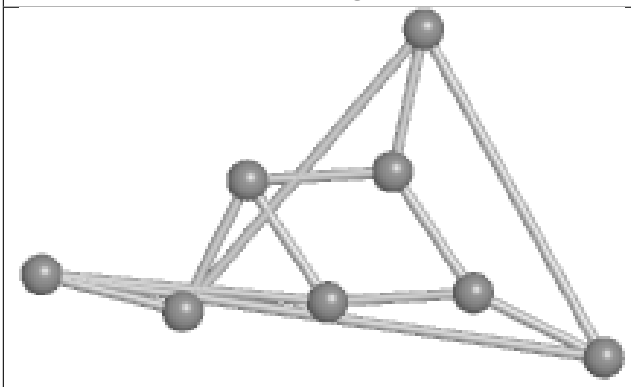
Ligand SF4 C 603



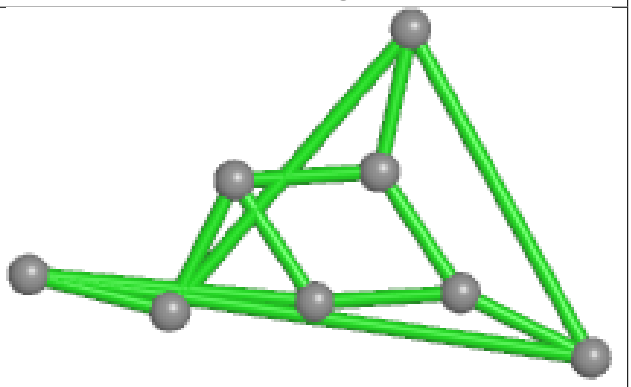
Bond lengths



Bond angles

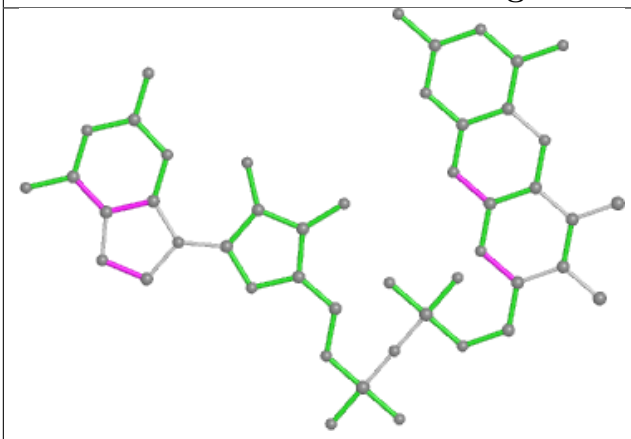


Torsions

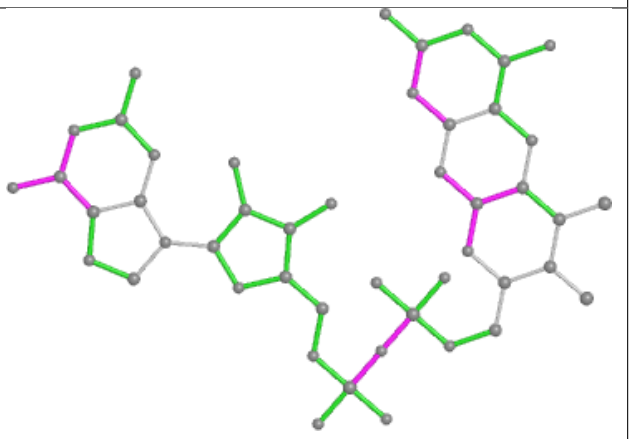


Rings

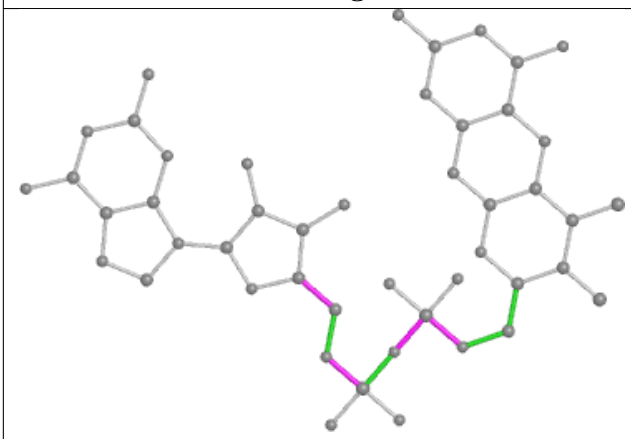
Ligand MGD A 1001



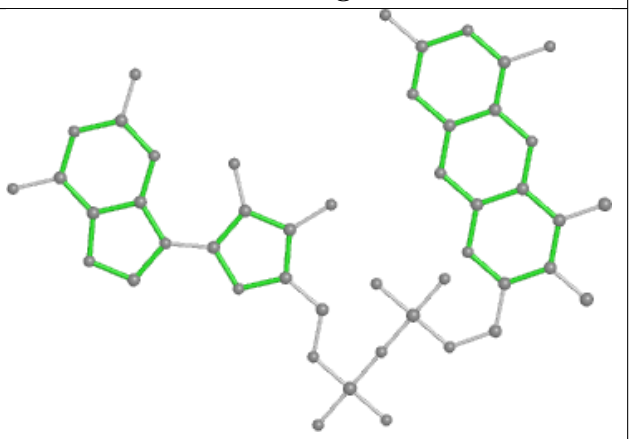
Bond lengths



Bond angles

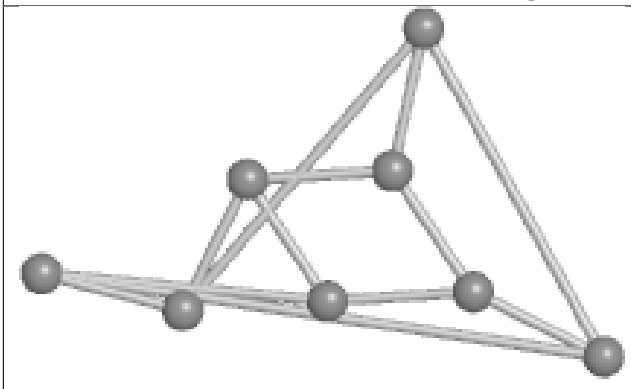


Torsions



Rings

Ligand SF4 B 1007



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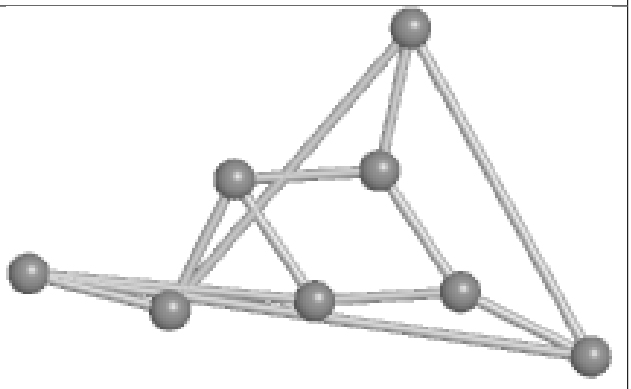
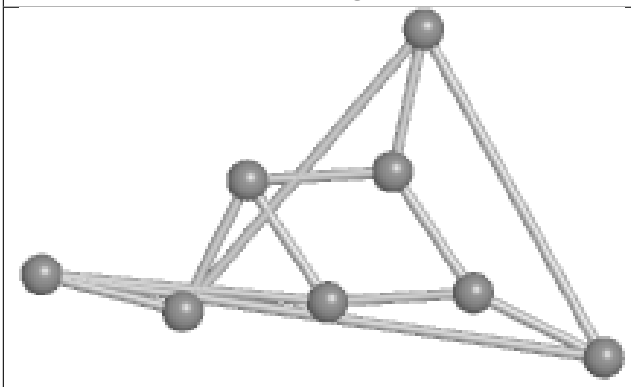
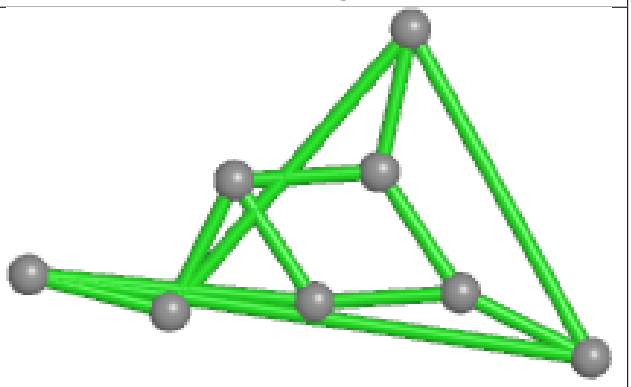


Bond angles

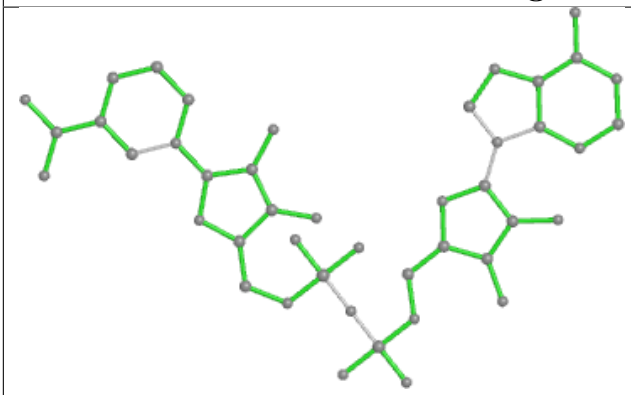


Torsions

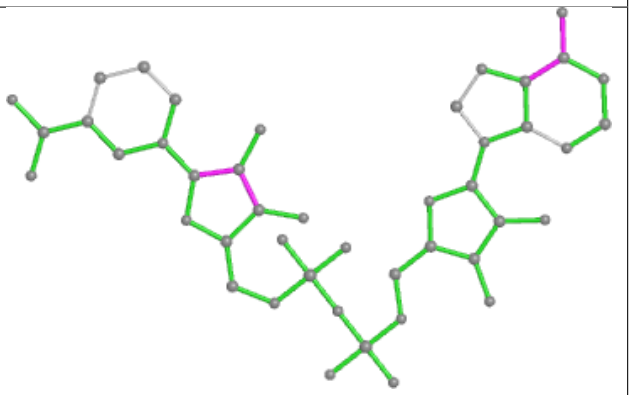


Rings

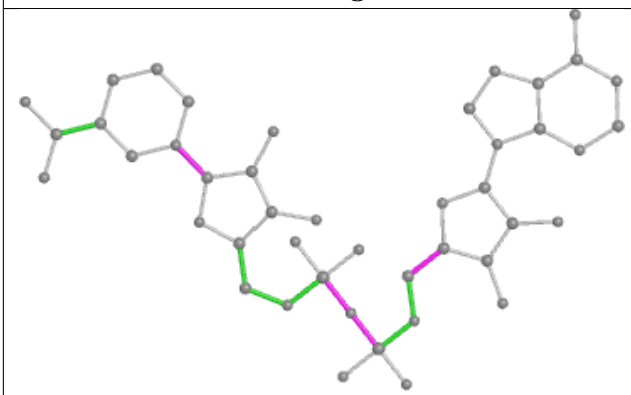
Ligand NAI C 601



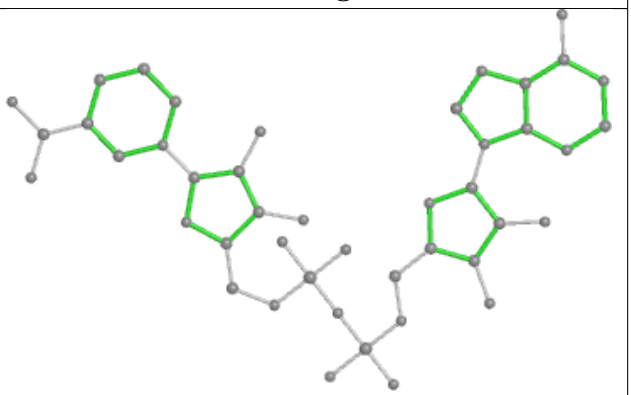
Bond lengths



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.

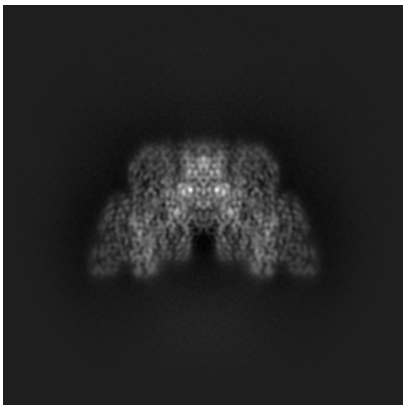
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-62562. These allow visual inspection of the internal detail of the map and identification of artifacts.

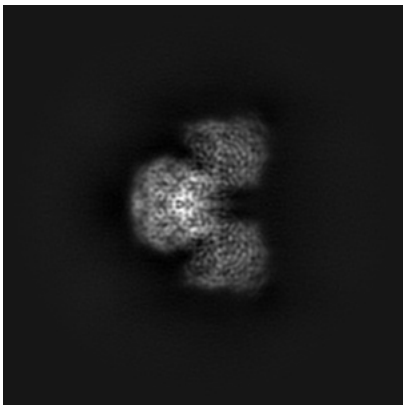
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

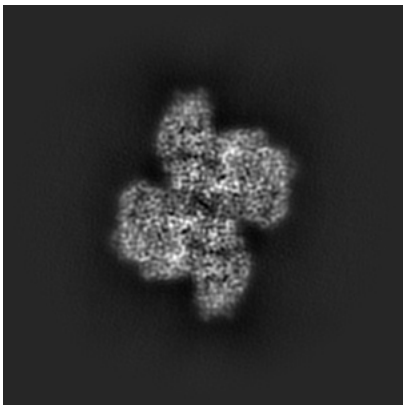
6.1.1 Primary map



X

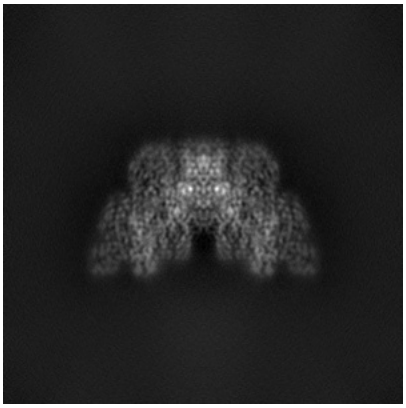


Y

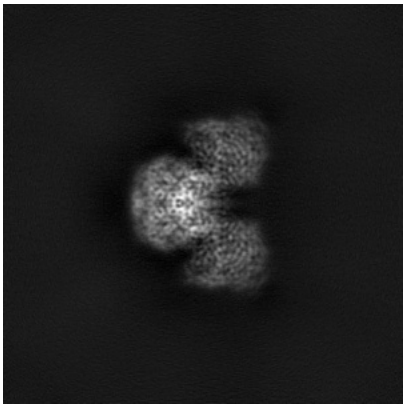


Z

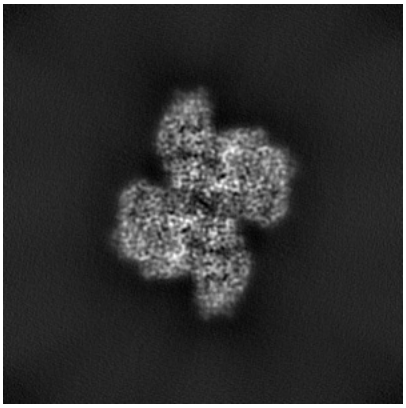
6.1.2 Raw map



X



Y

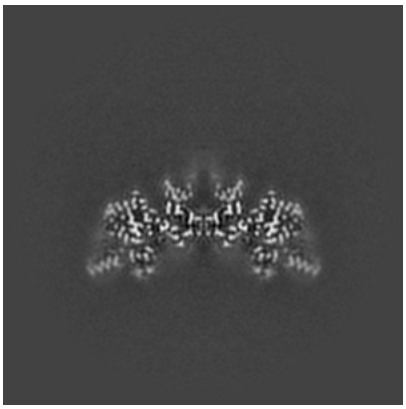


Z

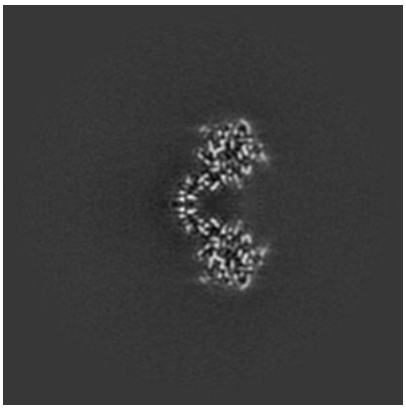
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

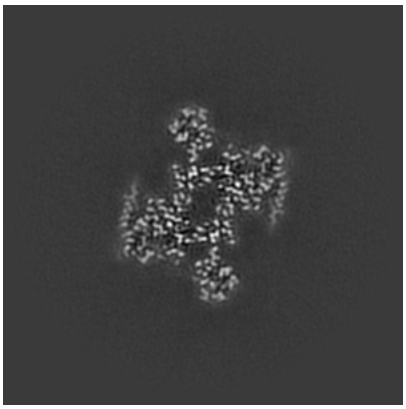
6.2.1 Primary map



X Index: 150

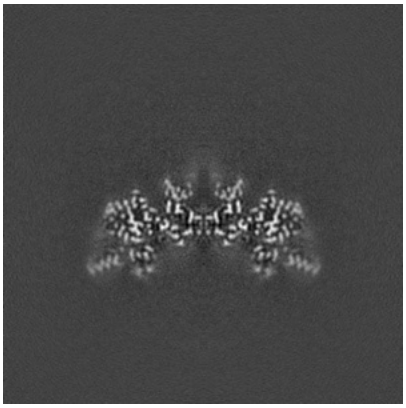


Y Index: 150

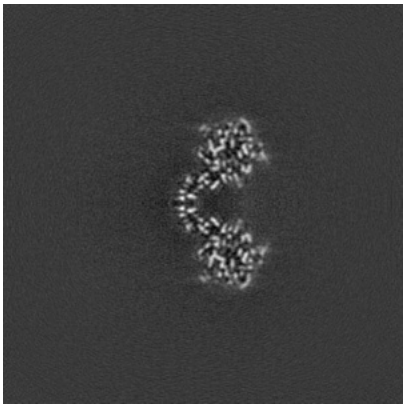


Z Index: 150

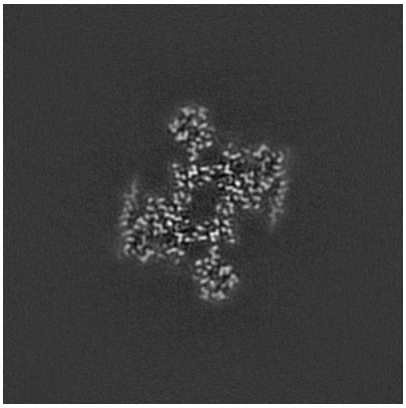
6.2.2 Raw map



X Index: 150



Y Index: 150

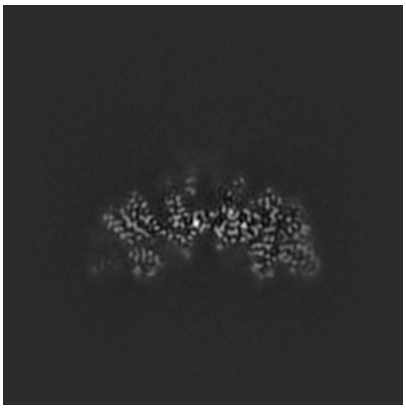


Z Index: 150

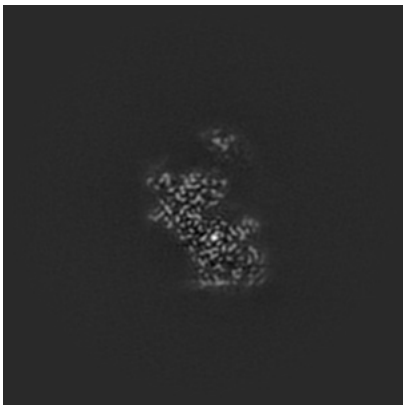
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

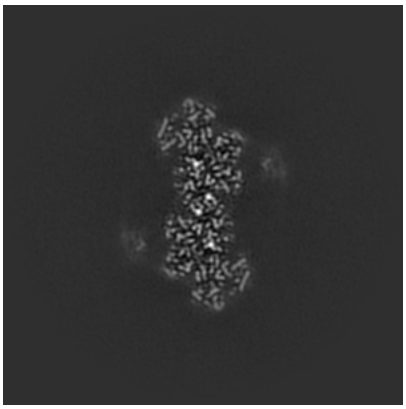
6.3.1 Primary map



X Index: 146

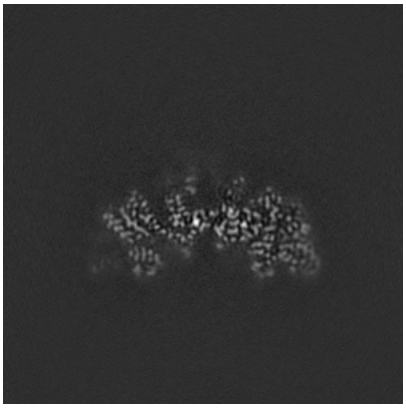


Y Index: 135

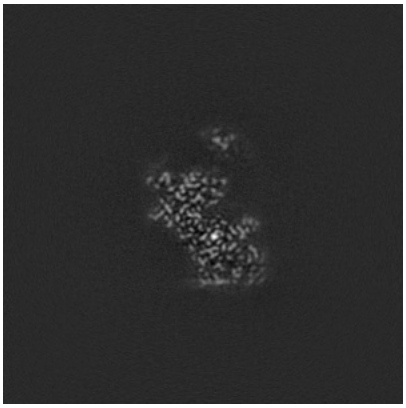


Z Index: 135

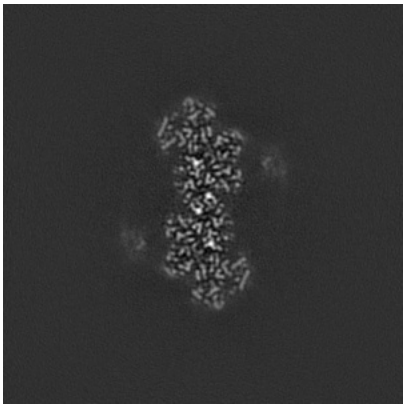
6.3.2 Raw map



X Index: 146



Y Index: 135

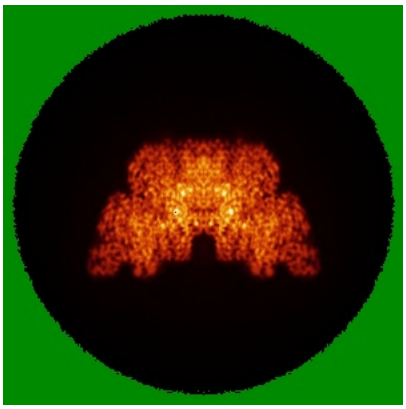


Z Index: 135

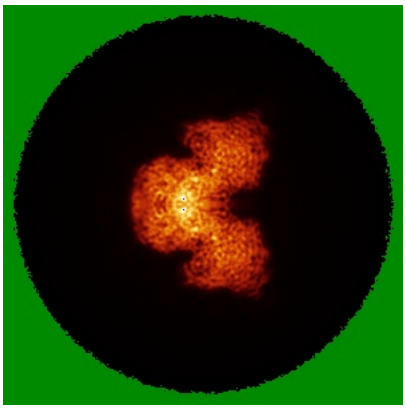
The images above show the largest variance slices of the map in three orthogonal directions.

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

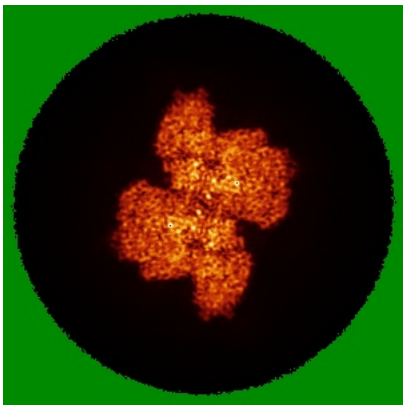
6.4.1 Primary map



X

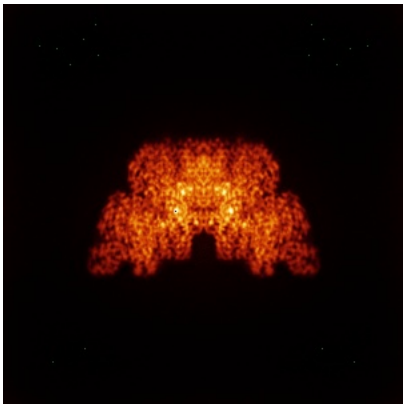


Y

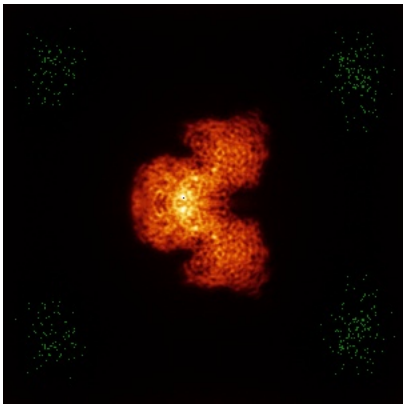


Z

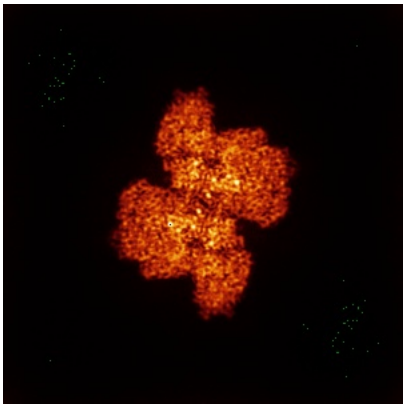
6.4.2 Raw map



X



Y

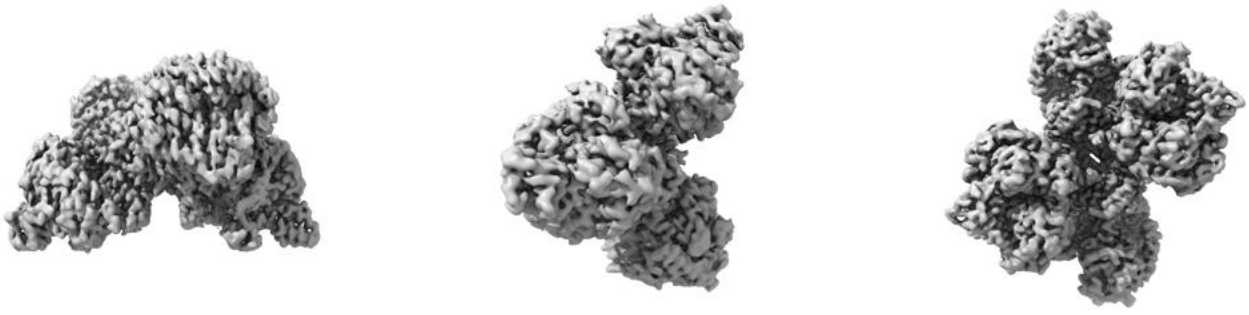


Z

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)

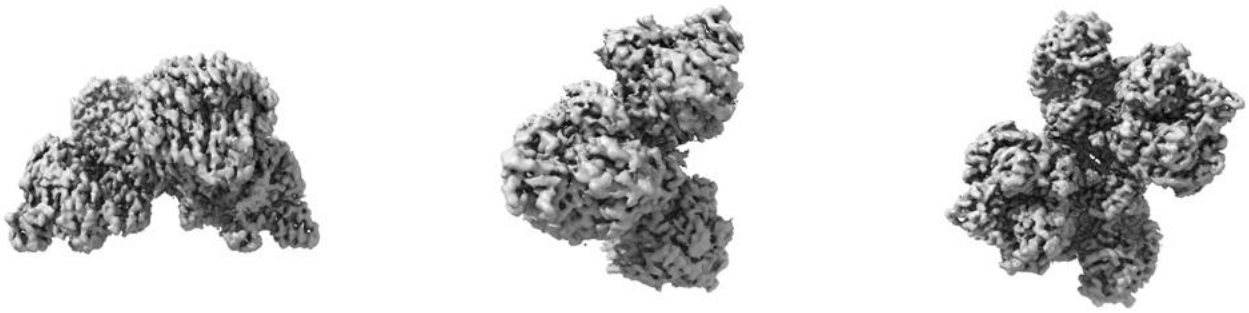
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.133. 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.

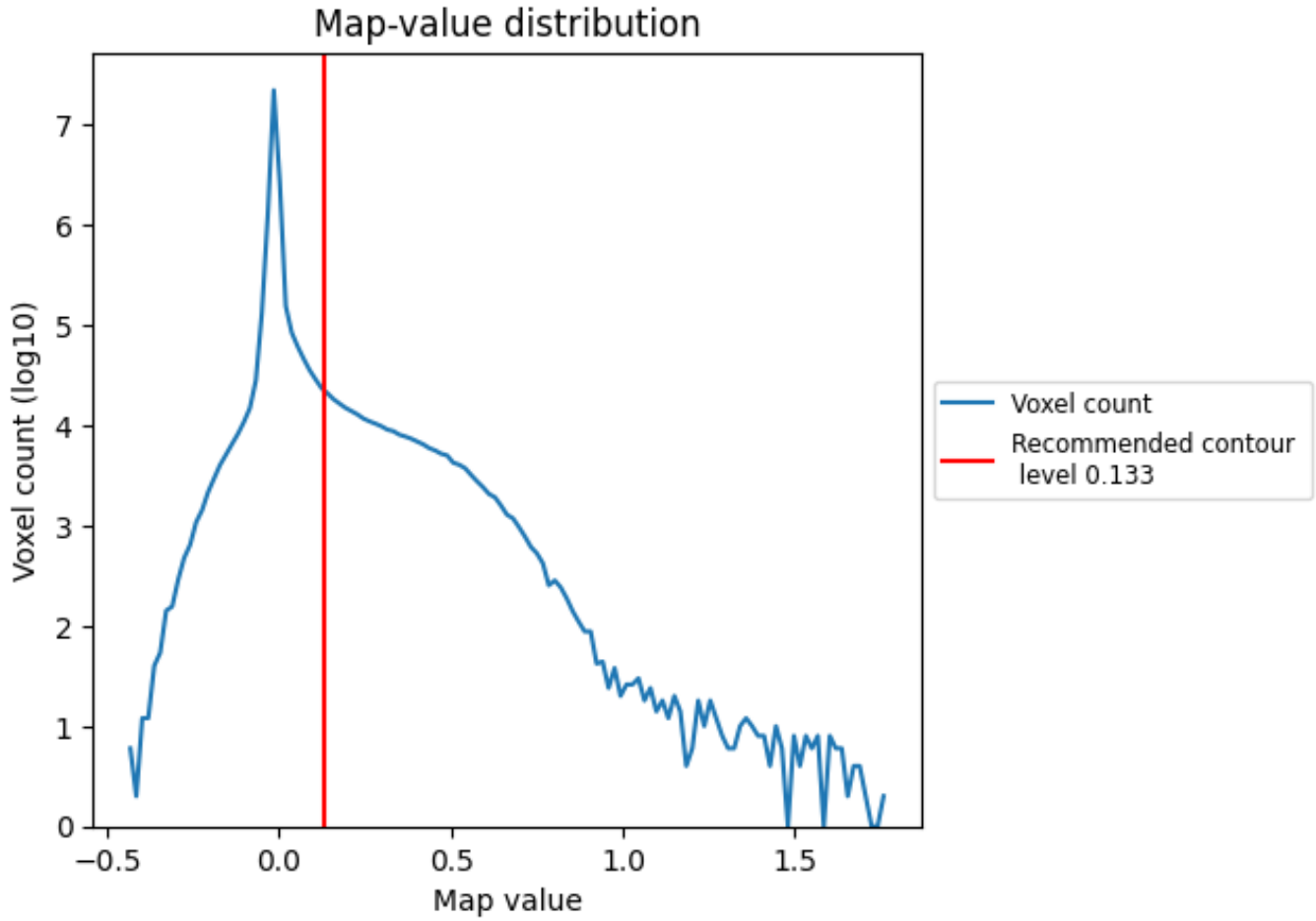
6.6 Mask visualisation (i)

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

7 Map analysis

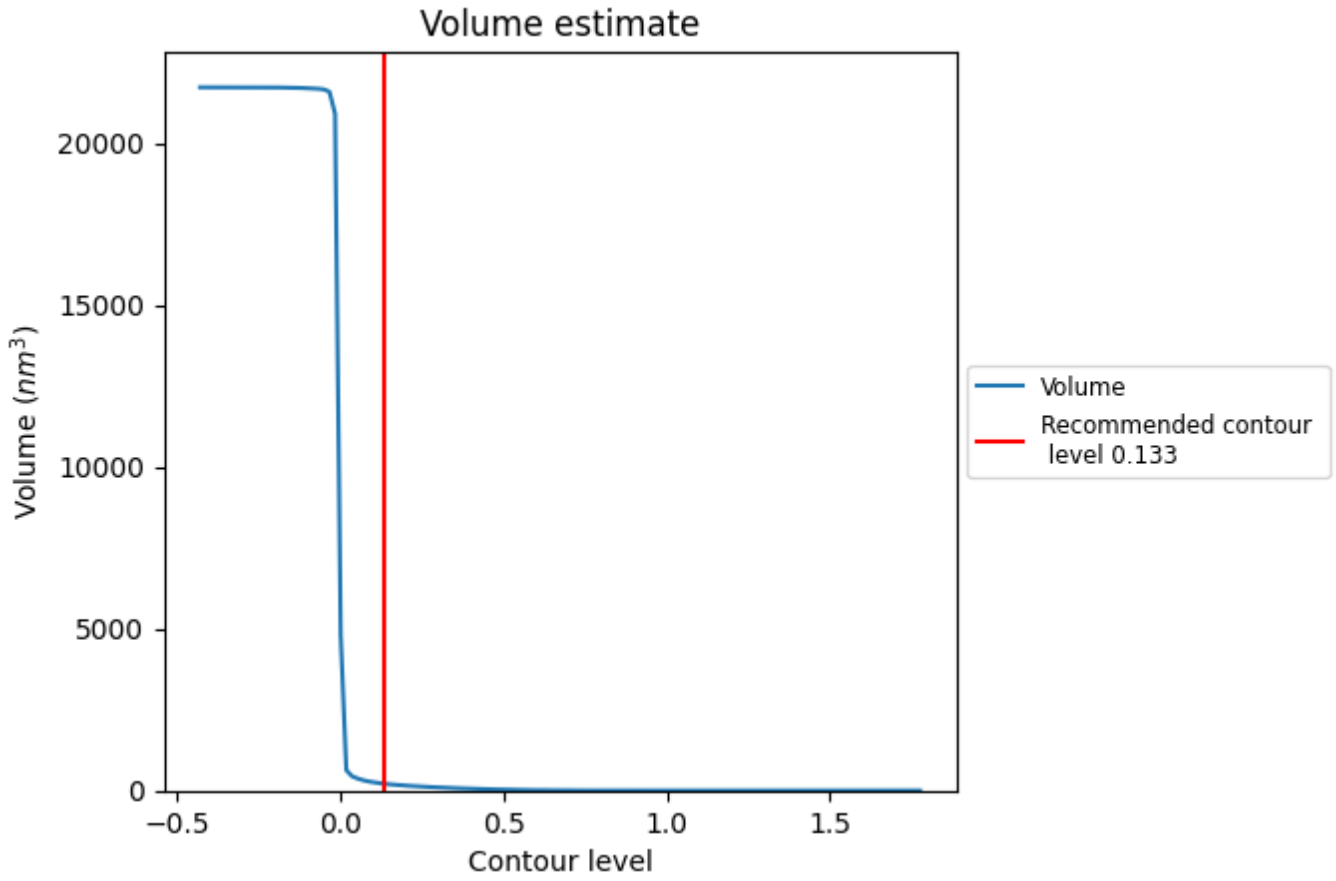
This section contains the results of statistical analysis of the map.

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.

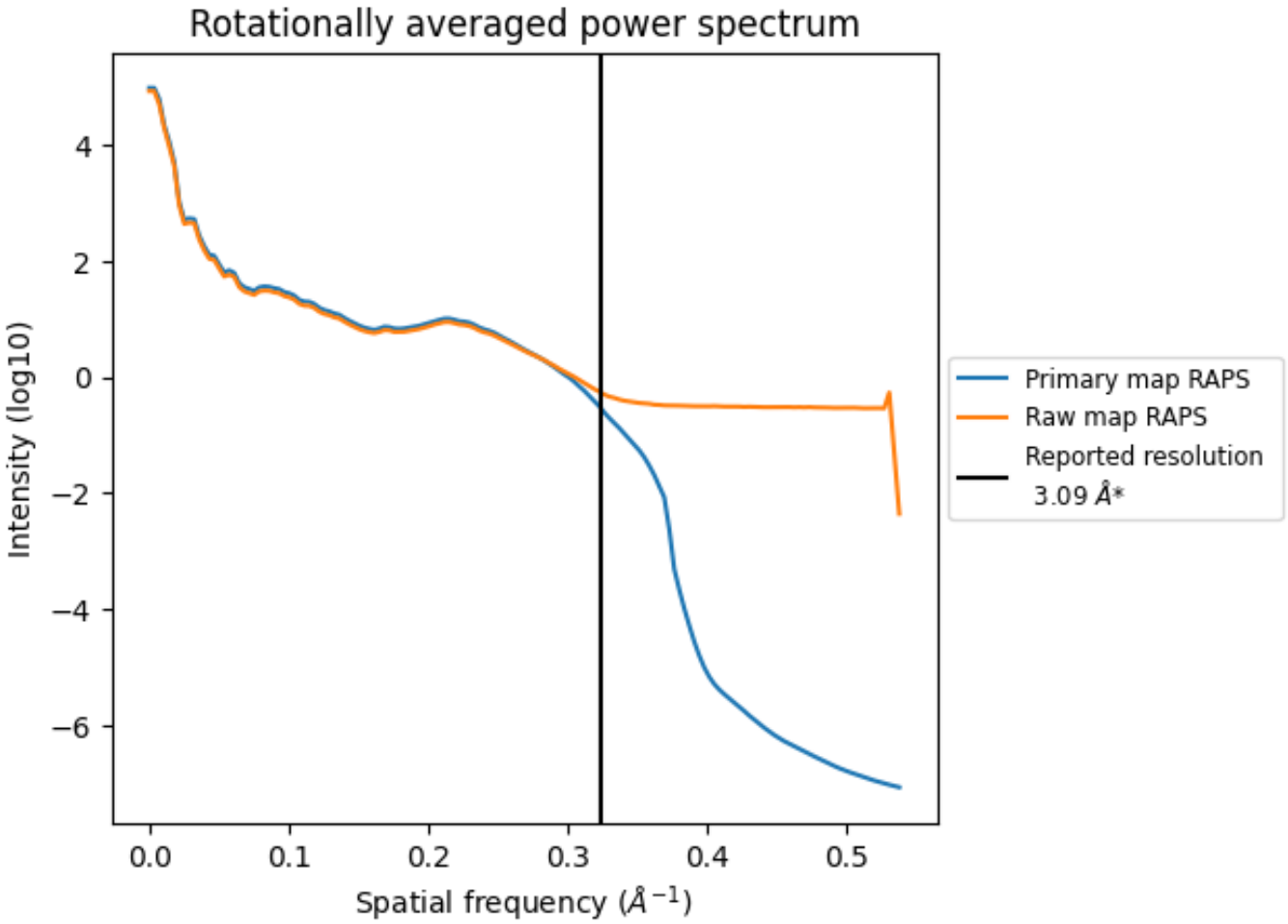
7.2 Volume estimate



The volume at the recommended contour level is 212 nm^3; this corresponds to an approximate mass of 191 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)

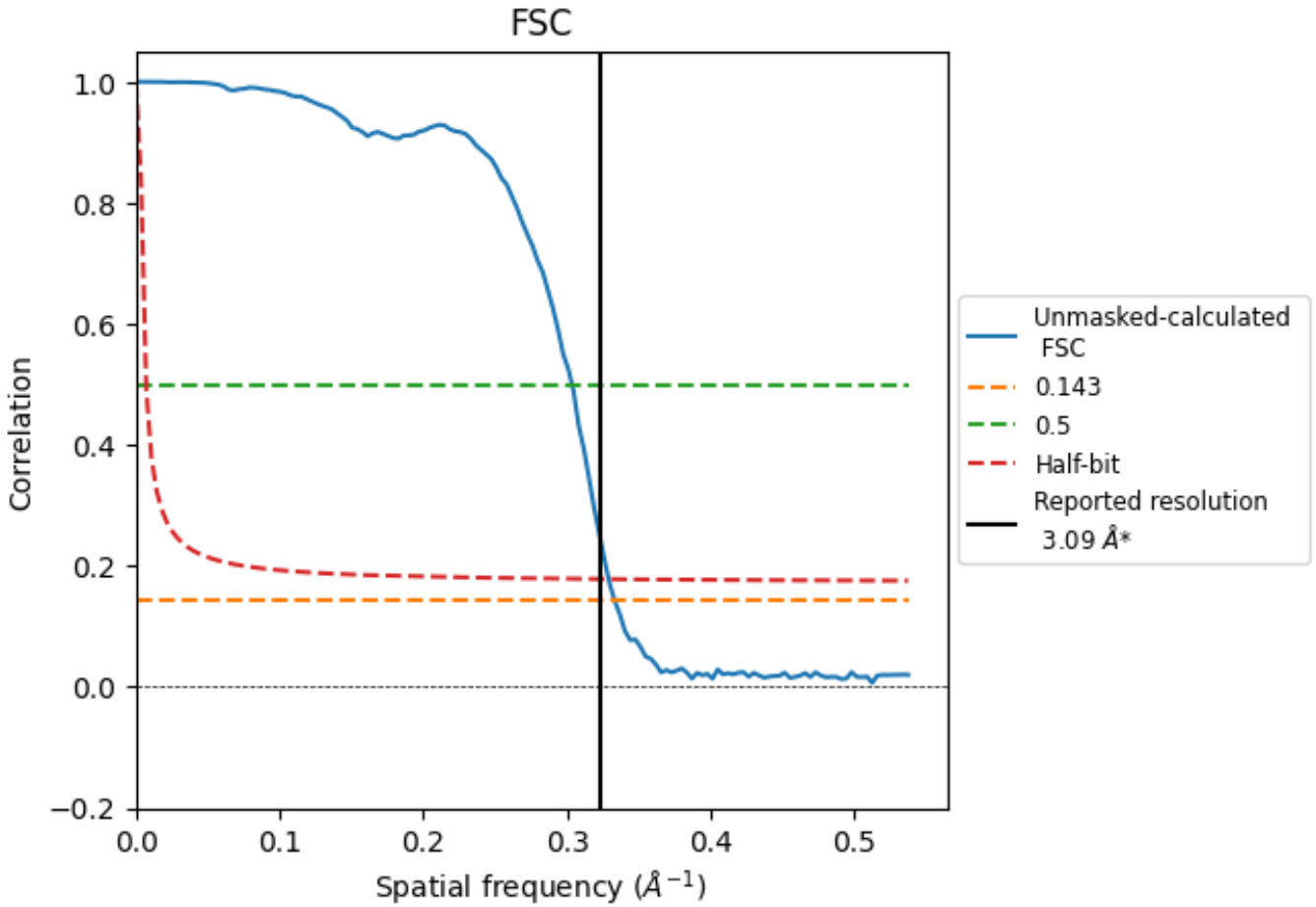


*Reported resolution corresponds to spatial frequency of 0.324 Å^{-1}

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 0.324 Å^{-1}

8.2 Resolution estimates (i)

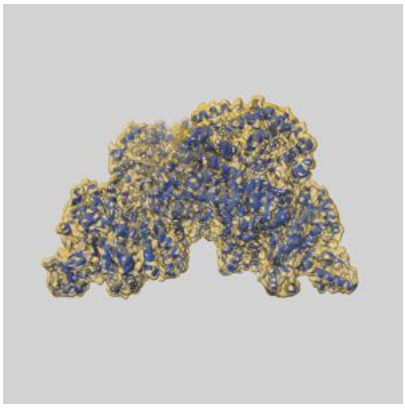
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.00	3.29	3.04

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

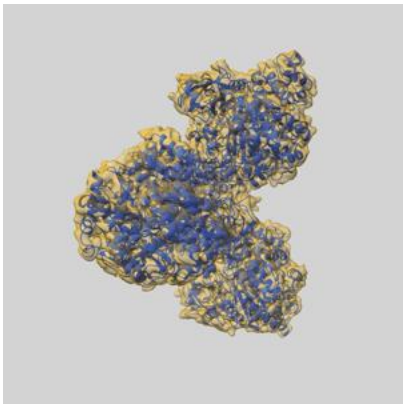
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-62562 and PDB model 9KTL. Per-residue inclusion information can be found in section 3 on page 9.

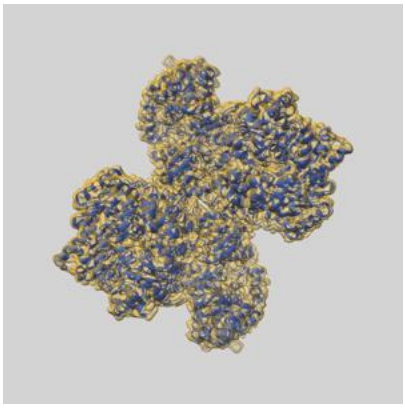
9.1 Map-model overlay



X



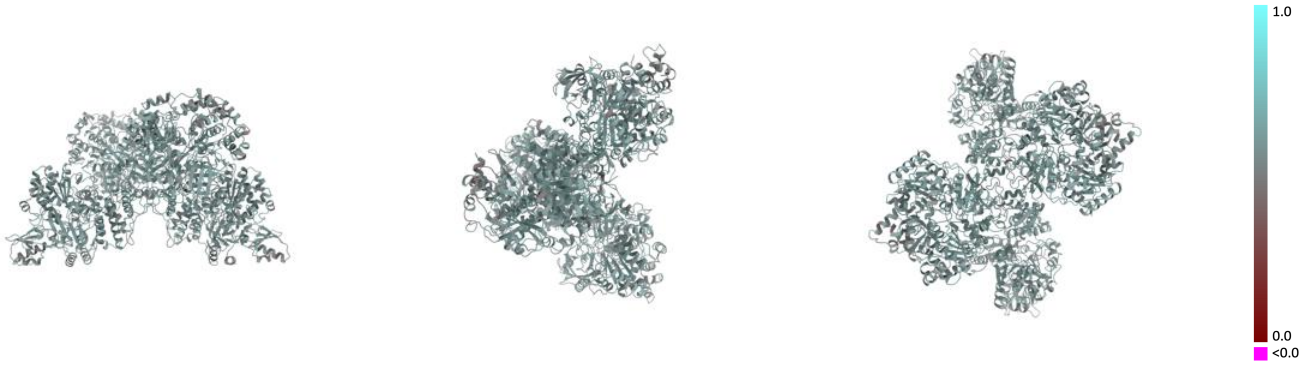
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.133 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.

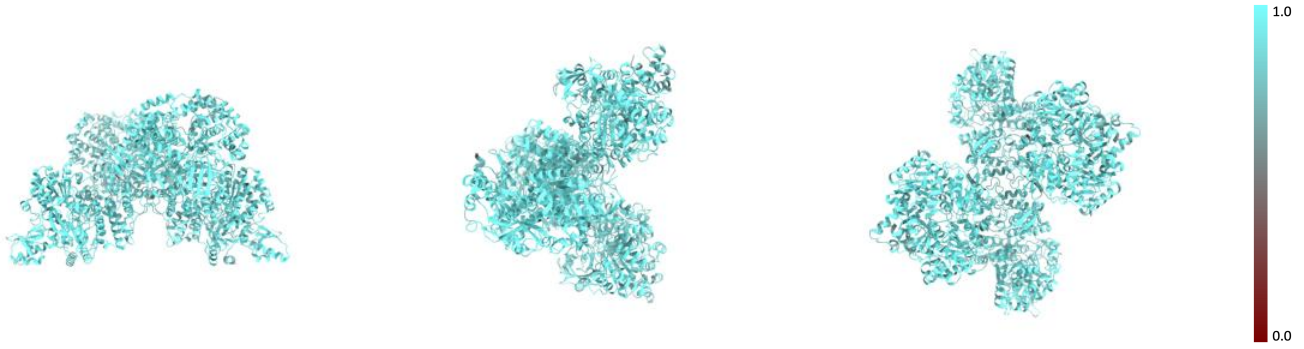
9.2 Q-score mapped to coordinate model (i)



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.

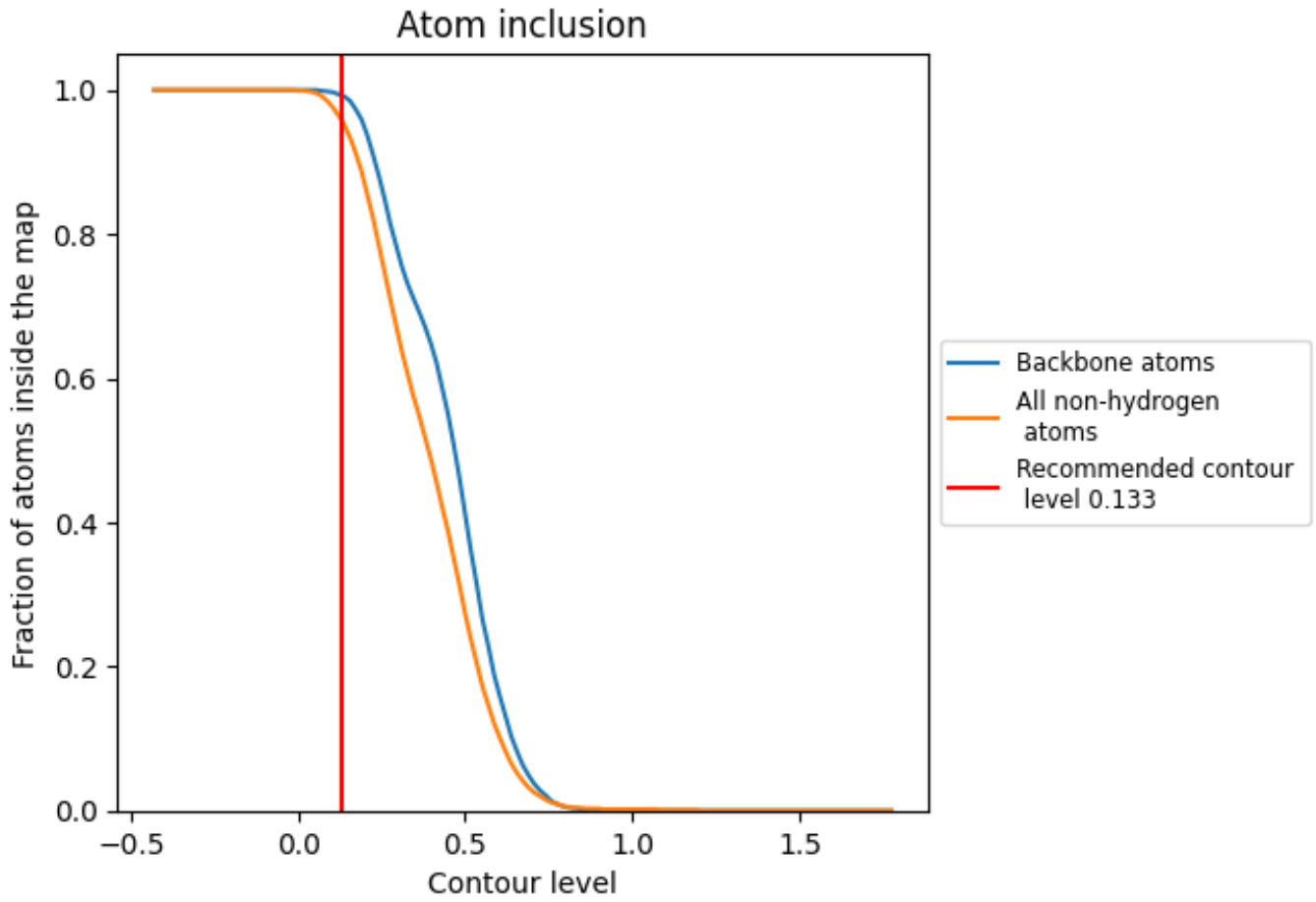
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.133).

9.4 Atom inclusion (i)



At the recommended contour level, 99% of all backbone atoms, 96% 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 (0.133) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9560	0.5730
A	0.9620	0.5820
B	0.9630	0.5810
C	0.9570	0.5690
D	0.9570	0.5690
E	0.9540	0.5580
F	0.9500	0.5570
G	0.8500	0.5180
H	0.8570	0.5270