Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:31 PM GMT

PDB ID	:	4FA4
Title	:	Crystal Structure of WT MauG in Complex with Pre-Methylamine Dehydrogenase Aged 10 Days
Authors	:	Yukl, E.T.; Wilmot, C.M.
Deposited on	:	2012-05-21
Resolution	:	2.14 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

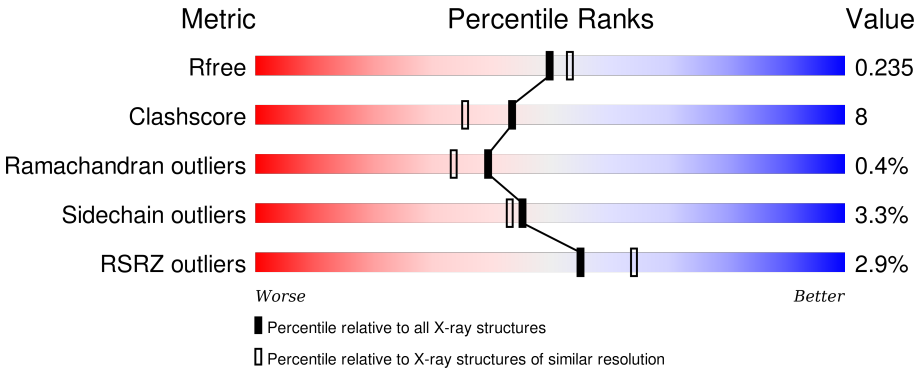
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.14 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1693 (2.16-2.12)
Clashscore	102246	1824 (2.16-2.12)
Ramachandran outliers	100387	1798 (2.16-2.12)
Sidechain outliers	100360	1798 (2.16-2.12)
RSRZ outliers	91569	1699 (2.16-2.12)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	373	75% 20% • 5%
1	B	373	81% 14% • •
2	C	137	5% 72% 23% • •
2	E	137	4% 72% 19% • 8%
3	D	385	6% 80% 17% • •

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Mol	Chain	Length	Quality of chain
3	F	385	2% 82% 15%

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
6	PGE	A	404	-	-	-	X
7	EDO	A	405	-	-	-	X
9	PO4	B	404	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 14775 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Methylamine utilization protein MauG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	354	Total	C	N	O	S	0	7	0
			2813	1752	514	536	11			
1	B	359	Total	C	N	O	S	0	1	0
			2781	1733	502	535	11			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	368	HIS	-	EXPRESSION TAG	UNP Q51658
A	369	HIS	-	EXPRESSION TAG	UNP Q51658
A	370	HIS	-	EXPRESSION TAG	UNP Q51658
A	371	HIS	-	EXPRESSION TAG	UNP Q51658
A	372	HIS	-	EXPRESSION TAG	UNP Q51658
A	373	HIS	-	EXPRESSION TAG	UNP Q51658
B	368	HIS	-	EXPRESSION TAG	UNP Q51658
B	369	HIS	-	EXPRESSION TAG	UNP Q51658
B	370	HIS	-	EXPRESSION TAG	UNP Q51658
B	371	HIS	-	EXPRESSION TAG	UNP Q51658
B	372	HIS	-	EXPRESSION TAG	UNP Q51658
B	373	HIS	-	EXPRESSION TAG	UNP Q51658

- Molecule 2 is a protein called Methylamine dehydrogenase light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	131	Total	C	N	O	S	0	1	0
			1017	628	179	196	14			
2	E	126	Total	C	N	O	S	0	3	0
			973	601	163	194	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	132	HIS	-	EXPRESSION TAG	UNP P22619
C	133	HIS	-	EXPRESSION TAG	UNP P22619
C	134	HIS	-	EXPRESSION TAG	UNP P22619
C	135	HIS	-	EXPRESSION TAG	UNP P22619
C	136	HIS	-	EXPRESSION TAG	UNP P22619
C	137	HIS	-	EXPRESSION TAG	UNP P22619
E	132	HIS	-	EXPRESSION TAG	UNP P22619
E	133	HIS	-	EXPRESSION TAG	UNP P22619
E	134	HIS	-	EXPRESSION TAG	UNP P22619
E	135	HIS	-	EXPRESSION TAG	UNP P22619
E	136	HIS	-	EXPRESSION TAG	UNP P22619
E	137	HIS	-	EXPRESSION TAG	UNP P22619

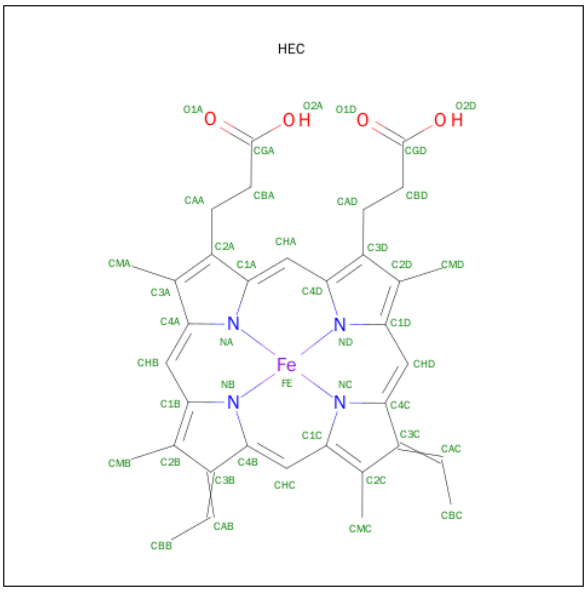
- Molecule 3 is a protein called Methylamine dehydrogenase heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	376	Total	C	N	O	S	0	5	0
			2959	1874	506	570	9			
3	F	376	Total	C	N	O	S	0	4	0
			2957	1872	511	565	9			

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

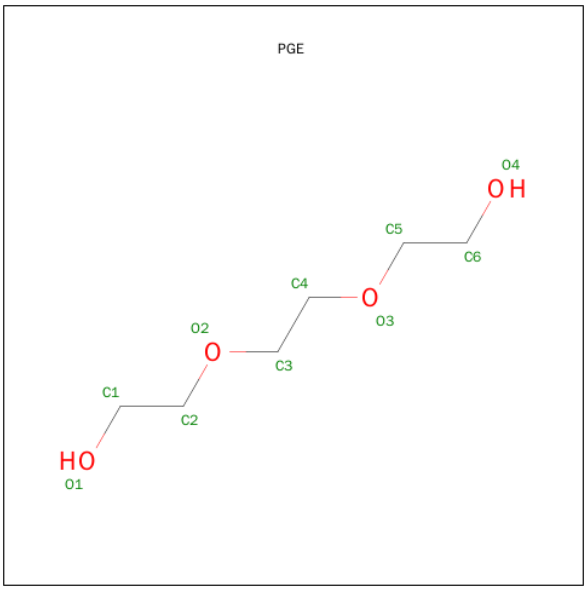
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Ca	0	0
			1	1		
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is HEME C (three-letter code: HEC) (formula: $C_{34}H_{34}FeN_4O_4$).



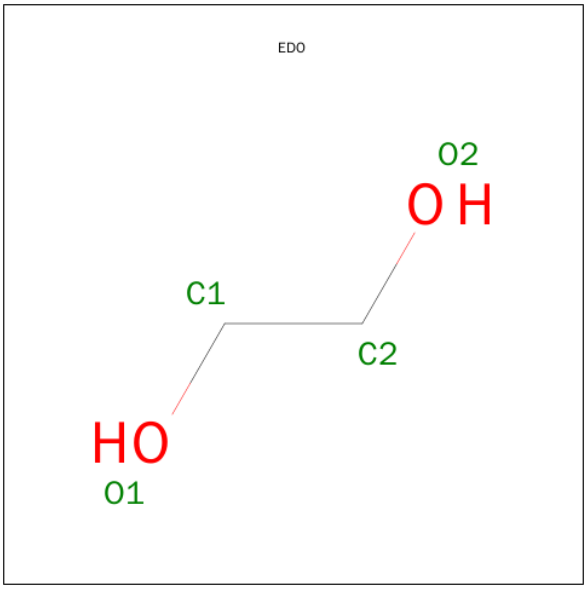
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
5	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 6 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 10 6 4	0	0

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

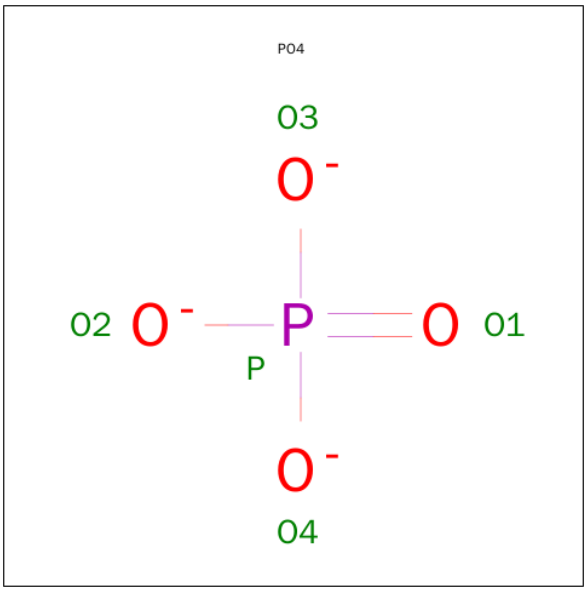


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	B	1	Total C O 4 2 2	0	0

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

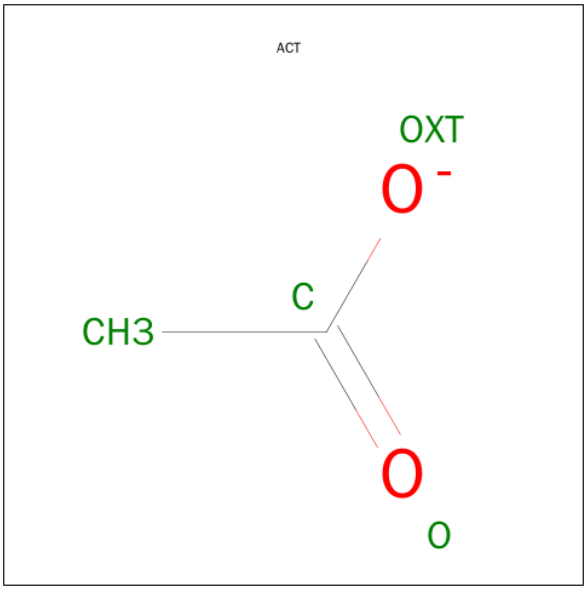
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	2	Total Na 2 2	0	0
8	A	1	Total Na 1 1	0	0

- Molecule 9 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	B	1	Total O P 5 4 1	0	0

- Molecule 10 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	D	1	Total C O 4 2 2	0	0
10	F	1	Total C O 4 2 2	0	0

- Molecule 11 is water.

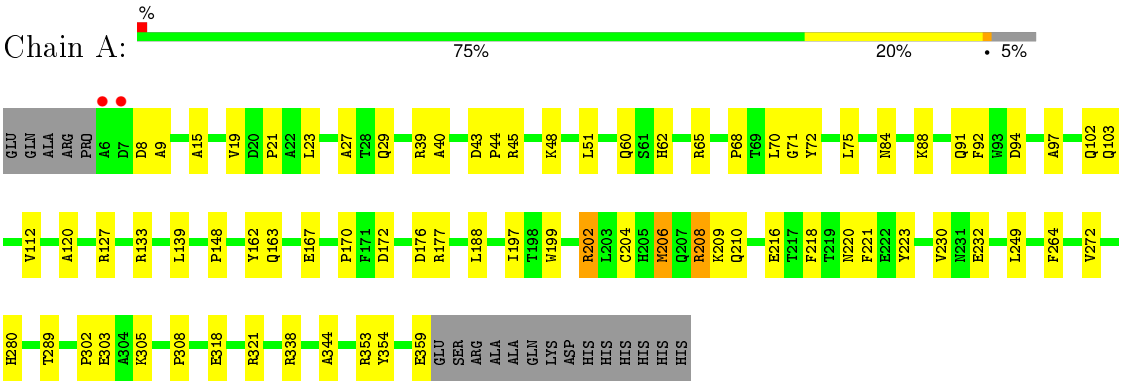
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	179	Total O 181 181	0	2
11	B	258	Total O 260 260	0	2
11	C	61	Total O 61 61	0	0
11	D	184	Total O 184 184	0	0
11	E	87	Total O 87 87	0	0
11	F	293	Total O 294 294	0	1

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

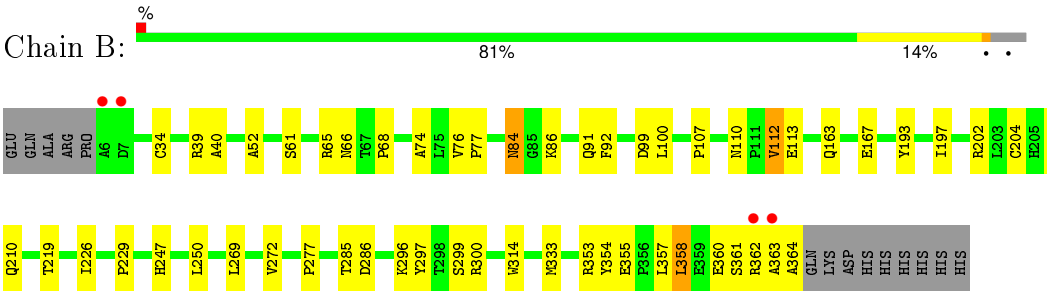
- Molecule 1: Methylamine utilization protein MauG

Chain A:



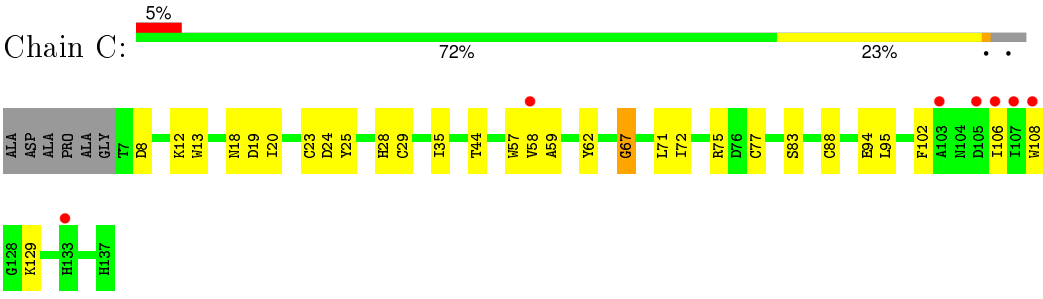
- Molecule 1: Methylamine utilization protein MauG

Chain B:



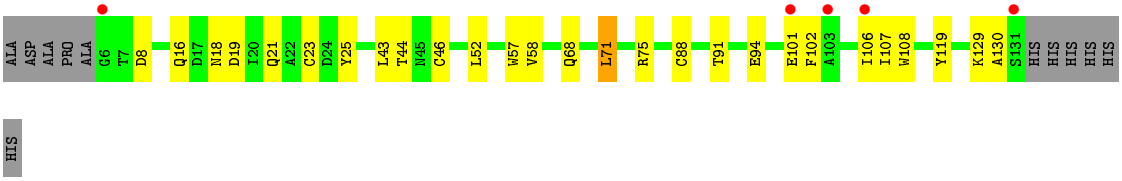
- Molecule 2: Methylamine dehydrogenase light chain

Chain C:

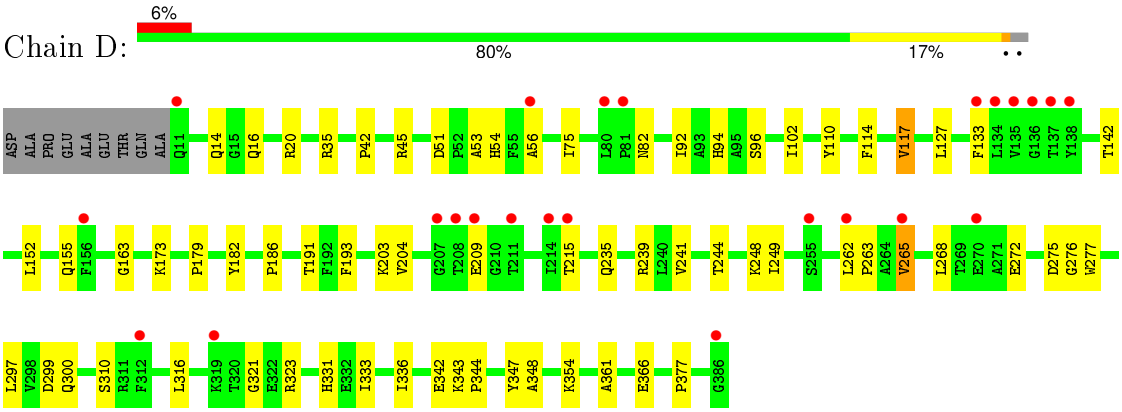


- Molecule 2: Methylamine dehydrogenase light chain

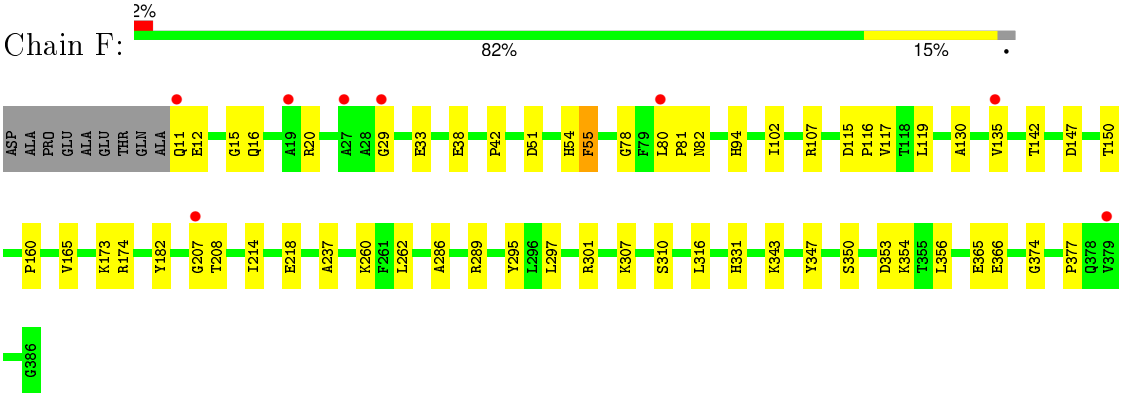
Chain E:



• Molecule 3: Methylamine dehydrogenase heavy chain



• Molecule 3: Methylamine dehydrogenase heavy chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	55.53Å 83.52Å 107.78Å 109.92° 91.52° 105.78°	Depositor
Resolution (Å)	43.46 – 2.14 37.17 – 2.14	Depositor EDS
% Data completeness (in resolution range)	97.4 (43.46-2.14) 84.9 (37.17-2.14)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.30 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.163 , 0.227 0.172 , 0.235	Depositor DCC
R_{free} test set	4829 reflections (5.45%)	DCC
Wilson B-factor (Å^2)	32.0	Xtriage
Anisotropy	0.043	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 39.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 93342 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14775	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PGE, NA, PO4, HEC, EDO, 0AF, ACT, CA

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	0.90	0/2880	0.88	2/3902 (0.1%)
1	B	1.04	0/2845	0.95	5/3859 (0.1%)
2	C	0.94	1/1035 (0.1%)	0.90	1/1413 (0.1%)
2	E	1.00	0/988	0.96	1/1348 (0.1%)
3	D	0.87	0/3040	0.88	1/4142 (0.0%)
3	F	1.02	1/3037 (0.0%)	0.95	0/4136
All	All	0.96	2/13825 (0.0%)	0.92	10/18800 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	77	CYS	CB-SG	-5.79	1.72	1.81
3	F	365	GLU	CG-CD	5.39	1.60	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	39	ARG	NE-CZ-NH2	-9.98	115.31	120.30
1	B	39	ARG	NE-CZ-NH1	8.53	124.57	120.30
1	B	65	ARG	NE-CZ-NH1	-5.91	117.35	120.30
3	D	35	ARG	NE-CZ-NH2	-5.75	117.42	120.30
1	B	353	ARG	NE-CZ-NH1	5.56	123.08	120.30
1	A	208	ARG	NE-CZ-NH2	-5.53	117.53	120.30
2	E	43	LEU	CB-CG-CD2	-5.39	101.83	111.00
2	C	8	ASP	CB-CG-OD1	5.34	123.10	118.30
1	B	99	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	338	ARG	NE-CZ-NH1	5.01	122.80	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2813	0	2695	66	0
1	B	2781	0	2655	38	0
2	C	1017	0	906	30	0
2	E	973	0	876	17	0
3	D	2959	0	2831	43	0
3	F	2957	0	2841	34	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	86	0	61	8	0
5	B	86	0	62	13	0
6	A	10	0	14	1	0
7	A	4	0	6	0	0
7	B	4	0	6	0	0
8	A	1	0	0	0	0
8	B	2	0	0	0	0
9	B	5	0	0	0	0
10	D	4	0	3	0	0
10	F	4	0	3	0	0
11	A	181	0	0	6	0
11	B	260	0	0	3	0
11	C	61	0	0	2	0
11	D	184	0	0	8	0
11	E	87	0	0	1	0
11	F	294	0	0	2	0
All	All	14775	0	12959	212	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 (212) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:CYS:SG	5:B:402:HEC:HAC	1.71	1.23
1:A:204:CYS:SG	5:A:403:HEC:HAC	1.81	1.16
1:A:133[B]:ARG:NH1	1:A:133[B]:ARG:HB3	1.64	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:CYS:SG	5:B:403:HEC:HAC	1.90	1.07
1:A:202[A]:ARG:HH22	2:C:127:VAL:HG11	1.31	0.96
1:A:202[A]:ARG:HB2	1:A:202[A]:ARG:HH11	1.33	0.94
2:C:57:0AF:CE3	2:C:108:TRP:CD1	2.54	0.90
1:B:285:THR:HG22	1:B:286:ASP:OD1	1.71	0.89
1:B:204:CYS:SG	5:B:403:HEC:C3C	2.65	0.85
1:A:204:CYS:HG	5:A:403:HEC:HAC	1.43	0.82
1:A:133[B]:ARG:HH11	1:A:133[B]:ARG:CB	1.92	0.81
1:B:210:GLN:HE22	2:E:44:THR:HG21	1.43	0.81
1:A:133[B]:ARG:HB3	1:A:133[B]:ARG:HH11	1.42	0.81
1:A:210:GLN:HE22	2:C:44:THR:HG21	1.45	0.80
1:B:34:CYS:SG	5:B:402:HEC:C3C	2.69	0.79
2:C:57:0AF:HE3	2:C:108:TRP:CD1	2.17	0.79
1:B:364:ALA:HB2	11:B:620:HOH:O	1.82	0.79
1:B:113:GLU:HG2	5:B:402:HEC:HBC2	1.67	0.77
1:A:204:CYS:SG	5:A:403:HEC:C3C	2.74	0.76
1:B:204:CYS:HG	5:B:403:HEC:HAC	1.47	0.76
2:C:23:CYS:HB3	2:C:88[B]:CYS:SG	2.26	0.76
1:A:133[B]:ARG:NH1	1:A:133[B]:ARG:CB	2.44	0.75
1:B:197:ILE:HG22	1:B:206:MET:CE	2.17	0.74
1:A:97:ALA:HA	1:A:102[B]:GLN:HE21	1.52	0.73
2:E:57:0AF:CE3	2:E:108:TRP:CD1	2.71	0.72
2:C:106:ILE:HG12	3:D:133:PHE:HZ	1.53	0.72
1:A:202[A]:ARG:NH1	1:A:202[A]:ARG:HB2	2.05	0.72
2:C:106:ILE:HG12	3:D:133:PHE:CZ	2.24	0.71
1:A:48:LYS:H	1:A:62:HIS:HE1	1.39	0.71
3:D:14:GLN:HE21	2:E:21:GLN:HE22	1.40	0.70
3:D:275:ASP:HB2	11:D:636:HOH:O	1.91	0.69
2:C:23:CYS:CB	2:C:88[B]:CYS:SG	2.80	0.69
1:B:197:ILE:HG22	1:B:206:MET:HE2	1.75	0.69
1:A:133[B]:ARG:HB3	1:A:133[B]:ARG:CZ	2.22	0.69
3:D:333:ILE:HD12	3:D:348:ALA:HB1	1.74	0.68
3:F:174[B]:ARG:CZ	3:F:208:THR:HA	2.24	0.68
3:D:51:ASP:HA	3:D:377:PRO:HA	1.77	0.67
1:A:133[B]:ARG:CA	1:A:133[B]:ARG:HH11	2.09	0.65
2:C:57:0AF:CE3	2:C:108:TRP:HD1	2.09	0.64
1:A:68:PRO:HG2	5:A:402:HEC:HBA1	1.79	0.64
3:D:342[A]:GLU:HA	11:D:653:HOH:O	1.98	0.63
3:D:268:LEU:HD22	3:D:277:TRP:HB3	1.81	0.63
1:A:9:ALA:HB3	1:A:139:LEU:HD21	1.81	0.62
1:B:91:GLN:O	1:B:92:PHE:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:54:HIS:O	3:F:55:PHE:HB2	2.00	0.61
3:D:342[B]:GLU:HA	11:D:653:HOH:O	2.00	0.61
1:A:202[A]:ARG:NH2	2:C:127:VAL:HG11	2.10	0.60
1:A:45:ARG:NH1	11:A:564:HOH:O	2.36	0.58
3:D:276:GLY:O	3:D:300:GLN:HA	2.03	0.58
1:A:39[A]:ARG:O	1:A:39[A]:ARG:HG2	2.03	0.58
3:D:193:PHE:CE2	3:D:203:LYS:HB2	2.39	0.58
1:A:209:LYS:HG2	3:F:33:GLU:HG3	1.85	0.58
3:F:82:ASN:HB3	3:F:142:THR:HB	1.85	0.57
5:A:403:HEC:HBC3	5:A:403:HEC:HMC1	1.87	0.57
3:D:275:ASP:CB	11:D:636:HOH:O	2.50	0.56
2:E:71:LEU:HD13	2:E:130:ALA:HB2	1.87	0.56
2:C:58:VAL:HG22	2:C:59:ALA:N	2.20	0.56
1:A:359:GLU:HA	11:A:647:HOH:O	2.06	0.56
1:A:199:TRP:O	1:A:202[A]:ARG:HG3	2.07	0.55
2:C:35:ILE:HD11	2:C:88[A]:CYS:SG	2.47	0.55
1:B:210:GLN:NE2	2:E:44:THR:HG21	2.19	0.55
3:F:12:GLU:OE1	3:F:20:ARG:NH1	2.39	0.55
3:F:174[B]:ARG:NH2	3:F:208:THR:HA	2.22	0.55
1:A:210:GLN:NE2	2:C:44:THR:HG21	2.21	0.54
2:C:62:TYR:CE1	2:C:67:GLY:HA2	2.43	0.54
1:A:359:GLU:CA	11:A:647:HOH:O	2.56	0.54
1:A:176:ASP:OD2	6:A:404:PGE:H6	2.08	0.54
1:A:127:ARG:HG2	1:A:133[C]:ARG:NH2	2.23	0.54
1:A:21:PRO:O	1:A:27:ALA:HA	2.08	0.53
2:C:62:TYR:CZ	2:C:67:GLY:HA2	2.43	0.53
1:A:172:ASP:O	1:A:177:ARG:NH1	2.41	0.53
3:D:45:ARG:NH2	3:D:343:LYS:O	2.42	0.53
1:B:208:ARG:HD2	11:B:687:HOH:O	2.08	0.53
1:A:70:LEU:HD13	1:A:163:GLN:NE2	2.24	0.52
1:A:208:ARG:NH2	3:F:29:GLY:O	2.36	0.52
3:D:297:LEU:HD11	3:D:333:ILE:HG22	1.92	0.52
2:C:12:LYS:NZ	11:C:219:HOH:O	2.40	0.52
1:A:272:VAL:HG21	5:A:403:HEC:HMA3	1.91	0.52
1:A:127:ARG:HG2	1:A:133[C]:ARG:HH21	1.74	0.51
3:F:331:HIS:HE1	3:F:366:GLU:OE1	1.93	0.51
3:D:336:ILE:HA	3:D:347:TYR:O	2.11	0.51
1:B:84:ASN:HD22	1:B:86:LYS:NZ	2.08	0.51
3:F:297:LEU:HD22	3:F:310:SER:HB2	1.92	0.50
3:F:42:PRO:HG3	3:F:116:PRO:HB2	1.92	0.50
3:D:20:ARG:NH1	11:D:562:HOH:O	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:244:THR:HG23	3:D:248:LYS:O	2.12	0.50
3:D:96:SER:HB3	3:D:110:TYR:CZ	2.46	0.50
1:B:299:SER:HB2	1:B:333:MET:HG3	1.94	0.49
3:D:344:PRO:HG2	3:D:361:ALA:HB3	1.94	0.49
1:B:226:ILE:O	1:B:297:TYR:OH	2.25	0.49
1:B:229:PRO:HG3	1:B:314:TRP:O	2.13	0.49
3:F:115:ASP:O	3:F:119:LEU:HA	2.11	0.49
1:A:303[B]:GLU:H	1:A:303[B]:GLU:CD	2.14	0.49
1:A:48:LYS:H	1:A:62:HIS:CE1	2.26	0.49
1:A:230:VAL:CG2	1:A:318:GLU:HG3	2.43	0.49
1:B:272:VAL:HG21	5:B:403:HEC:HMA3	1.94	0.48
3:D:239:ARG:HG3	3:D:241:VAL:HG23	1.95	0.48
2:E:46:CYS:SG	2:E:52:LEU:HD13	2.53	0.48
5:B:403:HEC:HBC3	5:B:403:HEC:HMC1	1.96	0.48
2:C:95:LEU:HD12	2:C:102:PHE:CD2	2.48	0.48
1:A:71:GLY:O	1:A:72:TYR:HB2	2.14	0.48
3:D:265:VAL:CG2	3:D:321:GLY:HA3	2.44	0.48
3:D:186:PRO:HB2	3:D:235:GLN:NE2	2.28	0.47
1:A:204:CYS:HA	1:A:220:ASN:ND2	2.29	0.47
3:D:155:GLN:NE2	11:D:621:HOH:O	2.28	0.47
3:F:80:LEU:N	3:F:81:PRO:CD	2.77	0.47
3:D:82:ASN:HB3	11:D:608:HOH:O	2.13	0.47
3:D:265:VAL:HG21	3:D:321:GLY:CA	2.45	0.47
1:A:91:GLN:O	1:A:92:PHE:HB2	2.14	0.47
1:A:353:ARG:NE	11:A:606:HOH:O	2.42	0.47
3:F:51:ASP:HA	3:F:377:PRO:HA	1.96	0.47
3:F:38:GLU:HB3	3:F:117:VAL:HG23	1.97	0.46
2:E:8:ASP:OD2	11:E:284:HOH:O	2.21	0.46
1:A:264:PHE:CE1	1:A:280:HIS:CE1	3.03	0.46
3:F:214:ILE:HD12	11:F:780:HOH:O	2.15	0.46
1:A:206:MET:HE2	1:A:216:GLU:CD	2.36	0.46
3:D:331:HIS:HE1	3:D:366:GLU:OE1	1.98	0.46
3:D:42:PRO:HD3	3:D:117:VAL:HG12	1.98	0.46
2:E:19:ASP:O	2:E:25:TYR:HB2	2.15	0.46
3:D:92:ILE:HG13	3:D:114:PHE:HB2	1.96	0.46
1:A:197:ILE:HA	1:A:202[A]:ARG:HB3	1.98	0.46
2:C:23:CYS:SG	2:C:88[B]:CYS:CB	3.04	0.46
3:F:350:SER:HB3	3:F:353:ASP:HB2	1.98	0.46
1:B:107:PRO:HG2	5:B:402:HEC:HBB2	1.97	0.46
1:A:102[A]:GLN:HG2	11:A:666:HOH:O	2.17	0.45
1:A:209:LYS:HE3	3:F:33:GLU:HG3	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300[A]:ARG:NH1	11:B:511:HOH:O	2.36	0.45
1:B:52:ALA:O	1:B:66:ASN:HA	2.16	0.45
2:E:91:THR:HG21	3:F:307:LYS:HD2	1.97	0.45
1:A:120:ALA:HA	1:A:148:PRO:HB3	1.97	0.45
3:F:286:ALA:HB3	3:F:295:TYR:HB2	1.98	0.45
2:C:94:GLU:HG2	2:C:102:PHE:O	2.16	0.45
1:A:29:GLN:HE22	5:A:402:HEC:HBC3	1.81	0.45
1:B:61:SER:HB3	1:B:112:VAL:HB	1.98	0.45
1:B:76:VAL:HG12	1:B:77:PRO:O	2.17	0.45
1:B:163:GLN:HE22	5:B:402:HEC:HMA1	1.81	0.45
1:A:206:MET:HE3	1:A:218:PHE:CD2	2.52	0.45
1:B:247:HIS:HB3	1:B:250:LEU:HB3	1.99	0.45
3:F:237:ALA:HB2	3:F:289:ARG:HG3	1.98	0.45
2:C:18:ASN:O	3:F:16:GLN:HA	2.16	0.45
3:F:354:LYS:HG2	3:F:374:GLY:O	2.17	0.45
1:B:110:ASN:HB3	1:B:113:GLU:HB2	1.99	0.45
2:E:57:0AF:HE3	2:E:108:TRP:CD1	2.50	0.45
3:D:299:ASP:OD1	3:D:300:GLN:N	2.45	0.45
1:B:34:CYS:CB	5:B:402:HEC:C3C	2.95	0.44
2:C:57:0AF:HE3	2:C:108:TRP:CG	2.52	0.44
2:C:23:CYS:SG	2:C:88[B]:CYS:HB2	2.57	0.44
2:E:23:CYS:CB	2:E:88[B]:CYS:SG	3.06	0.44
2:E:23:CYS:SG	2:E:88[B]:CYS:SG	3.15	0.44
1:B:91:GLN:HB3	5:B:402:HEC:HAA1	1.98	0.44
3:D:333:ILE:HD12	3:D:348:ALA:CB	2.46	0.44
3:D:82:ASN:HB3	3:D:142:THR:HB	2.00	0.44
1:B:202:ARG:HH21	2:E:75:ARG:HD2	1.83	0.44
1:A:289:THR:HG23	1:A:308:PRO:HD2	1.98	0.44
1:A:60:GLN:O	1:A:62:HIS:HD2	2.01	0.44
3:D:262:LEU:HB3	3:D:263:PRO:HD2	2.00	0.44
1:B:204:CYS:SG	5:B:403:HEC:CBC	2.97	0.44
3:F:260:LYS:NZ	3:F:260:LYS:HB3	2.33	0.43
3:F:174[A]:ARG:NH2	3:F:207:GLY:O	2.50	0.43
1:A:223:TYR:CG	1:A:249:LEU:HD22	2.53	0.43
1:A:206:MET:HE2	1:A:206:MET:HA	2.01	0.43
2:C:25:TYR:HB3	2:C:28:HIS:CD2	2.53	0.43
2:E:106:ILE:HA	3:F:135:VAL:HG23	2.00	0.43
1:A:112:VAL:O	1:A:112:VAL:HG23	2.17	0.43
3:F:347:TYR:HB3	3:F:356:LEU:HD11	2.01	0.43
1:A:40:ALA:HA	1:A:354:TYR:CZ	2.54	0.43
1:B:197:ILE:HG22	1:B:206:MET:HE1	1.97	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:107:ILE:HD12	2:E:119:TYR:HB2	2.00	0.42
1:A:170:PRO:HG3	1:A:353:ARG:HH12	1.83	0.42
3:D:54:HIS:HD2	11:D:625:HOH:O	2.01	0.42
3:F:147:ASP:OD1	3:F:147:ASP:C	2.58	0.42
2:C:83:SER:HB3	2:C:120:HIS:CE1	2.53	0.42
3:F:173:LYS:HB3	3:F:174[B]:ARG:NH2	2.34	0.42
3:D:191:THR:HA	3:D:204:VAL:O	2.19	0.42
1:A:43:ASP:HA	1:A:44:PRO:HD2	1.85	0.42
2:C:57:0AF:HBC1	2:C:108:TRP:NE1	2.34	0.42
1:A:163:GLN:HE22	5:A:402:HEC:HMA1	1.83	0.42
1:B:74:ALA:HA	1:B:100:LEU:HD11	2.01	0.42
2:C:19:ASP:OD1	3:F:15:GLY:HA3	2.20	0.42
1:A:15:ALA:HB2	1:A:162:TYR:CE1	2.54	0.42
1:A:21:PRO:HA	1:A:29:GLN:O	2.20	0.41
3:F:107:ARG:NE	3:F:130:ALA:HB1	2.35	0.41
3:D:297:LEU:HD22	3:D:310:SER:HB2	2.02	0.41
1:A:302:PRO:O	1:A:305:LYS:HG2	2.20	0.41
2:C:20:ILE:HG22	2:C:25:TYR:CZ	2.55	0.41
3:D:323:ARG:HB2	3:D:323:ARG:HE	1.73	0.41
2:C:75:ARG:HA	11:C:251:HOH:O	2.20	0.41
1:B:277:PRO:HB3	1:B:285:THR:HA	2.02	0.41
2:C:58:VAL:HA	2:C:72:ILE:O	2.20	0.41
2:E:94:GLU:HG2	2:E:102:PHE:O	2.20	0.41
3:F:11:GLN:HA	11:F:739:HOH:O	2.20	0.41
3:D:277:TRP:CE2	3:D:300:GLN:HG3	2.55	0.41
3:F:78:GLY:O	3:F:81:PRO:HD3	2.21	0.41
1:A:188:LEU:HD23	1:A:344:ALA:HB2	2.03	0.41
1:A:202[A]:ARG:HG3	1:A:202[A]:ARG:H	1.65	0.41
1:B:193:TYR:O	1:B:197:ILE:HG12	2.20	0.41
2:C:13:TRP:NE1	2:C:24:ASP:HA	2.36	0.41
1:A:103:GLN:C	1:A:103:GLN:OE1	2.59	0.41
1:A:88:LYS:HA	1:A:221:PHE:O	2.20	0.41
3:D:272:GLU:HB3	3:D:277:TRP:HB2	2.03	0.41
3:D:249:ILE:HB	3:D:265:VAL:HG12	2.03	0.41
1:A:65:ARG:HH12	1:A:94:ASP:CG	2.24	0.41
3:D:16:GLN:HA	2:E:18:ASN:O	2.21	0.41
3:D:53:ALA:HB3	3:D:56:ALA:HB3	2.03	0.41
1:B:40:ALA:HA	1:B:354:TYR:CZ	2.56	0.40
1:B:361:SER:O	1:B:363:ALA:N	2.54	0.40
3:F:150:THR:HA	3:F:165:VAL:O	2.22	0.40
3:D:152:LEU:HA	3:D:163:GLY:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:GLU:O	1:B:358:LEU:HB2	2.21	0.40
1:A:19:VAL:HG13	11:A:537:HOH:O	2.21	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 X-ray entries followed by that with respect to entries of similar resolution.

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	360/373 (96%)	342 (95%)	18 (5%)	0	100	100
1	B	358/373 (96%)	344 (96%)	13 (4%)	1 (0%)	46	41
2	C	129/137 (94%)	123 (95%)	5 (4%)	1 (1%)	24	14
2	E	126/137 (92%)	123 (98%)	3 (2%)	0	100	100
3	D	379/385 (98%)	360 (95%)	16 (4%)	3 (1%)	24	14
3	F	378/385 (98%)	363 (96%)	13 (3%)	2 (0%)	34	26
All	All	1730/1790 (97%)	1655 (96%)	68 (4%)	7 (0%)	39	33

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	362	ARG
3	D	102[A]	ILE
3	D	102[B]	ILE
3	F	55	PHE
2	C	67	GLY
3	F	102	ILE
3	D	179	PRO

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 X-ray entries followed by that with respect to entries of similar resolution.

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	284/292 (97%)	273 (96%)	11 (4%)	39	36
1	B	280/292 (96%)	270 (96%)	10 (4%)	42	39
2	C	111/112 (99%)	108 (97%)	3 (3%)	52	52
2	E	107/112 (96%)	100 (94%)	7 (6%)	21	15
3	D	309/310 (100%)	299 (97%)	10 (3%)	46	44
3	F	308/310 (99%)	301 (98%)	7 (2%)	58	60
All	All	1399/1428 (98%)	1351 (97%)	48 (3%)	45	41

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASP
1	A	23	LEU
1	A	51	LEU
1	A	75	LEU
1	A	84	ASN
1	A	167	GLU
1	A	202[A]	ARG
1	A	202[B]	ARG
1	A	206	MET
1	A	232	GLU
1	A	321	ARG
1	B	68	PRO
1	B	84	ASN
1	B	112	VAL
1	B	167	GLU
1	B	219	THR
1	B	269	LEU
1	B	296	LYS
1	B	357	LEU
1	B	358	LEU
1	B	360	GLU
2	C	29	CYS

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Mol	Chain	Res	Type
2	C	71	LEU
2	C	129	LYS
3	D	75	ILE
3	D	94	HIS
3	D	117	VAL
3	D	127	LEU
3	D	173	LYS
3	D	209	GLU
3	D	215	THR
3	D	265	VAL
3	D	316	LEU
3	D	354	LYS
2	E	16	GLN
2	E	58	VAL
2	E	68	GLN
2	E	71	LEU
2	E	101[A]	GLU
2	E	101[B]	GLU
2	E	129	LYS
3	F	94	HIS
3	F	160	PRO
3	F	218	GLU
3	F	262	LEU
3	F	301	ARG
3	F	316	LEU
3	F	343	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	GLN
1	A	60	GLN
1	A	62	HIS
1	A	91	GLN
1	A	163	GLN
1	A	210	GLN
1	B	16	GLN
1	B	29	GLN
1	B	84	ASN
1	B	91	GLN
1	B	163	GLN
1	B	210	GLN

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Mol	Chain	Res	Type
2	C	134	HIS
3	D	14	GLN
3	D	235	GLN
2	E	68	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	0AF	C	57	2	13,16,17	1.13	0	10,22,24	1.19	0
2	0AF	E	57	2	13,16,17	1.06	0	10,22,24	1.24	1 (10%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	0AF	C	57	2	-	0/3/6/8	0/2/2/2
2	0AF	E	57	2	-	0/3/6/8	0/2/2/2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	E	57	0AF	O-C-CA	-2.00	120.27	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	57	0AF	5	0
2	E	57	0AF	2	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 15 ligands modelled in this entry, 5 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
5	HEC	A	402	1,11	24,50,50	1.70	9 (37%)	19,82,82	3.13	10 (52%)
5	HEC	A	403	1	24,50,50	1.99	9 (37%)	19,82,82	3.26	6 (31%)
6	PGE	A	404	-	9,9,9	0.64	0	8,8,8	0.45	0
7	EDO	A	405	-	3,3,3	0.48	0	2,2,2	0.46	0
5	HEC	B	402	1,11	24,50,50	1.66	4 (16%)	19,82,82	3.37	11 (57%)
5	HEC	B	403	1	24,50,50	1.68	6 (25%)	19,82,82	3.51	9 (47%)
9	PO4	B	404	-	4,4,4	0.30	0	6,6,6	0.29	0
7	EDO	B	405	-	3,3,3	0.48	0	2,2,2	0.22	0
10	ACT	D	401	-	1,3,3	1.52	0	0,3,3	0.00	-
10	ACT	F	401	-	1,3,3	0.37	0	0,3,3	0.00	-

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
5	HEC	A	402	1,11	-	0/6/54/54	0/0/8/8
5	HEC	A	403	1	-	0/6/54/54	0/0/8/8
6	PGE	A	404	-	-	0/7/7/7	0/0/0/0
7	EDO	A	405	-	-	0/1/1/1	0/0/0/0
5	HEC	B	402	1,11	-	0/6/54/54	0/0/8/8
5	HEC	B	403	1	-	0/6/54/54	0/0/8/8
9	PO4	B	404	-	-	0/0/0/0	0/0/0/0
7	EDO	B	405	-	-	0/1/1/1	0/0/0/0
10	ACT	D	401	-	-	0/0/0/0	0/0/0/0
10	ACT	F	401	-	-	0/0/0/0	0/0/0/0

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	403	HEC	C4A-NA	-4.11	1.31	1.36
5	A	403	HEC	C4B-NB	-3.97	1.31	1.36
5	A	403	HEC	C4A-NA	-3.44	1.32	1.36
5	A	403	HEC	C4C-NC	-3.15	1.32	1.36
5	B	403	HEC	C4C-NC	-3.12	1.32	1.36
5	A	402	HEC	C4C-NC	-2.87	1.32	1.36
5	B	403	HEC	C4B-NB	-2.81	1.32	1.36
5	A	402	HEC	C4A-NA	-2.43	1.33	1.36
5	A	403	HEC	C3B-C2B	-2.38	1.38	1.40
5	A	402	HEC	C1A-NA	-2.07	1.33	1.36
5	B	402	HEC	C4D-CHA	2.18	1.45	1.39
5	B	403	HEC	C4D-CHA	2.19	1.45	1.39
5	A	402	HEC	C3C-C4C	2.25	1.47	1.42
5	A	402	HEC	C1B-CHB	2.39	1.46	1.39
5	B	403	HEC	C1C-CHC	2.51	1.46	1.39
5	A	403	HEC	C3B-C4B	2.59	1.48	1.42
5	A	403	HEC	C1C-CHC	2.61	1.47	1.39
5	A	402	HEC	C4D-CHA	2.68	1.47	1.39
5	A	402	HEC	C3B-C4B	2.74	1.49	1.42
5	A	403	HEC	C1D-CHD	2.77	1.47	1.39
5	A	402	HEC	C1D-CHD	2.78	1.47	1.39
5	B	402	HEC	C1B-CHB	2.97	1.48	1.39
5	A	403	HEC	C3C-C4C	3.05	1.49	1.42
5	A	403	HEC	C4D-CHA	3.09	1.48	1.39
5	B	402	HEC	C1C-CHC	3.15	1.48	1.39
5	B	403	HEC	C3C-C4C	3.31	1.50	1.42
5	A	402	HEC	C1C-CHC	3.49	1.49	1.39
5	B	402	HEC	C1D-CHD	3.91	1.50	1.39

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	B	403	HEC	CBB-CAB-C3B	-9.92	105.31	127.35
5	B	402	HEC	CBB-CAB-C3B	-9.75	105.68	127.35
5	A	403	HEC	CBB-CAB-C3B	-8.57	108.31	127.35
5	A	402	HEC	CBB-CAB-C3B	-7.14	111.49	127.35
5	B	403	HEC	CBC-CAC-C3C	-6.62	112.63	127.35
5	A	403	HEC	CBC-CAC-C3C	-6.57	112.75	127.35
5	A	402	HEC	CBC-CAC-C3C	-6.43	113.07	127.35
5	A	403	HEC	CBD-CAD-C3D	-6.06	101.67	112.53
5	B	403	HEC	CBD-CAD-C3D	-5.74	102.25	112.53
5	A	402	HEC	CBD-CAD-C3D	-5.04	103.49	112.53
5	B	402	HEC	CMB-C2B-C1B	-4.42	121.04	128.36
5	B	402	HEC	CBC-CAC-C3C	-4.18	118.07	127.35
5	A	403	HEC	CBA-CAA-C2A	-4.00	105.35	112.53
5	B	403	HEC	CBA-CAA-C2A	-3.93	105.48	112.53
5	A	402	HEC	CBA-CAA-C2A	-3.55	106.17	112.53
5	A	402	HEC	C4C-C3C-C2C	-3.54	102.53	106.35
5	B	402	HEC	C4C-C3C-C2C	-3.51	102.56	106.35
5	A	402	HEC	CAA-CBA-CGA	-3.45	106.42	112.75
5	B	403	HEC	CMC-C2C-C1C	-3.31	122.89	128.36
5	B	402	HEC	CBA-CAA-C2A	-3.07	107.02	112.53
5	B	402	HEC	CBD-CAD-C3D	-3.00	107.15	112.53
5	B	402	HEC	CMC-C2C-C1C	-2.78	123.76	128.36
5	B	402	HEC	C4B-C3B-C2B	-2.69	103.44	106.35
5	A	403	HEC	CAD-CBD-CGD	-2.38	108.39	112.75
5	A	403	HEC	C4C-C3C-C2C	-2.35	103.81	106.35
5	A	402	HEC	CMB-C2B-C1B	-2.14	124.83	128.36
5	B	403	HEC	C4C-C3C-C2C	-2.01	104.18	106.35
5	A	402	HEC	CMC-C2C-C1C	-2.01	125.04	128.36
5	A	402	HEC	C3C-C4C-NC	2.17	115.04	110.94
5	B	403	HEC	CMD-C2D-C3D	2.19	129.81	125.24
5	B	403	HEC	C3B-C4B-NB	2.20	115.09	110.94
5	B	403	HEC	CAA-C2A-C1A	2.28	129.48	127.01
5	B	402	HEC	C3C-C4C-NC	2.34	115.35	110.94
5	A	402	HEC	CMD-C2D-C3D	2.41	130.27	125.24
5	B	402	HEC	CAD-C3D-C4D	2.66	129.90	127.01
5	B	402	HEC	CAA-C2A-C1A	3.67	130.99	127.01

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	402	HEC	3	0
5	A	403	HEC	5	0
6	A	404	PGE	1	0
5	B	402	HEC	7	0
5	B	403	HEC	6	0

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 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	354/373 (94%)	-0.08	2 (0%)	90	92	29, 39, 55, 71	0
1	B	359/373 (96%)	-0.18	4 (1%)	82	86	22, 33, 51, 87	0
2	C	130/137 (94%)	0.34	7 (5%)	29	38	23, 36, 65, 82	0
2	E	125/137 (91%)	-0.03	5 (4%)	42	51	23, 29, 42, 69	0
3	D	376/385 (97%)	0.11	24 (6%)	23	30	25, 42, 67, 77	0
3	F	376/385 (97%)	-0.14	8 (2%)	67	73	21, 30, 47, 61	0
All	All	1720/1790 (96%)	-0.03	50 (2%)	55	64	21, 35, 58, 87	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	6	ALA	6.0
1	B	6	ALA	5.7
2	C	106	ILE	5.0
3	D	135	VAL	3.9
3	D	207	GLY	3.8
1	B	7	ASP	3.6
1	B	362	ARG	3.5
3	D	208	THR	3.4
1	B	363	ALA	3.4
2	C	58	VAL	3.4
2	C	107	ILE	3.3
3	D	211	THR	3.2
1	A	7	ASP	3.2
3	D	386	GLY	3.0
3	D	80	LEU	3.0
2	E	106	ILE	2.9
3	D	11	GLN	2.9
3	F	207	GLY	2.9
3	D	137	THR	2.9

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Mol	Chain	Res	Type	RSRZ
3	F	11	GLN	2.8
3	D	134	LEU	2.8
2	E	131	SER	2.7
2	E	6	GLY	2.7
3	D	133	PHE	2.7
2	C	108	TRP	2.6
3	D	255	SER	2.6
2	C	105	ASP	2.6
2	C	103	ALA	2.5
3	D	136	GLY	2.4
3	D	209	GLU	2.3
2	E	103	ALA	2.3
2	C	133	HIS	2.3
3	D	81	PRO	2.3
3	F	27	ALA	2.3
3	D	215	THR	2.2
3	D	262	LEU	2.2
3	D	312	PHE	2.2
3	D	265	VAL	2.2
3	D	56	ALA	2.2
3	D	270	GLU	2.2
2	E	101[A]	GLU	2.1
3	D	156	PHE	2.1
3	D	138	TYR	2.1
3	F	379	VAL	2.1
3	D	319	LYS	2.1
3	D	214	ILE	2.1
3	F	29	GLY	2.1
3	F	80	LEU	2.0
3	F	19	ALA	2.0
3	F	135	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	0AF	C	57	15/16	0.94	0.24	-	39,43,47,49	0
2	0AF	E	57	15/16	0.95	0.19	-	31,34,38,40	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
6	PGE	A	404	10/10	0.69	0.39	4.25	78,86,90,90	0
9	PO4	B	404	5/5	0.96	0.19	4.23	83,84,84,85	0
7	EDO	A	405	4/4	0.90	0.18	2.91	59,59,60,60	0
4	CA	B	401	1/1	1.00	0.13	1.78	26,26,26,26	0
5	HEC	B	403	43/43	0.99	0.17	1.06	16,22,26,29	0
8	NA	B	407	1/1	0.97	0.10	0.71	42,42,42,42	0
8	NA	A	406	1/1	0.95	0.12	0.65	61,61,61,61	0
5	HEC	A	402	43/43	0.97	0.13	0.50	27,35,38,40	0
5	HEC	B	402	43/43	0.98	0.13	0.39	20,27,31,31	0
4	CA	A	401	1/1	0.98	0.12	0.11	33,33,33,33	0
5	HEC	A	403	43/43	0.98	0.13	-0.00	27,31,35,38	0
7	EDO	B	405	4/4	0.95	0.07	-1.26	44,46,47,48	0
8	NA	B	406	1/1	0.95	0.08	-	38,38,38,38	0
10	ACT	F	401	4/4	0.98	0.14	-	42,44,46,46	0
10	ACT	D	401	4/4	0.96	0.13	-	46,47,47,48	0

6.5 Other polymers (i)

There are no such residues in this entry.