Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 06:49 AM GMT

PDB ID	:	2YGX
Title	:	Structure of the mixed-function P450 MycG in P21 space group
Authors	:	Li, S.; Kells, P.M.; Rutaganira, F.U.; Sherman, D.H.; Podust, L.M.
Deposited on	:	2011-04-22
Resolution	:	2.39 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 (i) symbol.

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

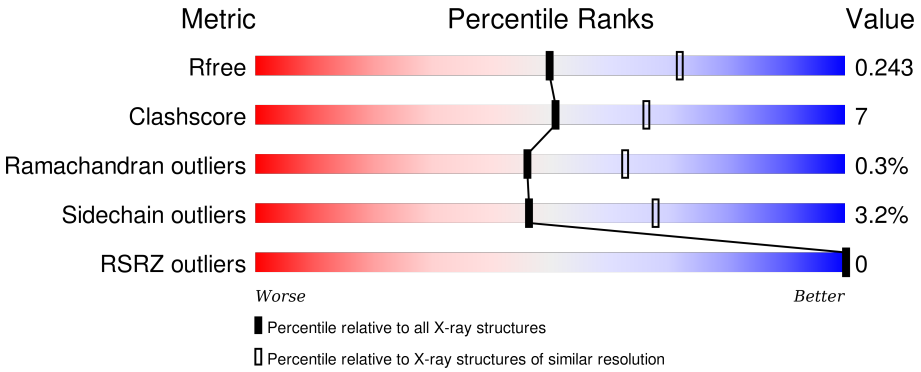
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 2.39 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	417	77% 16% • 6%
1	B	417	80% 13% • 6%
1	C	417	78% 15% 6%
1	D	417	78% 15% 6%

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
3	GOL	A	1399	-	-	-	X
3	GOL	B	1398	-	-	-	X
3	GOL	B	1401	-	-	X	-
3	GOL	C	1400	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12909 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 P-450-LIKE PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	1	0
			3056	1922	553	570	11			
1	B	393	Total	C	N	O	S	0	1	0
			3063	1926	555	571	11			
1	C	393	Total	C	N	O	S	0	0	0
			3043	1914	557	562	10			
1	D	393	Total	C	N	O	S	0	2	0
			3065	1927	558	569	11			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP Q59523
A	-18	GLY	-	EXPRESSION TAG	UNP Q59523
A	-17	SER	-	EXPRESSION TAG	UNP Q59523
A	-16	SER	-	EXPRESSION TAG	UNP Q59523
A	-15	HIS	-	EXPRESSION TAG	UNP Q59523
A	-14	HIS	-	EXPRESSION TAG	UNP Q59523
A	-13	HIS	-	EXPRESSION TAG	UNP Q59523
A	-12	HIS	-	EXPRESSION TAG	UNP Q59523
A	-11	HIS	-	EXPRESSION TAG	UNP Q59523
A	-10	HIS	-	EXPRESSION TAG	UNP Q59523
A	-9	SER	-	EXPRESSION TAG	UNP Q59523
A	-8	SER	-	EXPRESSION TAG	UNP Q59523
A	-7	GLY	-	EXPRESSION TAG	UNP Q59523
A	-6	LEU	-	EXPRESSION TAG	UNP Q59523
A	-5	VAL	-	EXPRESSION TAG	UNP Q59523
A	-4	PRO	-	EXPRESSION TAG	UNP Q59523
A	-3	ARG	-	EXPRESSION TAG	UNP Q59523
A	-2	GLY	-	EXPRESSION TAG	UNP Q59523
A	-1	SER	-	EXPRESSION TAG	UNP Q59523
A	0	HIS	-	EXPRESSION TAG	UNP Q59523
B	-19	MET	-	EXPRESSION TAG	UNP Q59523

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q59523
B	-17	SER	-	EXPRESSION TAG	UNP Q59523
B	-16	SER	-	EXPRESSION TAG	UNP Q59523
B	-15	HIS	-	EXPRESSION TAG	UNP Q59523
B	-14	HIS	-	EXPRESSION TAG	UNP Q59523
B	-13	HIS	-	EXPRESSION TAG	UNP Q59523
B	-12	HIS	-	EXPRESSION TAG	UNP Q59523
B	-11	HIS	-	EXPRESSION TAG	UNP Q59523
B	-10	HIS	-	EXPRESSION TAG	UNP Q59523
B	-9	SER	-	EXPRESSION TAG	UNP Q59523
B	-8	SER	-	EXPRESSION TAG	UNP Q59523
B	-7	GLY	-	EXPRESSION TAG	UNP Q59523
B	-6	LEU	-	EXPRESSION TAG	UNP Q59523
B	-5	VAL	-	EXPRESSION TAG	UNP Q59523
B	-4	PRO	-	EXPRESSION TAG	UNP Q59523
B	-3	ARG	-	EXPRESSION TAG	UNP Q59523
B	-2	GLY	-	EXPRESSION TAG	UNP Q59523
B	-1	SER	-	EXPRESSION TAG	UNP Q59523
B	0	HIS	-	EXPRESSION TAG	UNP Q59523
C	-19	MET	-	EXPRESSION TAG	UNP Q59523
C	-18	GLY	-	EXPRESSION TAG	UNP Q59523
C	-17	SER	-	EXPRESSION TAG	UNP Q59523
C	-16	SER	-	EXPRESSION TAG	UNP Q59523
C	-15	HIS	-	EXPRESSION TAG	UNP Q59523
C	-14	HIS	-	EXPRESSION TAG	UNP Q59523
C	-13	HIS	-	EXPRESSION TAG	UNP Q59523
C	-12	HIS	-	EXPRESSION TAG	UNP Q59523
C	-11	HIS	-	EXPRESSION TAG	UNP Q59523
C	-10	HIS	-	EXPRESSION TAG	UNP Q59523
C	-9	SER	-	EXPRESSION TAG	UNP Q59523
C	-8	SER	-	EXPRESSION TAG	UNP Q59523
C	-7	GLY	-	EXPRESSION TAG	UNP Q59523
C	-6	LEU	-	EXPRESSION TAG	UNP Q59523
C	-5	VAL	-	EXPRESSION TAG	UNP Q59523
C	-4	PRO	-	EXPRESSION TAG	UNP Q59523
C	-3	ARG	-	EXPRESSION TAG	UNP Q59523
C	-2	GLY	-	EXPRESSION TAG	UNP Q59523
C	-1	SER	-	EXPRESSION TAG	UNP Q59523
C	0	HIS	-	EXPRESSION TAG	UNP Q59523
D	-19	MET	-	EXPRESSION TAG	UNP Q59523
D	-18	GLY	-	EXPRESSION TAG	UNP Q59523
D	-17	SER	-	EXPRESSION TAG	UNP Q59523

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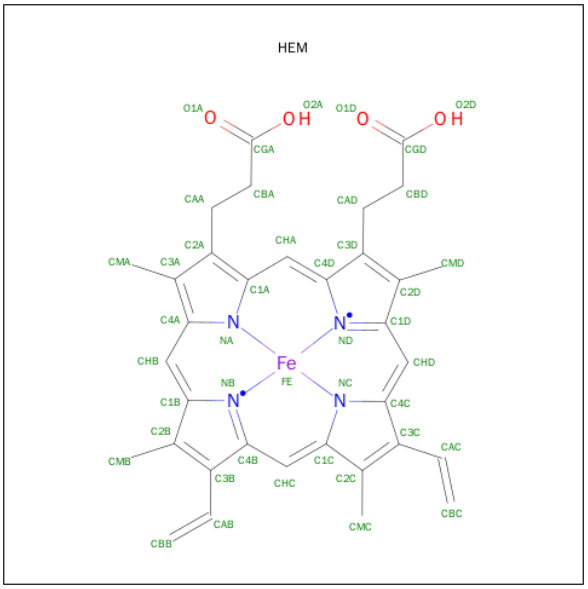
Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP Q59523
D	-15	HIS	-	EXPRESSION TAG	UNP Q59523
D	-14	HIS	-	EXPRESSION TAG	UNP Q59523
D	-13	HIS	-	EXPRESSION TAG	UNP Q59523
D	-12	HIS	-	EXPRESSION TAG	UNP Q59523
D	-11	HIS	-	EXPRESSION TAG	UNP Q59523
D	-10	HIS	-	EXPRESSION TAG	UNP Q59523
D	-9	SER	-	EXPRESSION TAG	UNP Q59523
D	-8	SER	-	EXPRESSION TAG	UNP Q59523
D	-7	GLY	-	EXPRESSION TAG	UNP Q59523
D	-6	LEU	-	EXPRESSION TAG	UNP Q59523
D	-5	VAL	-	EXPRESSION TAG	UNP Q59523
D	-4	PRO	-	EXPRESSION TAG	UNP Q59523
D	-3	ARG	-	EXPRESSION TAG	UNP Q59523
D	-2	GLY	-	EXPRESSION TAG	UNP Q59523
D	-1	SER	-	EXPRESSION TAG	UNP Q59523
D	0	HIS	-	EXPRESSION TAG	UNP Q59523

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

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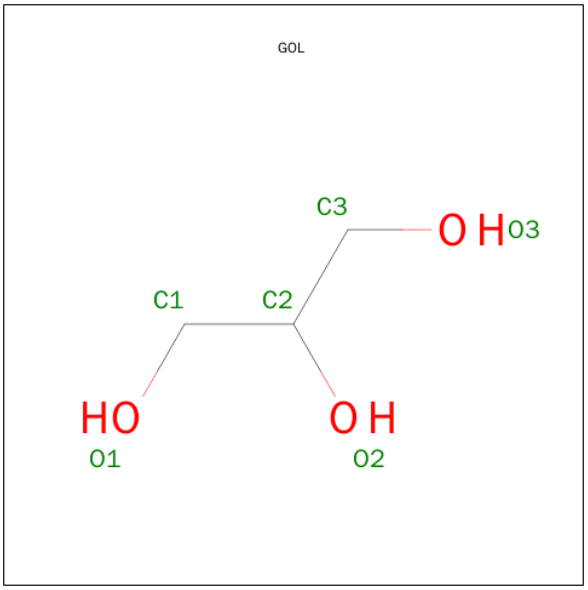
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	D	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		

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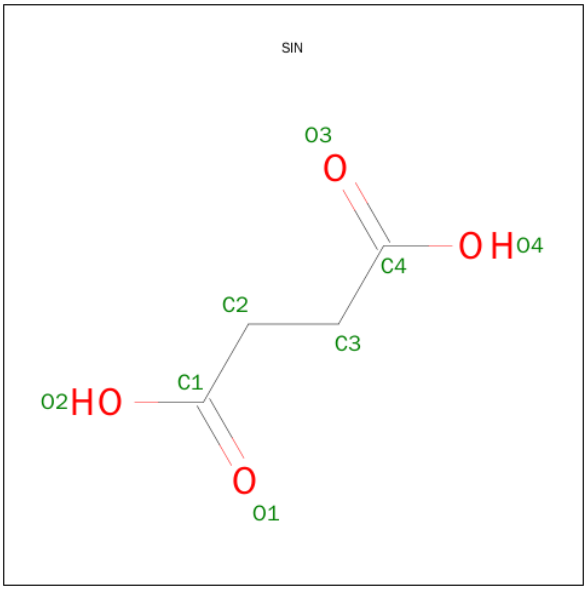
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0
3	D	1	Total C O 6 3 3	0	0

- Molecule 4 is SUCCINIC ACID (three-letter code: SIN) (formula: $C_4H_6O_4$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 8 4 4	0	0

- Molecule 5 is water.

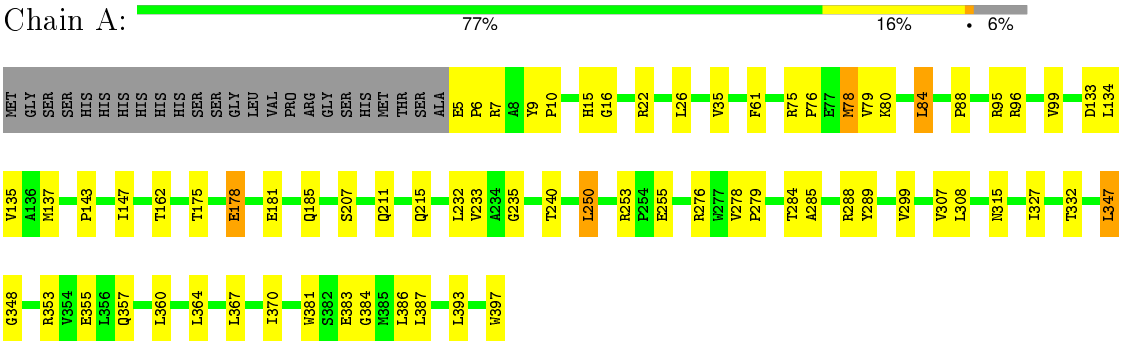
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	113	Total O 113 113	0	0
5	B	102	Total O 102 102	0	0
5	C	108	Total O 108 108	0	0
5	D	107	Total O 107 107	0	0

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.

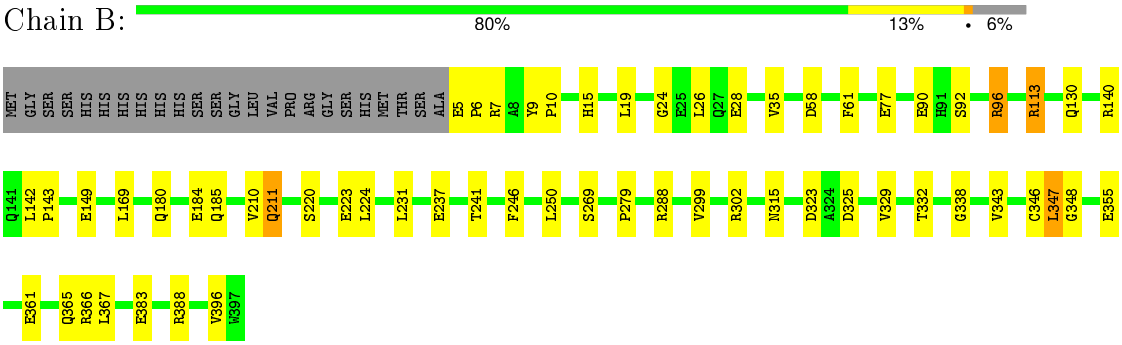
- Molecule 1: P-450-LIKE PROTEIN

Chain A:



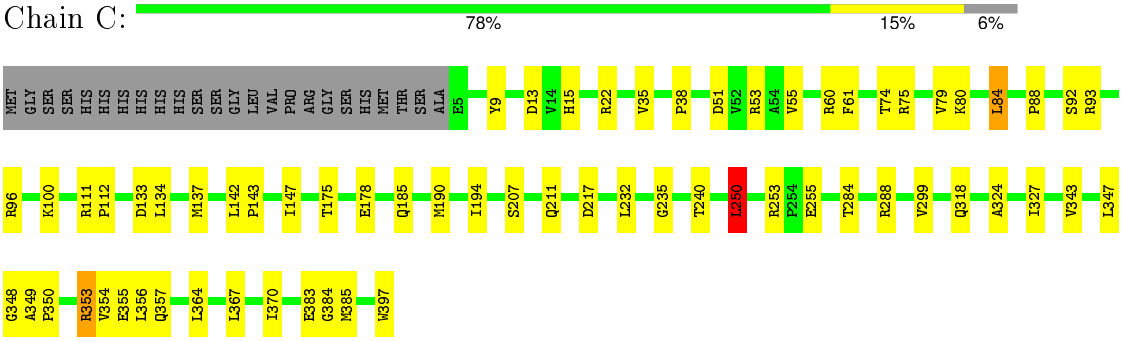
- Molecule 1: P-450-LIKE PROTEIN

Chain B:



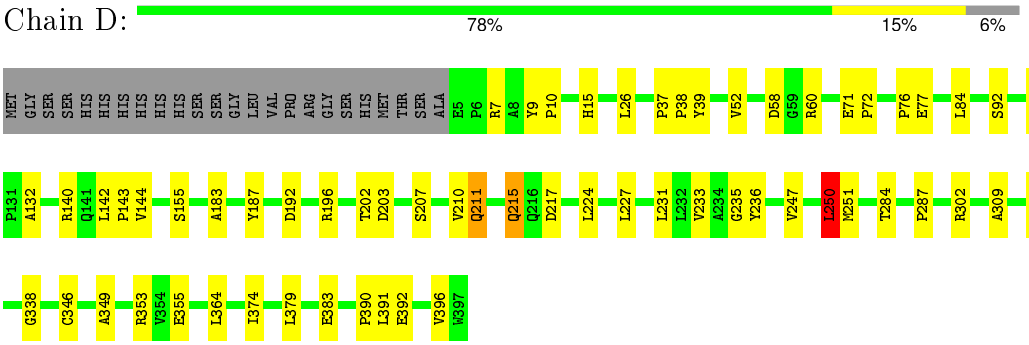
- Molecule 1: P-450-LIKE PROTEIN

Chain C:



- Molecule 1: P-450-LIKE PROTEIN

Chain D:


78%
15%
6%
MET GLY SER SER HIS HIS HIS HIS HIS HIS SER SER GLY LEU VAL PRO ARG GLY SER HIS MET THR SER ALA E5 P6 R7 A8 Y9 P10 H15 L26 P37 P38 Y39 V52 D58 G59 R60 E71 P72 P76 E77 L84 S92 R96 M125 Q130
P131 A132 R140 Q141 L142 P143 V144 S155 A183 Y187 D192 R196 T202 D203 S207 V210 Q211 Q215 Q216 D217 L224 L227 L231 L232 V233 A234 G235 Y236 V247 L250 M251 T284 P287 R302 A309 N315 D330 R331 T332
G338 C346 A349 R353 V354 E355 L364 I374 L379 E383 P390 L391 E392 V396 W397

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	57.15Å 161.98Å 100.11Å 90.00° 89.99° 90.00°	Depositor
Resolution (Å)	80.99 – 2.39 80.99 – 2.39	Depositor EDS
% Data completeness (in resolution range)	87.4 (80.99-2.39) 87.4 (80.99-2.39)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.80 (at 2.40Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.184 , 0.247 0.183 , 0.243	Depositor DCC
R_{free} test set	3191 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	21.7	Xtriage
Anisotropy	0.280	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 5.2	EDS
Estimated twinning fraction	0.478 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 62819 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	12909	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 47.77 % of the origin peak, indicating pseudo translational symmetry.The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 9.4580e-05.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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: GOL, SIN, HEM

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	0.82	1/3123 (0.0%)	0.83	0/4253
1	B	0.80	0/3127	0.83	1/4258 (0.0%)
1	C	0.83	0/3106	0.85	4/4231 (0.1%)
1	D	0.81	1/3130 (0.0%)	0.85	1/4263 (0.0%)
All	All	0.81	2/12486 (0.0%)	0.84	6/17005 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	346	CYS	CB-SG	5.91	1.92	1.82
1	A	289	TYR	CD2-CE2	-5.82	1.30	1.39

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	250	LEU	CA-CB-CG	6.65	130.59	115.30
1	D	250	LEU	CA-CB-CG	-6.24	100.94	115.30
1	B	58	ASP	CB-CG-OD1	5.67	123.40	118.30
1	C	253	ARG	NE-CZ-NH2	-5.40	117.60	120.30
1	C	60	ARG	NE-CZ-NH1	5.39	123.00	120.30
1	C	353	ARG	NE-CZ-NH2	-5.16	117.72	120.30

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	3056	0	3022	39	0
1	B	3063	0	3032	46	0
1	C	3043	0	3019	44	0
1	D	3065	0	3021	36	0
2	A	43	0	30	3	0
2	B	43	0	30	6	0
2	C	43	0	30	4	0
2	D	43	0	30	3	0
3	A	24	0	32	6	0
3	B	18	0	24	8	0
3	C	18	0	24	8	0
3	D	12	0	16	2	0
4	B	8	0	4	0	0
5	A	113	0	0	3	0
5	B	102	0	0	0	0
5	C	108	0	0	1	0
5	D	107	0	0	1	0
All	All	12909	0	12314	170	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 7.

All (170) 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:140:ARG:HH21	3:B:1401:GOL:H12	1.19	1.08
1:C:343:VAL:HG22	3:C:1398:GOL:H31	1.51	0.91
2:D:450:HEM:HBC2	2:D:450:HEM:HMC2	1.58	0.85
1:B:24:GLY:HA3	3:B:1398:GOL:H32	1.59	0.83
1:B:140:ARG:HH21	3:B:1401:GOL:C1	1.91	0.82
1:C:143:PRO:HA	1:C:355:GLU:OE1	1.86	0.76
1:D:52:VAL:HG13	1:D:309:ALA:HB1	1.74	0.69
1:D:96:ARG:HD3	5:D:2040:HOH:O	1.93	0.67
1:C:38:PRO:HG2	1:C:74:THR:HA	1.76	0.67
1:A:327:ILE:HB	3:A:1401:GOL:H32	1.78	0.66
2:D:450:HEM:HBC2	2:D:450:HEM:CMC	2.24	0.65
1:B:9:TYR:CG	1:B:10:PRO:HA	2.32	0.65
2:B:450:HEM:HBC2	2:B:450:HEM:HMC2	1.79	0.64
1:B:241:THR:HA	3:B:1401:GOL:H32	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:PRO:HA	1:D:355:GLU:OE1	1.99	0.62
1:C:51:ASP:O	1:C:55:VAL:HG23	1.99	0.62
1:B:113:ARG:HE	1:B:149:GLU:CD	2.02	0.61
1:C:250:LEU:HD11	1:C:364:LEU:HD21	1.83	0.61
3:A:1398:GOL:H11	1:B:325:ASP:OD2	2.00	0.61
1:D:250:LEU:HD21	1:D:364:LEU:HD21	1.83	0.60
1:B:343:VAL:HG22	3:B:1400:GOL:C3	2.32	0.60
1:B:279:PRO:HG2	1:B:388:ARG:NH2	2.17	0.60
1:C:343:VAL:CG2	3:C:1398:GOL:H31	2.30	0.60
3:A:1401:GOL:H31	5:A:2100:HOH:O	2.01	0.60
1:C:147:ILE:HD13	1:C:232:LEU:HA	1.82	0.60
1:A:367:LEU:O	1:A:370:ILE:HG22	2.02	0.59
1:C:96:ARG:HD3	5:C:2041:HOH:O	2.01	0.58
1:D:142:LEU:HB3	1:D:143:PRO:HD3	1.84	0.57
1:C:9:TYR:HB2	1:C:35:VAL:HB	1.87	0.57
1:C:134:LEU:O	1:C:134:LEU:HG	2.03	0.57
1:A:88:PRO:HB2	1:B:323:ASP:HA	1.86	0.57
1:B:140:ARG:NH2	3:B:1401:GOL:H12	2.04	0.57
1:A:353:ARG:O	1:A:357:GLN:HG3	2.05	0.56
1:A:9:TYR:CG	1:A:10:PRO:HA	2.41	0.56
1:D:9:TYR:CG	1:D:10:PRO:HA	2.41	0.56
2:B:450:HEM:HMB1	2:B:450:HEM:HBB2	1.88	0.55
1:B:343:VAL:HG22	3:B:1400:GOL:H32	1.88	0.55
1:A:147:ILE:HD13	1:A:232:LEU:HA	1.88	0.55
1:D:58:ASP:OD1	1:D:60:ARG:HB2	2.06	0.55
1:C:349:ALA:O	1:C:353:ARG:HG3	2.07	0.55
1:C:175:THR:OG1	1:C:178:GLU:HG3	2.07	0.55
1:A:135:VAL:HG23	1:A:393:LEU:HB2	1.87	0.55
2:B:450:HEM:CMC	2:B:450:HEM:HBC2	2.37	0.54
1:A:143:PRO:HA	1:A:355:GLU:OE1	2.06	0.54
1:D:71:GLU:OE2	1:D:287:PRO:HG2	2.08	0.53
1:A:240:THR:HG22	3:A:1400:GOL:H12	1.91	0.53
1:B:130:GLN:HB3	1:B:396:VAL:HG12	1.90	0.53
1:C:240:THR:HG22	3:C:1399:GOL:H32	1.90	0.53
1:D:183:ALA:O	1:D:187:TYR:HD1	1.91	0.53
1:C:350:PRO:O	1:C:354:VAL:HG23	2.09	0.53
1:B:366:ARG:O	1:B:367:LEU:HD23	2.09	0.52
1:D:9:TYR:CD1	1:D:10:PRO:HA	2.43	0.52
1:D:207:SER:O	1:D:211:GLN:HG2	2.09	0.52
1:A:175:THR:OG1	1:A:178:GLU:HB2	2.10	0.52
1:C:61:PHE:HB3	1:C:288:ARG:HB3	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:269:SER:OG	1:B:329:VAL:O	2.27	0.51
1:A:5:GLU:N	1:A:6:PRO:HD2	2.24	0.51
1:B:220:SER:OG	1:B:223:GLU:HG3	2.10	0.51
1:C:207:SER:O	1:C:211:GLN:HG2	2.11	0.51
1:A:250:LEU:HD22	1:A:364:LEU:HD21	1.93	0.51
1:C:347:LEU:HD12	1:C:347:LEU:C	2.32	0.50
1:C:15:HIS:HE1	1:C:383:GLU:OE2	1.94	0.50
1:B:7:ARG:CZ	1:B:26:LEU:HD21	2.42	0.50
3:A:1398:GOL:C1	1:B:325:ASP:OD2	2.60	0.49
1:C:367:LEU:O	1:C:370:ILE:HG22	2.12	0.49
1:B:15:HIS:HE1	1:B:383:GLU:OE2	1.94	0.49
1:C:348:GLY:HA3	2:C:450:HEM:C3C	2.48	0.49
1:D:349:ALA:O	1:D:353:ARG:HG3	2.12	0.49
1:A:134:LEU:HG	1:A:134:LEU:O	2.12	0.49
1:A:9:TYR:HB2	1:A:35:VAL:HB	1.94	0.49
1:C:384:GLY:O	1:C:385:MET:HB2	2.13	0.49
1:A:250:LEU:CD1	1:A:360:LEU:HD22	2.42	0.49
1:C:255:GLU:HB2	3:C:1400:GOL:H32	1.95	0.49
1:C:318:GLN:HE22	1:C:324:ALA:H	1.61	0.48
1:C:142:LEU:HB3	1:C:143:PRO:HD3	1.94	0.48
1:C:327:ILE:HB	3:C:1400:GOL:H12	1.96	0.48
1:C:190:MET:O	1:C:194:ILE:HD12	2.13	0.48
1:C:353:ARG:O	1:C:357:GLN:HG3	2.13	0.48
1:D:39:TYR:CZ	1:D:76:PRO:HG3	2.48	0.48
1:A:78:MET:HB2	5:A:2037:HOH:O	2.14	0.48
1:D:390:PRO:O	3:D:1398:GOL:H32	2.13	0.48
1:C:13:ASP:OD1	1:C:15:HIS:HD2	1.98	0.47
1:B:142:LEU:HB3	1:B:143:PRO:HD3	1.96	0.47
1:C:255:GLU:HB2	3:C:1400:GOL:C3	2.44	0.47
1:C:327:ILE:O	3:C:1400:GOL:H12	2.14	0.47
1:D:302:ARG:HH11	1:D:302:ARG:HG2	1.79	0.47
1:A:207:SER:O	1:A:211:GLN:HG2	2.14	0.47
1:C:133:ASP:O	1:C:137:MET:HG3	2.15	0.47
1:D:140:ARG:HH21	3:D:1398:GOL:H31	1.78	0.47
1:A:288:ARG:O	1:A:307:VAL:N	2.48	0.47
1:C:318:GLN:NE2	1:C:324:ALA:H	2.13	0.47
1:A:347:LEU:C	1:A:347:LEU:HD12	2.36	0.47
1:D:247:VAL:O	1:D:251:MET:HG3	2.14	0.46
1:B:9:TYR:CD1	1:B:10:PRO:HA	2.50	0.46
1:B:113:ARG:HG2	1:B:113:ARG:HH11	1.80	0.46
1:C:13:ASP:OD1	1:C:15:HIS:CD2	2.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:GLU:HB3	1:B:6:PRO:HD3	1.97	0.46
1:B:169:LEU:HD22	1:B:237:GLU:HG3	1.98	0.46
1:B:9:TYR:HB2	1:B:35:VAL:HB	1.97	0.46
1:D:9:TYR:O	1:D:38:PRO:HD3	2.15	0.46
1:C:75:ARG:HD2	1:C:384:GLY:O	2.16	0.46
1:A:84:LEU:HD22	2:A:450:HEM:HAD2	1.97	0.45
1:A:284:THR:OG1	1:A:308:LEU:HB3	2.16	0.45
1:A:96:ARG:HD3	5:A:2050:HOH:O	2.15	0.45
1:D:211:GLN:HB3	1:D:211:GLN:HE21	1.53	0.45
1:B:92:SER:O	1:B:96:ARG:HB2	2.17	0.45
1:D:37:PRO:HG3	1:D:72:PRO:HB3	1.99	0.45
1:B:143:PRO:HA	1:B:355:GLU:OE1	2.17	0.45
1:B:343:VAL:HG22	3:B:1400:GOL:H31	1.97	0.44
1:B:231:LEU:HA	1:B:231:LEU:HD23	1.77	0.44
1:A:15:HIS:HE1	1:A:383:GLU:OE2	2.00	0.44
1:B:361:GLU:O	1:B:365:GLN:HB2	2.17	0.44
1:A:7:ARG:NH1	1:A:26:LEU:HD21	2.32	0.44
1:B:246:PHE:O	1:B:250:LEU:HD23	2.17	0.44
1:B:61:PHE:HB3	1:B:288:ARG:HB3	1.99	0.44
1:D:210:VAL:HG22	1:D:224:LEU:HD13	1.99	0.44
1:D:7:ARG:CZ	1:D:26:LEU:HD21	2.47	0.44
1:A:386:LEU:O	1:A:387:LEU:HD23	2.16	0.44
1:D:227:LEU:O	1:D:231:LEU:HG	2.17	0.44
1:B:279:PRO:HG2	1:B:388:ARG:HH22	1.81	0.44
1:A:367:LEU:HD22	1:A:397:TRP:CG	2.52	0.44
1:B:302:ARG:HG2	1:B:302:ARG:HH11	1.83	0.44
1:B:347:LEU:HD12	1:B:347:LEU:C	2.38	0.44
1:B:346:CYS:HB2	2:B:450:HEM:NA	2.33	0.43
1:C:88:PRO:HB3	1:C:92:SER:OG	2.17	0.43
1:D:235:GLY:HA2	2:D:450:HEM:C2C	2.54	0.43
1:A:133:ASP:O	1:A:137:MET:HG3	2.19	0.43
1:C:93:ARG:NE	1:C:217:ASP:OD2	2.43	0.43
1:D:192[B]:ASP:O	1:D:196:ARG:HG3	2.19	0.43
1:A:95:ARG:O	1:A:99:VAL:HG22	2.17	0.43
1:D:130:GLN:HB3	1:D:396:VAL:HG12	2.01	0.43
1:C:92:SER:O	1:C:96:ARG:HB2	2.19	0.43
1:C:240:THR:HG22	3:C:1399:GOL:C3	2.48	0.43
1:D:144:VAL:HB	1:D:236:TYR:CE1	2.54	0.43
1:A:276:ARG:O	1:A:315:ASN:HB3	2.19	0.43
1:A:75:ARG:HD3	1:A:384:GLY:O	2.19	0.43
1:B:211:GLN:HB3	1:B:211:GLN:HE21	1.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:92:SER:O	1:D:96:ARG:HB2	2.19	0.42
1:B:210:VAL:HG22	1:B:224:LEU:HD13	2.00	0.42
1:B:348:GLY:HA3	2:B:450:HEM:C3C	2.54	0.42
1:B:15:HIS:CE1	1:B:383:GLU:OE2	2.73	0.42
1:A:250:LEU:CD2	1:A:364:LEU:HD21	2.50	0.42
1:A:16:GLY:HA2	1:A:381:TRP:CZ2	2.53	0.42
1:A:61:PHE:HB3	1:A:288:ARG:HB3	2.01	0.42
1:D:315:ASN:HD21	1:D:338:GLY:N	2.18	0.42
1:B:180:GLN:NE2	1:B:184:GLU:OE2	2.50	0.42
1:A:253:ARG:HD3	3:A:1401:GOL:O3	2.20	0.42
1:C:235:GLY:HA2	2:C:450:HEM:C2C	2.54	0.42
1:D:125:MET:HE2	1:D:132:ALA:HB3	2.01	0.42
1:C:9:TYR:O	1:C:38:PRO:HD3	2.20	0.41
1:B:9:TYR:CD2	1:B:10:PRO:HA	2.55	0.41
1:C:367:LEU:HD22	1:C:397:TRP:CG	2.55	0.41
1:C:356:LEU:HD11	2:C:450:HEM:HBB1	2.02	0.41
2:B:450:HEM:CMB	2:B:450:HEM:HBB2	2.51	0.41
1:A:235:GLY:HA2	2:A:450:HEM:C2C	2.55	0.41
1:A:99:VAL:HG21	1:B:28:GLU:HG3	2.03	0.41
1:D:391:LEU:HA	1:D:391:LEU:HD23	1.85	0.41
1:B:315:ASN:HD21	1:B:338:GLY:N	2.19	0.41
1:D:215:GLN:C	1:D:217:ASP:H	2.23	0.41
1:B:19:LEU:HD12	1:B:19:LEU:HA	1.83	0.41
1:D:202:THR:HB	1:D:203:ASP:H	1.60	0.41
1:A:181:GLU:O	1:A:185:GLN:HG2	2.21	0.41
1:D:374:ILE:HD11	1:D:379:LEU:HD23	2.03	0.41
1:A:348:GLY:HA3	2:A:450:HEM:C3C	2.56	0.41
1:B:90:GLU:CD	1:B:90:GLU:H	2.25	0.40
1:C:111:ARG:HB3	1:C:112:PRO:HD3	2.03	0.40
1:D:15:HIS:HE1	1:D:383:GLU:OE2	2.04	0.40
1:D:9:TYR:OH	1:D:284:THR:HG23	2.21	0.40
1:C:84:LEU:HD13	2:C:450:HEM:O1D	2.20	0.40
1:A:278:VAL:HA	1:A:279:PRO:HD3	1.99	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	392/417 (94%)	373 (95%)	16 (4%)	3 (1%)	24 35
1	B	392/417 (94%)	376 (96%)	16 (4%)	0	100 100
1	C	391/417 (94%)	372 (95%)	19 (5%)	0	100 100
1	D	393/417 (94%)	378 (96%)	14 (4%)	1 (0%)	46 63
All	All	1568/1668 (94%)	1499 (96%)	65 (4%)	4 (0%)	46 63

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	215	GLN
1	A	215	GLN
1	A	285	ALA
1	A	76	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	317/346 (92%)	304 (96%)	13 (4%)	37 57
1	B	318/346 (92%)	310 (98%)	8 (2%)	55 76
1	C	314/346 (91%)	304 (97%)	10 (3%)	46 68
1	D	316/346 (91%)	307 (97%)	9 (3%)	51 72
All	All	1265/1384 (91%)	1225 (97%)	40 (3%)	46 68

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	78	MET
1	A	79	VAL
1	A	80	LYS
1	A	84	LEU
1	A	162	THR
1	A	178	GLU
1	A	233	VAL
1	A	250	LEU
1	A	255	GLU
1	A	299	VAL
1	A	332	THR
1	A	347	LEU
1	B	77	GLU
1	B	96	ARG
1	B	113	ARG
1	B	185	GLN
1	B	211	GLN
1	B	299	VAL
1	B	332	THR
1	B	347	LEU
1	C	22	ARG
1	C	53	ARG
1	C	79	VAL
1	C	80	LYS
1	C	84	LEU
1	C	100	LYS
1	C	185	GLN
1	C	250	LEU
1	C	284	THR
1	C	299	VAL
1	D	77	GLU
1	D	84	LEU
1	D	155	SER
1	D	211	GLN
1	D	233	VAL
1	D	250	LEU
1	D	330	ASP
1	D	332	THR
1	D	392	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	15	HIS
1	A	130	GLN
1	A	211	GLN
1	A	259	GLN
1	A	318	GLN
1	B	15	HIS
1	B	130	GLN
1	B	185	GLN
1	B	211	GLN
1	B	259	GLN
1	B	318	GLN
1	B	320	GLN
1	B	335	GLN
1	C	15	HIS
1	C	130	GLN
1	C	211	GLN
1	C	259	GLN
1	C	318	GLN
1	C	320	GLN
1	C	335	GLN
1	C	365	GLN
1	C	378	GLN
1	D	15	HIS
1	D	130	GLN
1	D	211	GLN
1	D	222	GLN
1	D	259	GLN
1	D	318	GLN
1	D	320	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

17 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	GOL	A	1398	-	5,5,5	0.31	0	5,5,5	0.92	0
3	GOL	A	1399	-	5,5,5	0.17	0	5,5,5	0.65	0
3	GOL	A	1400	-	5,5,5	0.38	0	5,5,5	0.39	0
3	GOL	A	1401	-	5,5,5	0.49	0	5,5,5	1.38	1 (20%)
2	HEM	A	450	1,5	30,50,50	2.13	7 (23%)	24,82,82	2.41	10 (41%)
3	GOL	B	1398	-	5,5,5	0.50	0	5,5,5	0.89	0
4	SIN	B	1399	-	1,7,7	0.07	0	2,8,8	1.03	0
3	GOL	B	1400	-	5,5,5	0.46	0	5,5,5	0.53	0
3	GOL	B	1401	-	5,5,5	0.50	0	5,5,5	1.09	0
2	HEM	B	450	1,5	30,50,50	2.15	6 (20%)	24,82,82	2.42	13 (54%)
3	GOL	C	1398	-	5,5,5	0.25	0	5,5,5	0.85	0
3	GOL	C	1399	-	5,5,5	0.30	0	5,5,5	1.01	0
3	GOL	C	1400	-	5,5,5	0.25	0	5,5,5	1.18	0
2	HEM	C	450	1,5	30,50,50	2.21	9 (30%)	24,82,82	2.52	12 (50%)
3	GOL	D	1398	-	5,5,5	0.30	0	5,5,5	0.97	0
3	GOL	D	1399	-	5,5,5	0.46	0	5,5,5	0.98	0
2	HEM	D	450	1,5	30,50,50	1.95	3 (10%)	24,82,82	2.44	10 (41%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1398	-	-	0/4/4/4	0/0/0/0
3	GOL	A	1399	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1400	-	-	0/4/4/4	0/0/0/0
3	GOL	A	1401	-	-	0/4/4/4	0/0/0/0
2	HEM	A	450	1,5	-	0/10/54/54	0/0/8/8
3	GOL	B	1398	-	-	0/4/4/4	0/0/0/0
4	SIN	B	1399	-	-	0/1/5/5	0/0/0/0
3	GOL	B	1400	-	-	0/4/4/4	0/0/0/0
3	GOL	B	1401	-	-	0/4/4/4	0/0/0/0
2	HEM	B	450	1,5	-	0/10/54/54	0/0/8/8
3	GOL	C	1398	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1399	-	-	0/4/4/4	0/0/0/0
3	GOL	C	1400	-	-	0/4/4/4	0/0/0/0
2	HEM	C	450	1,5	-	0/10/54/54	0/0/8/8
3	GOL	D	1398	-	-	0/4/4/4	0/0/0/0
3	GOL	D	1399	-	-	0/4/4/4	0/0/0/0
2	HEM	D	450	1,5	-	0/10/54/54	0/0/8/8

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	450	HEM	C3B-C4B	-8.33	1.44	1.51
2	C	450	HEM	C3B-C4B	-7.64	1.45	1.51
2	D	450	HEM	C3B-C4B	-6.49	1.46	1.51
2	A	450	HEM	C3B-C4B	-6.37	1.46	1.51
2	A	450	HEM	C3D-C4D	-5.53	1.44	1.51
2	D	450	HEM	C3D-C4D	-4.96	1.45	1.51
2	A	450	HEM	C2C-C1C	-4.27	1.44	1.52
2	C	450	HEM	C3D-C4D	-3.99	1.46	1.51
2	B	450	HEM	C3D-C4D	-3.97	1.46	1.51
2	D	450	HEM	C2C-C1C	-3.94	1.45	1.52
2	C	450	HEM	C2C-C1C	-3.53	1.45	1.52
2	B	450	HEM	C2C-C1C	-2.95	1.47	1.52
2	A	450	HEM	C2D-C1D	-2.47	1.43	1.51
2	B	450	HEM	C2B-C1B	-2.41	1.44	1.51
2	C	450	HEM	C2D-C1D	-2.37	1.44	1.51
2	C	450	HEM	C2B-C1B	-2.36	1.44	1.51
2	A	450	HEM	C2B-C1B	-2.28	1.44	1.51
2	B	450	HEM	C1C-NC	2.07	1.38	1.36
2	A	450	HEM	C3C-CAC	2.29	1.55	1.51
2	C	450	HEM	C3C-CAC	2.33	1.55	1.51
2	C	450	HEM	FE-ND	2.40	2.10	1.97
2	B	450	HEM	FE-ND	2.74	2.12	1.97
2	A	450	HEM	FE-NC	3.03	2.07	1.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	450	HEM	C1C-NC	3.23	1.40	1.36
2	C	450	HEM	FE-NC	3.41	2.09	1.95

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	450	HEM	C3C-CAC-CBC	-4.73	117.20	124.46
2	C	450	HEM	CMA-C3A-C4A	-3.54	122.50	128.36
2	C	450	HEM	C3B-C4B-NB	-2.75	106.36	111.63
2	A	450	HEM	CMA-C3A-C4A	-2.63	124.01	128.36
2	B	450	HEM	CAA-C2A-C1A	-2.62	124.16	127.01
2	B	450	HEM	C3B-C4B-NB	-2.62	106.63	111.63
2	D	450	HEM	CBA-CAA-C2A	-2.58	107.90	112.53
2	B	450	HEM	CBA-CAA-C2A	-2.53	108.00	112.53
2	C	450	HEM	C3B-CAB-CBB	-2.47	120.66	124.46
2	B	450	HEM	CMA-C3A-C4A	-2.43	124.35	128.36
2	A	450	HEM	CBA-CAA-C2A	-2.40	108.23	112.53
2	A	450	HEM	CBD-CAD-C3D	-2.37	106.65	113.55
2	C	450	HEM	CAA-C2A-C1A	-2.37	124.44	127.01
2	B	450	HEM	C3C-CAC-CBC	-2.34	120.87	124.46
2	D	450	HEM	CBD-CAD-C3D	-2.33	106.78	113.55
2	A	450	HEM	C3B-C4B-NB	-2.21	107.41	111.63
2	B	450	HEM	CBD-CAD-C3D	-2.04	107.62	113.55
2	A	450	HEM	C2C-C1C-CHC	2.02	126.76	123.68
2	C	450	HEM	CMA-C3A-C2A	2.11	129.64	125.24
2	B	450	HEM	C3B-C4B-CHC	2.12	126.15	123.16
2	C	450	HEM	C2D-C3D-C4D	2.15	105.14	101.50
2	B	450	HEM	CMD-C2D-C3D	2.18	124.01	114.35
3	A	1401	GOL	O2-C2-C3	2.29	119.17	108.65
2	D	450	HEM	CMD-C2D-C3D	2.31	124.57	114.35
2	D	450	HEM	C2C-C1C-CHC	2.48	127.45	123.68
2	C	450	HEM	C3B-C4B-CHC	2.51	126.70	123.16
2	B	450	HEM	C2D-C3D-C4D	2.74	106.14	101.50
2	A	450	HEM	CMD-C2D-C3D	2.81	126.80	114.35
2	D	450	HEM	C2D-C3D-C4D	2.97	106.54	101.50
2	C	450	HEM	CMD-C2D-C3D	3.15	128.27	114.35
2	D	450	HEM	CMB-C2B-C3B	3.90	126.26	116.53
2	C	450	HEM	CMB-C2B-C3B	4.09	126.75	116.53
2	A	450	HEM	CMB-C2B-C3B	4.15	126.90	116.53
2	B	450	HEM	CAD-C3D-C2D	4.17	125.19	113.22
2	D	450	HEM	CAD-C3D-C4D	4.20	127.28	112.47
2	B	450	HEM	CMB-C2B-C3B	4.40	127.53	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	450	HEM	CAD-C3D-C2D	4.49	126.14	113.22
2	D	450	HEM	CAD-C3D-C2D	4.50	126.14	113.22
2	A	450	HEM	CAD-C3D-C4D	4.51	128.38	112.47
2	B	450	HEM	CAD-C3D-C4D	4.59	128.65	112.47
2	C	450	HEM	CAD-C3D-C4D	4.60	128.70	112.47
2	D	450	HEM	CMC-C2C-C3C	4.72	128.30	116.53
2	A	450	HEM	CAD-C3D-C2D	4.77	126.92	113.22
2	B	450	HEM	CMC-C2C-C3C	4.86	128.65	116.53
2	C	450	HEM	CMC-C2C-C3C	4.87	128.69	116.53
2	A	450	HEM	CMC-C2C-C3C	5.35	129.88	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 40 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1398	GOL	2	0
3	A	1400	GOL	1	0
3	A	1401	GOL	3	0
2	A	450	HEM	3	0
3	B	1398	GOL	1	0
3	B	1400	GOL	3	0
3	B	1401	GOL	4	0
2	B	450	HEM	6	0
3	C	1398	GOL	2	0
3	C	1399	GOL	2	0
3	C	1400	GOL	4	0
2	C	450	HEM	4	0
3	D	1398	GOL	2	0
2	D	450	HEM	3	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	393/417 (94%)	-0.88	0	100	100	8, 21, 37, 54	0
1	B	393/417 (94%)	-0.91	0	100	100	7, 20, 37, 56	0
1	C	393/417 (94%)	-0.88	0	100	100	9, 21, 37, 51	0
1	D	393/417 (94%)	-0.91	0	100	100	8, 20, 37, 51	0
All	All	1572/1668 (94%)	-0.90	0	100	100	7, 20, 37, 56	0

There are no RSRZ outliers to report.

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

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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
3	GOL	B	1398	6/6	0.98	0.20	15.42	48,51,52,52	0
3	GOL	A	1399	6/6	0.98	0.14	6.01	36,38,40,43	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	GOL	C	1400	6/6	0.99	0.11	3.61	32,35,38,39	0
3	GOL	B	1401	6/6	0.99	0.09	0.96	25,30,32,35	0
3	GOL	D	1399	6/6	0.99	0.09	0.89	12,19,20,24	0
3	GOL	D	1398	6/6	1.00	0.09	0.74	23,28,29,29	0
3	GOL	C	1398	6/6	0.99	0.08	0.45	14,15,18,24	0
2	HEM	B	450	43/43	0.99	0.09	0.20	2,10,14,19	0
2	HEM	C	450	43/43	0.99	0.09	0.09	2,10,14,16	0
2	HEM	D	450	43/43	1.00	0.09	0.05	4,9,14,15	0
3	GOL	B	1400	6/6	0.99	0.07	-0.42	10,21,23,25	0
2	HEM	A	450	43/43	1.00	0.08	-0.54	5,11,14,17	0
3	GOL	A	1400	6/6	0.99	0.07	-0.70	22,26,27,28	0
3	GOL	C	1399	6/6	1.00	0.07	-1.15	20,22,23,24	0
3	GOL	A	1401	6/6	0.99	0.07	-1.25	30,36,38,40	0
3	GOL	A	1398	6/6	0.99	0.07	-1.63	12,18,19,20	0
4	SIN	B	1399	8/8	0.93	0.31	-	69,70,74,75	0

6.5 Other polymers (i)

There are no such residues in this entry.