



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:51 PM GMT

PDB ID : 3V8D
Title : Crystal structure of human CYP7A1 in complex with 7-ketocholesterol
Authors : Strushkevich, N.; Tempel, W.; MacKenzie, F.; Wernimont, A.K.; Arrowsmith, C.H.; Edwards, A.M.; Bountra, C.; Weigelt, J.; Usanov, S.A.; Park, H.; Structural Genomics Consortium (SGC)
Deposited on : 2011-12-22
Resolution : 1.90 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 ⓘ](#)) 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

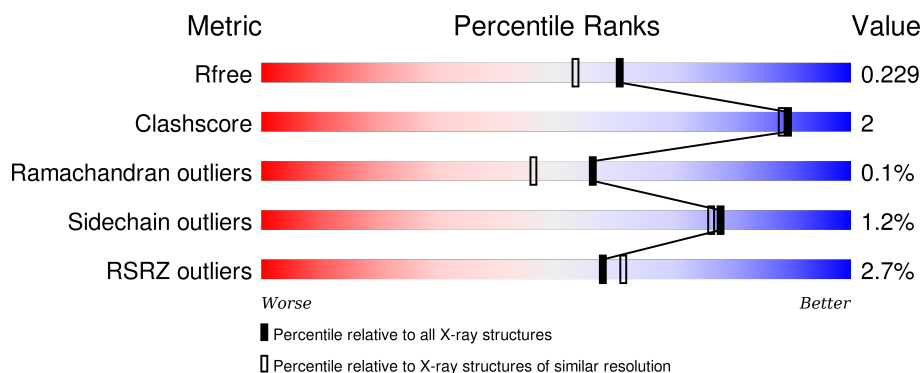
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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 $\leq 5\%$. 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	491	 2% 92% 5% 3%
1	B	491	 3% 90% 5% 5%

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
5	UNX	A	607	-	-	-	X
5	UNX	B	607	-	-	-	X
5	UNX	B	612	-	-	-	X
5	UNX	B	614	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8129 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 Cholesterol 7-alpha-monooxygenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	0	13	0
			3861	2493	655	690	23			
1	B	467	Total	C	N	O	S	0	9	0
			3723	2408	625	668	22			

There are 26 discrepancies between the modelled and reference sequences:

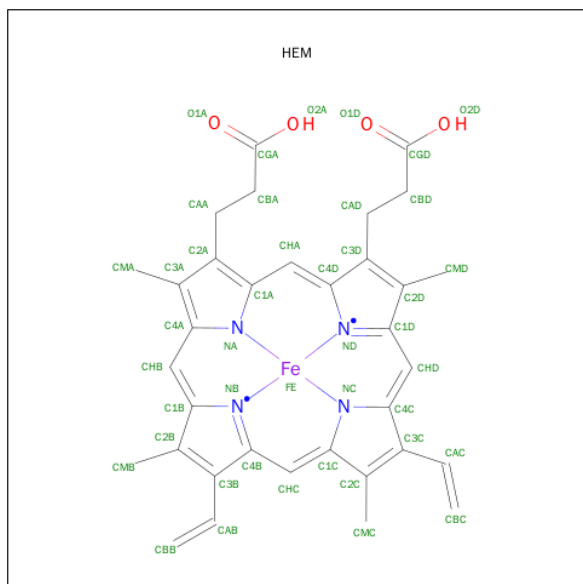
Chain	Residue	Modelled	Actual	Comment	Reference
A	18	MET	-	EXPRESSION TAG	UNP P22680
A	19	ALA	-	EXPRESSION TAG	UNP P22680
A	20	LYS	-	EXPRESSION TAG	UNP P22680
A	21	LYS	-	EXPRESSION TAG	UNP P22680
A	22	THR	-	EXPRESSION TAG	UNP P22680
A	23	SER	-	EXPRESSION TAG	UNP P22680
A	24	SER	-	EXPRESSION TAG	UNP P22680
A	104	LEU	THR	ENGINEERED MUTATION	UNP P22680
A	504	HIS	-	EXPRESSION TAG	UNP P22680
A	505	HIS	-	EXPRESSION TAG	UNP P22680
A	506	HIS	-	EXPRESSION TAG	UNP P22680
A	507	HIS	-	EXPRESSION TAG	UNP P22680
A	508	HIS	-	EXPRESSION TAG	UNP P22680
B	18	MET	-	EXPRESSION TAG	UNP P22680
B	19	ALA	-	EXPRESSION TAG	UNP P22680
B	20	LYS	-	EXPRESSION TAG	UNP P22680
B	21	LYS	-	EXPRESSION TAG	UNP P22680
B	22	THR	-	EXPRESSION TAG	UNP P22680
B	23	SER	-	EXPRESSION TAG	UNP P22680
B	24	SER	-	EXPRESSION TAG	UNP P22680
B	104	LEU	THR	ENGINEERED MUTATION	UNP P22680
B	504	HIS	-	EXPRESSION TAG	UNP P22680
B	505	HIS	-	EXPRESSION TAG	UNP P22680
B	506	HIS	-	EXPRESSION TAG	UNP P22680
B	507	HIS	-	EXPRESSION TAG	UNP P22680

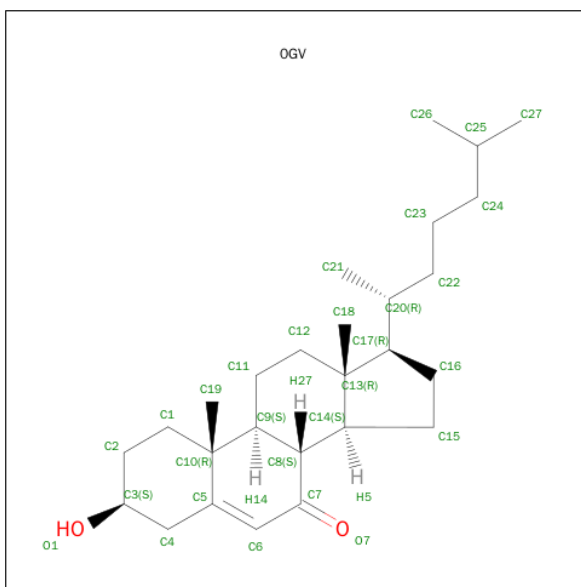
Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	508	HIS	-	EXPRESSION TAG	UNP P22680

- 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
3	A	1	Total	C	O	0	0
			29	27	2		
3	B	1	Total	C	O	0	0
			29	27	2		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	9	Total	X	0	0
			9	9		
5	A	5	Total	X	0	0
			5	5		

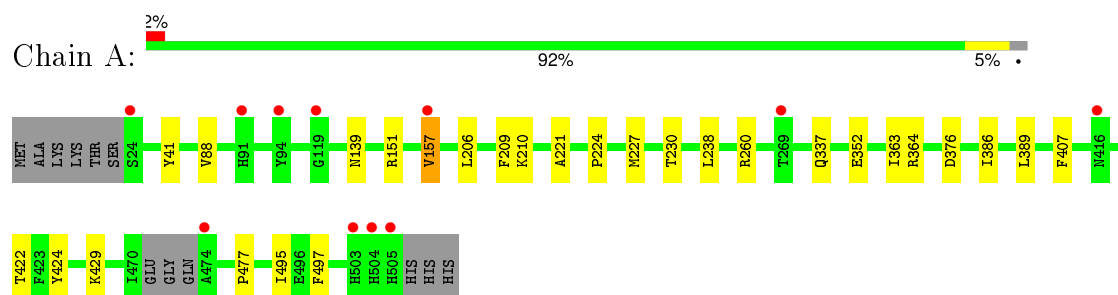
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	193	Total	O	0	2
			195	195		
6	B	161	Total	O	0	1
			162	162		

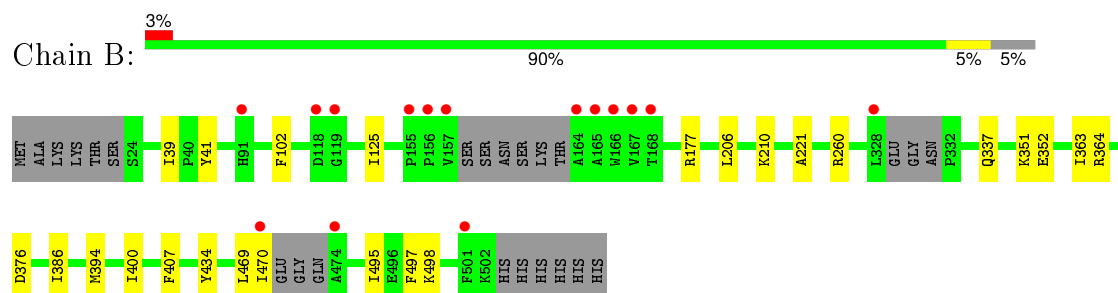
3 Residue-property plots [i](#)

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: Cholesterol 7-alpha-monooxygenase



• Molecule 1: Cholesterol 7-alpha-monooxygenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	55.62Å 74.22Å 87.93Å 66.33° 75.53° 69.62°	Depositor
Resolution (Å)	50.00 – 1.90 43.67 – 1.90	Depositor EDS
% Data completeness (in resolution range)	97.6 (50.00-1.90) 85.4 (43.67-1.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.81 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.185 , 0.225 0.191 , 0.229	Depositor DCC
R_{free} test set	2116 reflections (2.35%)	DCC
Wilson B-factor (Å ²)	28.6	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 92143 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8129	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: UNX, OGV, SO4, 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	0.71	0/3999	0.52	0/5417
1	B	0.70	0/3844	0.52	0/5209
All	All	0.71	0/7843	0.52	0/10626

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	3861	0	3805	20	0
1	B	3723	0	3618	11	0
2	A	43	0	30	1	0
2	B	43	0	30	3	0
3	A	29	0	44	1	0
3	B	29	0	44	1	0
4	A	15	0	0	1	0
4	B	15	0	0	0	0
5	A	5	0	0	0	0
5	B	9	0	0	0	0
6	A	195	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	162	0	0	0	0
All	All	8129	0	7571	36	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 2.

All (36) 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:A:151[B]:ARG:HB3	1:A:151[B]:ARG:NH2	1.92	0.85
1:A:151[B]:ARG:HB3	1:A:151[B]:ARG:HH21	1.52	0.72
1:A:88:VAL:HG21	1:A:389:LEU:HD21	1.78	0.65
1:A:151[B]:ARG:CB	1:A:151[B]:ARG:NH2	2.63	0.61
1:B:206:LEU:HD21	1:B:210:LYS:HE3	1.85	0.58
1:A:227[B]:MET:HE1	1:B:39:ILE:HG12	1.85	0.58
1:B:41:TYR:HB3	1:B:221:ALA:HB2	1.89	0.55
1:A:139:ASN:OD1	1:A:337:GLN:NE2	2.40	0.54
1:B:102:PHE:HE2	1:B:125:ILE:HD11	1.72	0.54
1:A:151[B]:ARG:CZ	1:A:151[B]:ARG:CB	2.86	0.54
2:B:601:HEM:HBB2	2:B:601:HEM:HMB2	1.89	0.54
1:A:363:ILE:HG23	1:A:386:ILE:HG23	1.92	0.51
2:A:601:HEM:HBC2	2:A:601:HEM:HHD	1.92	0.51
2:B:601:HEM:HHD	2:B:601:HEM:HBC2	1.93	0.51
1:B:469:LEU:HD22	1:B:495:ILE:HD13	1.93	0.51
1:A:422[B]:THR:HG23	1:A:429:LYS:HE3	1.94	0.49
1:B:363:ILE:HG23	1:B:386:ILE:HG23	1.95	0.47
1:A:352:GLU:HG3	1:A:407:PHE:CD1	2.51	0.46
1:B:177:ARG:HA	1:B:206:LEU:HD11	1.98	0.46
1:B:351:LYS:HG2	1:B:434:TYR:CZ	2.51	0.45
1:A:422[A]:THR:HG22	1:A:429:LYS:HE3	1.97	0.45
1:B:352:GLU:HG3	1:B:407:PHE:CD1	2.52	0.45
1:A:376:ASP:HB2	4:A:603:SO4:O1	2.17	0.45
1:A:206:LEU:C	1:A:206:LEU:HD23	2.38	0.44
1:A:209:PHE:HA	1:A:238:LEU:HD11	2.00	0.44
3:B:602:0GV:H30	3:B:602:0GV:H3	1.99	0.44
2:B:601:HEM:HBB2	2:B:601:HEM:CMB	2.48	0.43
1:A:41:TYR:HB3	1:A:221:ALA:HB2	2.00	0.43
1:B:470:ILE:HD11	1:B:498:LYS:HG2	2.00	0.43
3:A:602:0GV:H3	3:A:602:0GV:H30	2.00	0.42
1:B:394[B]:MET:HG2	1:B:400:ILE:HD12	2.01	0.42
1:A:224:PRO:O	1:A:227[B]:MET:HG2	2.18	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:LEU:HD21	1:A:210:LYS:HE3	1.99	0.42
1:A:157:VAL:O	1:A:157:VAL:HG13	2.20	0.42
1:A:477:PRO:HG3	1:A:495:ILE:CG2	2.50	0.42
1:A:422[B]:THR:HG22	1:A:424:TYR:CZ	2.56	0.41

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	488/491 (99%)	480 (98%)	7 (1%)	1 (0%)	52	42
1	B	468/491 (95%)	464 (99%)	4 (1%)	0	100	100
All	All	956/982 (97%)	944 (99%)	11 (1%)	1 (0%)	56	46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	157	VAL

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	411/433 (95%)	406 (99%)	5 (1%)	78	76

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	387/433 (89%)	382 (99%)	5 (1%)	76	73
All	All	798/866 (92%)	788 (99%)	10 (1%)	78	73

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	230[A]	THR
1	A	230[B]	THR
1	A	260	ARG
1	A	364	ARG
1	A	497	PHE
1	B	260	ARG
1	B	337	GLN
1	B	364	ARG
1	B	376	ASP
1	B	497	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	GLN
1	A	337	GLN
1	B	60	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 24 ligands modelled in this entry, 14 are unknown - 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
2	HEM	A	601	1,6	30,50,50	2.78	11 (36%)	24,82,82	2.46	7 (29%)
3	0GV	A	602	-	32,32,32	1.70	4 (12%)	48,50,50	1.13	4 (8%)
4	SO4	A	603	-	4,4,4	0.29	0	6,6,6	0.20	0
4	SO4	A	604	-	4,4,4	0.48	0	6,6,6	0.09	0
4	SO4	A	605	-	4,4,4	0.48	0	6,6,6	0.09	0
2	HEM	B	601	1,6	30,50,50	2.42	11 (36%)	24,82,82	2.40	7 (29%)
3	0GV	B	602	-	32,32,32	1.82	8 (25%)	48,50,50	1.30	7 (14%)
4	SO4	B	603	-	4,4,4	0.25	0	6,6,6	0.36	0
4	SO4	B	604	-	4,4,4	0.35	0	6,6,6	0.29	0
4	SO4	B	605	-	4,4,4	0.52	0	6,6,6	0.16	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	601	1,6	-	0/10/54/54	0/0/8/8
3	0GV	A	602	-	-	0/10/71/71	0/4/4/4
4	SO4	A	603	-	-	0/0/0/0	0/0/0/0
4	SO4	A	604	-	-	0/0/0/0	0/0/0/0
4	SO4	A	605	-	-	0/0/0/0	0/0/0/0
2	HEM	B	601	1,6	-	0/10/54/54	0/0/8/8
3	0GV	B	602	-	-	0/10/71/71	0/4/4/4
4	SO4	B	603	-	-	0/0/0/0	0/0/0/0
4	SO4	B	604	-	-	0/0/0/0	0/0/0/0
4	SO4	B	605	-	-	0/0/0/0	0/0/0/0

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	HEM	C3B-C4B	-8.32	1.44	1.51
2	B	601	HEM	C3B-C4B	-6.15	1.46	1.51
3	B	602	0GV	C8-C7	-5.22	1.43	1.51
3	A	602	0GV	C8-C7	-4.47	1.44	1.51
2	A	601	HEM	C2D-C3D	-4.09	1.42	1.54
2	B	601	HEM	C2D-C3D	-3.89	1.42	1.54
2	B	601	HEM	C2C-C1C	-3.70	1.45	1.52
2	A	601	HEM	C3D-C4D	-3.57	1.47	1.51
3	B	602	0GV	C4-C5	-3.28	1.43	1.51
2	A	601	HEM	C2C-C1C	-3.27	1.46	1.52
3	B	602	0GV	C10-C5	-3.21	1.45	1.52
3	A	602	0GV	C10-C5	-2.70	1.47	1.52
2	A	601	HEM	CAA-C2A	-2.64	1.47	1.52
3	B	602	0GV	C6-C7	-2.58	1.40	1.45
2	A	601	HEM	C2B-C1B	-2.26	1.44	1.51
2	B	601	HEM	C3D-C4D	-2.18	1.48	1.51
2	B	601	HEM	CAA-C2A	-2.11	1.48	1.52
2	B	601	HEM	C2B-C1B	-2.02	1.45	1.51
3	B	602	0GV	C11-C9	2.07	1.57	1.53
2	B	601	HEM	FE-NC	2.08	2.04	1.95
3	B	602	0GV	C10-C9	2.26	1.60	1.56
2	A	601	HEM	C2A-C3A	2.46	1.45	1.37
3	B	602	0GV	C13-C14	2.53	1.60	1.55
2	A	601	HEM	CHD-C4C	2.62	1.42	1.36
2	B	601	HEM	C2A-C3A	2.71	1.45	1.37
2	B	601	HEM	CHD-C4C	2.83	1.43	1.36
2	A	601	HEM	FE-NC	3.08	2.07	1.95
3	A	602	0GV	C11-C9	3.91	1.60	1.53
3	A	602	0GV	C6-C5	4.04	1.39	1.34
3	B	602	0GV	C6-C5	4.17	1.39	1.34
2	B	601	HEM	C4C-NC	4.69	1.41	1.36
2	A	601	HEM	C4C-NC	4.98	1.42	1.36
2	B	601	HEM	C1C-NC	5.12	1.42	1.36
2	A	601	HEM	C1C-NC	6.09	1.43	1.36

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	601	HEM	CBA-CAA-C2A	-3.38	106.47	112.53
3	B	602	0GV	O7-C7-C6	-3.05	116.54	121.62
2	B	601	HEM	CAA-CBA-CGA	-2.82	107.58	112.75
2	A	601	HEM	CAA-CBA-CGA	-2.81	107.59	112.75
3	B	602	0GV	C4-C5-C6	-2.58	116.79	121.11

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	0GV	C14-C13-C17	-2.44	97.23	100.09
3	A	602	0GV	O7-C7-C6	-2.37	117.67	121.62
3	B	602	0GV	C16-C17-C13	-2.25	100.90	103.82
3	A	602	0GV	C16-C17-C13	-2.22	100.93	103.82
3	B	602	0GV	C9-C8-C14	-2.20	106.48	109.97
3	B	602	0GV	C10-C5-C6	-2.17	120.22	122.69
2	B	601	HEM	CBA-CAA-C2A	-2.11	108.75	112.53
3	B	602	0GV	C11-C12-C13	-2.02	109.23	112.84
2	B	601	HEM	CMD-C2D-C3D	3.14	128.22	114.35
2	A	601	HEM	CMD-C2D-C3D	3.21	128.57	114.35
3	A	602	0GV	C4-C5-C10	3.45	121.45	116.43
3	B	602	0GV	C4-C5-C10	4.36	122.78	116.43
2	B	601	HEM	CAD-C3D-C2D	4.68	126.67	113.22
2	A	601	HEM	CMC-C2C-C3C	4.71	128.29	116.53
2	A	601	HEM	CAD-C3D-C4D	4.72	129.13	112.47
2	B	601	HEM	CAD-C3D-C4D	4.85	129.57	112.47
2	A	601	HEM	CAD-C3D-C2D	4.92	127.36	113.22
2	B	601	HEM	CMC-C2C-C3C	5.09	129.24	116.53
2	B	601	HEM	CMB-C2B-C3B	5.68	130.70	116.53
2	A	601	HEM	CMB-C2B-C3B	6.06	131.65	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	1	0
3	A	602	0GV	1	0
4	A	603	SO4	1	0
2	B	601	HEM	3	0
3	B	602	0GV	1	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, 95th 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	479/491 (97%)	-0.05	11 (2%) 64 67	19, 29, 48, 70	1 (0%)
1	B	467/491 (95%)	0.02	15 (3%) 51 54	20, 29, 49, 86	1 (0%)
All	All	946/982 (96%)	-0.02	26 (2%) 58 61	19, 29, 49, 86	2 (0%)

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	157	VAL	8.9
1	B	164	ALA	5.0
1	B	165	ALA	4.7
1	B	474	ALA	4.6
1	B	156	PRO	4.1
1	B	91	HIS	3.9
1	B	328	LEU	3.6
1	A	503	HIS	3.6
1	A	474	ALA	3.5
1	B	167	VAL	3.0
1	B	155	PRO	3.0
1	B	470	ILE	2.9
1	A	94	TYR	2.9
1	A	416	ASN	2.8
1	A	91	HIS	2.7
1	A	504	HIS	2.6
1	A	157	VAL	2.5
1	A	24	SER	2.4
1	A	119	GLY	2.3
1	B	168	THR	2.3
1	A	505	HIS	2.2
1	B	166	TRP	2.2
1	A	269	THR	2.2
1	B	501	PHE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	118	ASP	2.0
1	B	119	GLY	2.0

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

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

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, 95th 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
5	UNX	B	614	1/1	0.94	0.20	9.22	30,30,30,30	0
5	UNX	A	607	1/1	0.86	0.31	8.98	30,30,30,30	0
5	UNX	B	607	1/1	0.67	0.22	6.13	30,30,30,30	0
5	UNX	B	612	1/1	0.97	0.15	4.74	30,30,30,30	0
2	HEM	B	601	43/43	0.98	0.15	1.49	19,20,27,28	0
3	0GV	B	602	29/29	0.95	0.15	1.17	20,21,23,23	0
2	HEM	A	601	43/43	0.98	0.13	0.85	20,21,26,27	0
4	SO4	B	604	5/5	0.98	0.11	0.28	38,40,42,43	0
5	UNX	B	609	1/1	0.75	0.14	0.16	30,30,30,30	0
4	SO4	A	604	5/5	0.97	0.16	0.10	61,61,64,64	0
4	SO4	B	603	5/5	0.99	0.07	-0.21	40,41,42,42	0
4	SO4	A	605	5/5	0.93	0.11	-0.39	80,81,82,84	0
5	UNX	B	610	1/1	0.96	0.10	-0.48	30,30,30,30	0
3	0GV	A	602	29/29	0.96	0.08	-0.59	20,21,24,24	0
4	SO4	A	603	5/5	0.98	0.07	-0.59	40,41,43,43	0
5	UNX	B	606	1/1	0.90	0.09	-0.66	30,30,30,30	0
4	SO4	B	605	5/5	0.95	0.08	-1.17	71,73,75,75	0
5	UNX	A	606	1/1	0.85	0.18	-	30,30,30,30	0
5	UNX	B	611	1/1	0.91	0.25	-	30,30,30,30	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	UNX	A	608	1/1	0.90	0.37	-	30,30,30,30	0
5	UNX	A	610	1/1	0.92	0.20	-	30,30,30,30	0
5	UNX	A	609	1/1	0.90	0.23	-	30,30,30,30	0
5	UNX	B	613	1/1	0.94	0.05	-	30,30,30,30	0
5	UNX	B	608	1/1	0.96	0.30	-	30,30,30,30	0

6.5 Other polymers [i](#)

There are no such residues in this entry.