Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:11 PM GMT

PDB ID	:	4X0L
Title	:	Human haptoglobin-haemoglobin complex
Authors	:	Lane-Serff, H.; MacGregor, P.; Lowe, E.D.; Carrington, M.; Higgins, M.K.
Deposited on	:	2014-11-21
Resolution	:	2.05 Å(reported)

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 (i)

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

The reported resolution of this entry is 2.05 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.
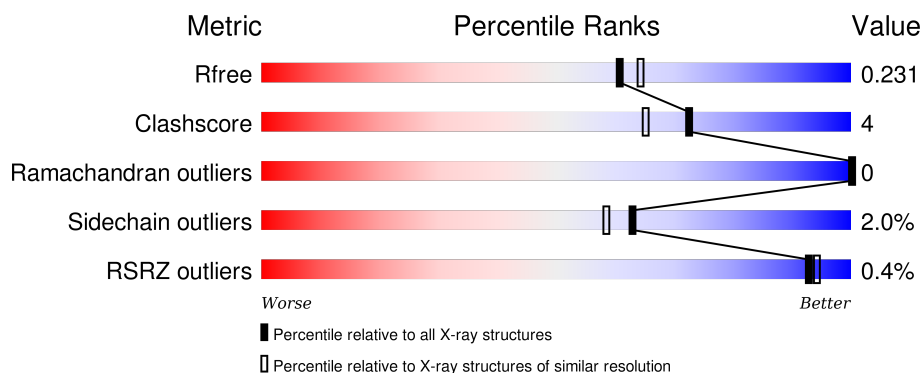
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1192 (2.04-2.04)
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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	141	89% ... 11%
2	B	146	% 84% ... 14% ..
3	C	259	89% ... 9% .

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	OXY	A	202	-	-	-	X
6	GOL	C	504	-	-	-	X
7	NAG	C	501	-	-	-	X
9	CAC	C	505	-	-	X	X

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 4551 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 Hemoglobin subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	141	1069	685	187	194	3	0	0	0

- Molecule 2 is a protein called Hemoglobin subunit beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	144	1105	713	191	198	3	0	0	0

- Molecule 3 is a protein called Haptoglobin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	259	2024	1290	344	380	10	0	0	0

- Molecule 4 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).
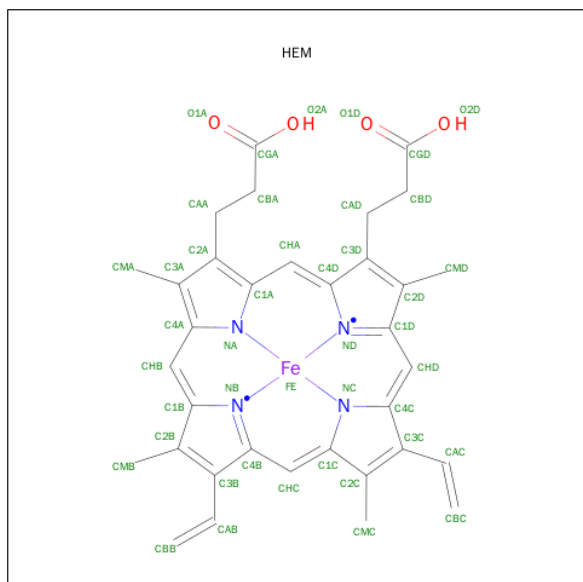
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
4	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 5 is OXYGEN MOLECULE (three-letter code: OXY) (formula: O_2).
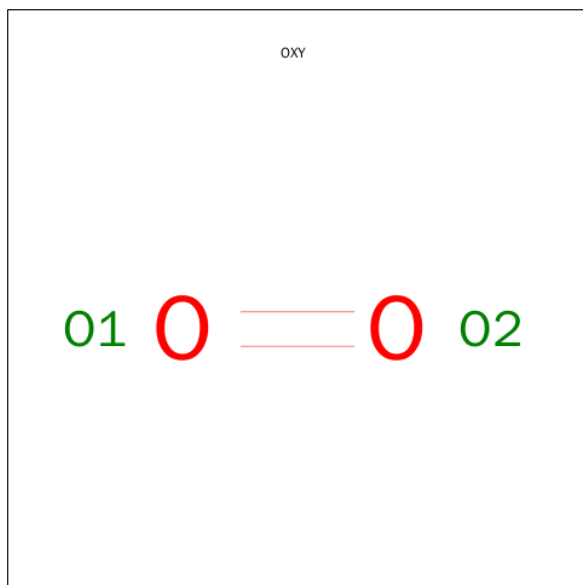
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	O	0	0
			2	2		
5	B	1	Total	O	0	0
			2	2		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

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

- Molecule 7 is a polymer of unknown type called SUGAR (ALPHA-L-FUCOSE).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	C	2	Total 24	C 14	N 1	O 9	0	0

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O_4S).
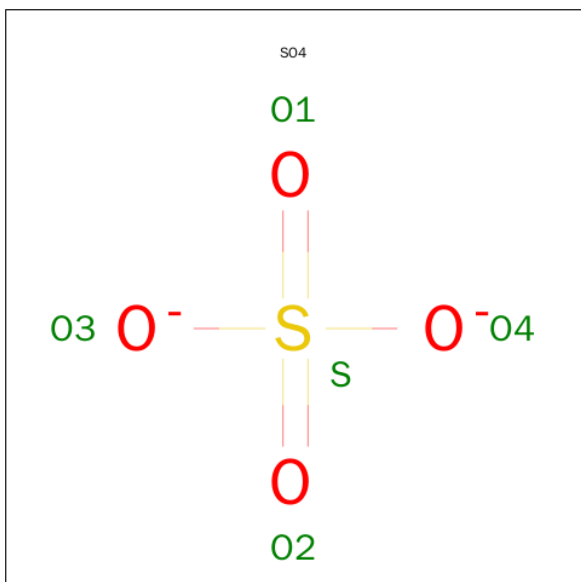
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total 5	O 4	S 1	0	0

- Molecule 9 is CACODYLATE ION (three-letter code: CAC) (formula: $C_2H_6AsO_2$).
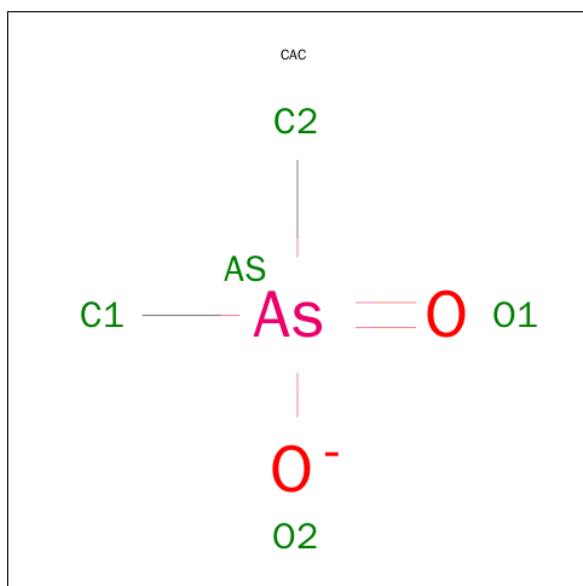
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	1	Total 5	As 1	C 2	O 2	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	55	Total 55	O 55	0	0
10	B	28	Total 28	O 28	0	0
10	C	134	Total 134	O 134	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: Hemoglobin subunit alpha

Chain A:

- Molecule 2: Hemoglobin subunit beta

Chain B:

- Molecule 3: Haptoglobin

Chain C:

4   Data and refinement statistics (i)

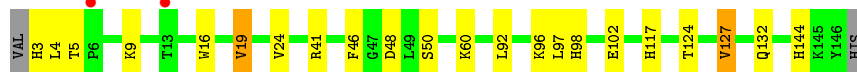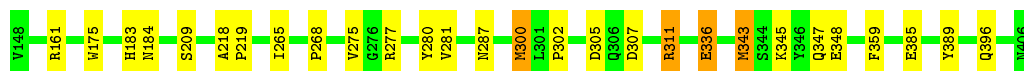| Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	96.60Å 96.60Å 132.77Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	39.93 – 2.05 39.90 – 2.05	Depositor EDS
% Data completeness (in resolution range)	99.8 (39.93-2.05) 99.9 (39.90-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.94 (at 2.05Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.180 , 0.224 0.188 , 0.231	Depositor DCC
R_{free} test set	2295 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	21.7	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 51.5	EDS
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Outliers	0 of 45465 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4551	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.95% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, OXY, FUC, CAC, HEM, SO4

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	1.00	0/1097	1.00	4/1491 (0.3%)
2	B	0.90	0/1134	0.90	2/1541 (0.1%)
3	C	1.01	2/2073 (0.1%)	1.01	7/2818 (0.2%)
All	All	0.98	2/4304 (0.0%)	0.98	13/5850 (0.2%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	348	GLU	CD-OE2	7.03	1.33	1.25
3	C	336	GLU	CG-CD	5.20	1.59	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	311	ARG	NE-CZ-NH1	11.29	125.94	120.30
1	A	32	ARG	NE-CZ-NH1	10.42	125.51	120.30
1	A	48	ASP	CB-CG-OD1	7.68	125.21	118.30
3	C	305	ASP	CB-CG-OD1	6.73	124.36	118.30
1	A	32	ARG	NE-CZ-NH2	-6.36	117.12	120.30
3	C	343	MET	CG-SD-CE	6.27	110.23	100.20
3	C	300	MET	CG-SD-CE	-5.80	90.92	100.20
3	C	311	ARG	NE-CZ-NH2	-5.76	117.42	120.30
3	C	305	ASP	CB-CG-OD2	-5.44	113.40	118.30
3	C	161	ARG	NE-CZ-NH1	5.44	123.02	120.30
2	B	41	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	93	ARG	NE-CZ-NH1	5.38	122.99	120.30
2	B	41	ARG	NE-CZ-NH2	-5.28	117.66	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	1069	0	1070	6	0
2	B	1105	0	1099	13	0
3	C	2024	0	2000	19	0
4	A	43	0	30	0	0
4	B	43	0	30	2	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	B	6	0	8	0	0
6	C	6	0	7	0	0
7	C	24	0	22	0	0
8	C	5	0	0	1	0
9	C	5	0	0	3	2
10	A	55	0	0	0	0
10	B	28	0	0	1	0
10	C	134	0	0	6	0
All	All	4551	0	4266	36	2

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 4.

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)
3:C:275:VAL:HB	10:C:632:HOH:O	1.31	1.23
3:C:336:GLU:OE2	10:C:601:HOH:O	1.60	1.18
1:A:8:LYS:NZ	1:A:75:ASP:OD1	2.10	0.84
3:C:385:GLU:OE2	9:C:505:CAC:O2	1.97	0.81
3:C:343:MET:HB2	9:C:505:CAC:C1	2.23	0.69
2:B:98:HIS:HD2	8:C:503:SO4:O3	1.85	0.58
2:B:102:GLU:OE1	3:C:287:ASN:HB2	2.04	0.58
3:C:307:ASP:HB3	3:C:311:ARG:NH1	2.21	0.55
4:B:201:HEM:HMC2	4:B:201:HEM:HBC2	1.89	0.54
2:B:16:TRP:O	2:B:19:VAL:HG13	2.08	0.53
2:B:92:LEU:HD12	2:B:96:LYS:HE2	1.90	0.52
3:C:275:VAL:CB	10:C:632:HOH:O	2.12	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:124:THR:OG1	2:B:127:VAL:HG13	2.10	0.52
3:C:343:MET:HA	9:C:505:CAC:O2	2.10	0.51
2:B:4:LEU:C	2:B:5:THR:O	2.48	0.50
3:C:275:VAL:CG2	10:C:632:HOH:O	2.50	0.50
3:C:175:TRP:CE2	3:C:265:ILE:HD12	2.47	0.50
3:C:281:VAL:HG22	3:C:359:PHE:HA	1.95	0.49
2:B:4:LEU:HD23	2:B:9:LYS:HA	1.96	0.48
3:C:280:TYR:CE2	3:C:300:MET:HE3	2.49	0.47
1:A:115:PRO:O	2:B:117:HIS:HE1	1.98	0.47
2:B:46:PHE:HA	2:B:60:LYS:HD2	1.99	0.45
1:A:3:LEU:HD12	1:A:74:VAL:HG11	1.99	0.44
3:C:268:PRO:O	3:C:396:GLN:NE2	2.50	0.44
1:A:97:VAL:HG23	1:A:98:ASN:N	2.33	0.44
2:B:144:HIS:HB3	10:B:315:HOH:O	2.17	0.43
3:C:345:LYS:O	3:C:347:GLN:HG2	2.19	0.43
3:C:281:VAL:HG21	3:C:389:TYR:OH	2.18	0.43
3:C:184:ASN:ND2	10:C:712:HOH:O	2.37	0.43
1:A:71:VAL:O	1:A:74:VAL:HG23	2.20	0.41
2:B:97:LEU:HD13	4:B:201:HEM:C2D	2.55	0.41
3:C:218:ALA:N	3:C:219:PRO:HD2	2.36	0.41
3:C:311:ARG:HD3	10:C:631:HOH:O	2.19	0.41
2:B:48:ASP:OD1	2:B:50:SER:OG	2.38	0.41
1:A:36:SER:HB3	2:B:132:GLN:HG3	2.02	0.41
3:C:277:ARG:O	3:C:302:PRO:HA	2.22	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:505:CAC:C1	9:C:505:CAC:C1[5_554]	1.32	0.88
9:C:505:CAC:AS	9:C:505:CAC:C1[5_554]	1.84	0.36

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	139/141 (99%)	139 (100%)	0	0	100	100
2	B	142/146 (97%)	133 (94%)	9 (6%)	0	100	100
3	C	257/259 (99%)	246 (96%)	11 (4%)	0	100	100
All	All	538/546 (98%)	518 (96%)	20 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2   Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	113/113 (100%)	110 (97%)	3 (3%)	52	45
2	B	116/118 (98%)	112 (97%)	4 (3%)	44	36
3	C	222/222 (100%)	220 (99%)	2 (1%)	84	84
All	All	451/453 (100%)	442 (98%)	9 (2%)	63	58

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	VAL
1	A	79	ASN
1	A	96	PRO
2	B	3	HIS
2	B	19	VAL
2	B	24	VAL
2	B	127	VAL
3	C	183	HIS
3	C	209	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	98	HIS
2	B	117	HIS
2	B	140	ASN
3	C	195	GLN
3	C	207	ASN
3	C	396	GLN
3	C	406	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

2 carbohydrates 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	#$|Z| > 2$
7	NAG	C	501	3,7	14,14,15	0.69	0	15,19,21	1.64	2 (13%)
7	FUC	C	502	7	10,10,11	0.91	0	14,14,16	1.70	2 (14%)

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
7	NAG	C	501	3,7	-	0/6/23/26	0/1/1/1
7	FUC	C	502	7	-	0/0/17/20	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
7	C	501	NAG	C3-C4-C5	-2.61	105.65	110.20
7	C	502	FUC	C1-O5-C5	2.59	116.38	112.38
7	C	501	NAG	C2-N2-C7	3.24	127.20	123.04
7	C	502	FUC	O5-C5-C6	4.72	113.93	106.13

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry (i)

8 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	#$|Z| > 2$
4	HEM	A	201	1,5	30,50,50	2.33	3 (10%)	24,82,82	2.29	6 (25%)
5	OXY	A	202	4	1,1,1	0.24	0	0,0,0	0.00	-
4	HEM	B	201	2,5	30,50,50	2.15	10 (33%)	24,82,82	2.63	11 (45%)
5	OXY	B	202	4	1,1,1	0.29	0	0,0,0	0.00	-
6	GOL	B	203	-	5,5,5	0.37	0	5,5,5	0.82	0
8	SO4	C	503	-	4,4,4	0.61	0	6,6,6	0.92	0
6	GOL	C	504	-	5,5,5	0.83	0	5,5,5	1.73	1 (20%)
9	CAC	C	505	-	0,4,4	0.00	-	0,6,6	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
4	HEM	A	201	1,5	-	0/10/54/54	0/0/8/8
5	OXY	A	202	4	-	0/0/0/0	0/0/0/0
4	HEM	B	201	2,5	-	0/10/54/54	0/0/8/8
5	OXY	B	202	4	-	0/0/0/0	0/0/0/0
6	GOL	B	203	-	-	0/4/4/4	0/0/0/0
8	SO4	C	503	-	-	0/0/0/0	0/0/0/0
6	GOL	C	504	-	-	0/4/4/4	0/0/0/0
9	CAC	C	505	-	-	0/0/0/0	0/0/0/0

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	201	HEM	C2D-C3D	-7.52	1.31	1.54
4	A	201	HEM	C2C-C1C	-6.52	1.40	1.52
4	B	201	HEM	C2D-C3D	-5.95	1.36	1.54
4	A	201	HEM	C3B-C4B	-5.69	1.46	1.51
4	B	201	HEM	C2C-C1C	-5.28	1.42	1.52
4	B	201	HEM	C3B-C4B	-3.38	1.48	1.51
4	B	201	HEM	C2B-C1B	-3.08	1.41	1.51
4	B	201	HEM	C3D-C4D	-2.38	1.48	1.51
4	B	201	HEM	C1C-NC	-2.37	1.33	1.36
4	B	201	HEM	C4C-NC	-2.18	1.33	1.36
4	B	201	HEM	FE-NB	2.10	2.08	1.97
4	B	201	HEM	CHC-C1C	2.66	1.42	1.36
4	B	201	HEM	FE-NC	3.45	2.09	1.95

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	201	HEM	CBA-CAA-C2A	-4.79	103.94	112.53
6	C	504	GOL	C3-C2-C1	-3.22	98.48	111.12
4	B	201	HEM	CBD-CAD-C3D	-2.72	105.62	113.55
4	B	201	HEM	C3B-C4B-NB	-2.50	106.85	111.63
4	A	201	HEM	CAA-CBA-CGA	-2.01	109.07	112.75
4	B	201	HEM	CAA-CBA-CGA	2.01	116.43	112.75
4	B	201	HEM	CMD-C2D-C3D	2.41	125.00	114.35
4	B	201	HEM	C3C-CAC-CBC	2.42	128.18	124.46
4	B	201	HEM	C2D-C3D-C4D	2.46	105.67	101.50
4	A	201	HEM	CMD-C2D-C3D	2.83	126.88	114.35
4	A	201	HEM	CMC-C2C-C3C	4.09	126.73	116.53
4	A	201	HEM	CAD-C3D-C4D	4.27	127.54	112.47
4	B	201	HEM	CAD-C3D-C2D	4.28	125.54	113.22
4	B	201	HEM	CMC-C2C-C3C	4.55	127.88	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	201	HEM	CAD-C3D-C4D	4.62	128.76	112.47
4	A	201	HEM	CMB-C2B-C3B	5.21	129.53	116.53
4	A	201	HEM	CAD-C3D-C2D	5.34	128.57	113.22
4	B	201	HEM	CMB-C2B-C3B	5.83	131.08	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	201	HEM	2	0
8	C	503	SO4	1	0
9	C	505	CAC	3	2

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	141/141 (100%)	-0.54	0	100	100	13, 20, 33, 39	0
2	B	144/146 (98%)	-0.02	2 (1%)	78	82	16, 29, 44, 58	0
3	C	259/259 (100%)	-0.22	0	100	100	11, 19, 39, 57	0
All	All	544/546 (99%)	-0.25	2 (0%)	93	94	11, 21, 40, 58	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	6	PRO	3.1
2	B	13	THR	2.4

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)

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
7	NAG	C	501	14/15	0.95	0.15	3.12	23,26,30,33	0
7	FUC	C	502	10/11	0.96	0.20	-	26,30,32,32	0

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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(Å²)	Q<0.9
5	OXY	A	202	2/2	0.97	0.23	14.99	31,31,31,48	0
9	CAC	C	505	5/5	0.90	0.36	13.92	47,137,178,198	2
6	GOL	C	504	6/6	0.95	0.15	3.30	23,24,28,32	0
5	OXY	B	202	2/2	0.99	0.11	1.11	23,23,23,29	0
4	HEM	A	201	43/43	0.98	0.10	0.91	12,15,32,43	0
4	HEM	B	201	43/43	0.96	0.12	0.30	19,26,41,47	0
6	GOL	B	203	6/6	0.94	0.12	-0.10	32,35,37,44	0
8	SO4	C	503	5/5	0.99	0.07	-1.74	15,20,21,21	0

6.5 Other polymers (i)

There are no such residues in this entry.