



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:48 AM GMT

PDB ID : 2IPS
Title : Crystal structure of a ternary complex of bovine lactoperoxidase with thiocyanate and iodide at 3.1 Å resolution
Authors : Singh, A.K.; Singh, N.; Sharma, S.; Singh, T.P.
Deposited on : 2006-10-12
Resolution : 3.10 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) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

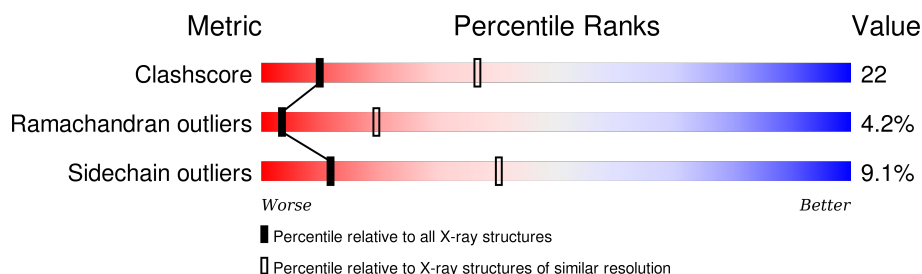
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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))
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)

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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	595	

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	SCN	A	702	-	X	-	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 5138 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 Lactoperoxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	595	Total	C	N	O	S	0	0	0
			4770	3037	847	860	26			

- Molecule 2 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	3	Total	C	N	O	0	0
			39	22	2	15		
2	A	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 3 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	2	Total	C	N	O	0	0
			28	16	2	10		

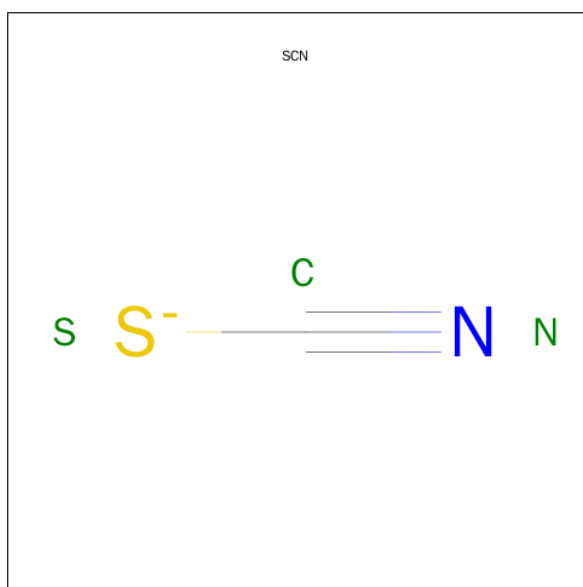
- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

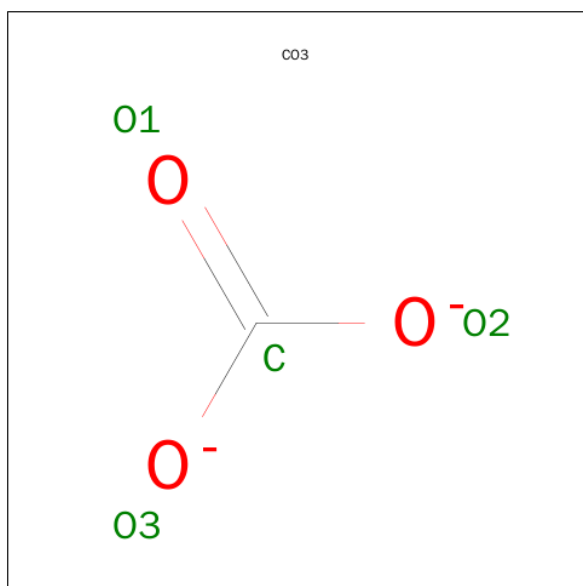
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Ca	0	0
			1	1		

- Molecule 6 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 7 is CARBONATE ION (three-letter code: CO3) (formula: CO₃).

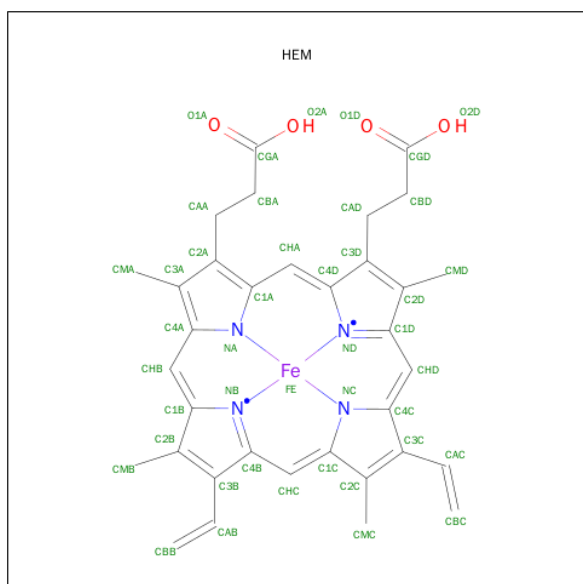


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	1	3		

- Molecule 8 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	6	Total 1 6 6	0	0

- Molecule 9 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 10 is water.

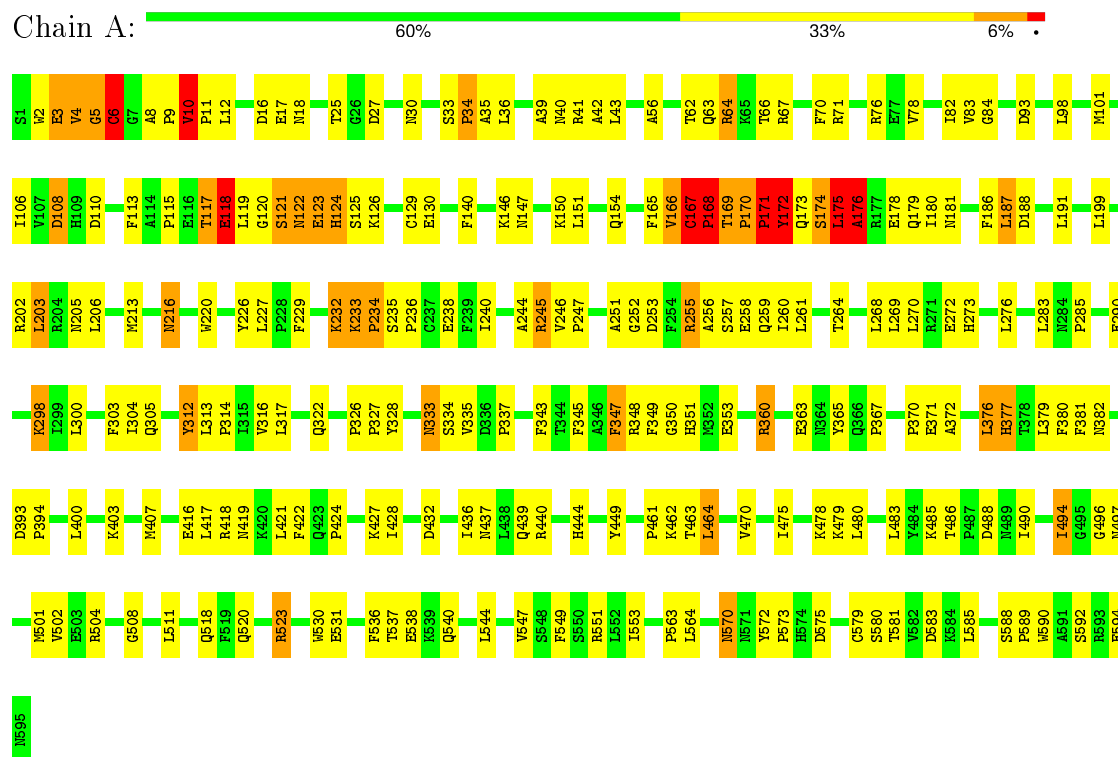
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	177	Total O 177 177	0	0

3 Residue-property plots

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.

Note EDS was not executed.

- Molecule 1: Lactoperoxidase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	55.54Å 80.59Å 77.92Å 90.00° 102.69° 90.00°	Depositor
Resolution (Å)	17.07 – 3.10	Depositor
% Data completeness (in resolution range)	97.4 (17.07-3.10)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.193 , 0.235	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5138	wwPDB-VP
Average B, all atoms (Å ²)	27.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CO3, SCN, NAG, CA, NDG, HEM, IOD, MAN

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	0.53	4/4898 (0.1%)	0.93	16/6645 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	11	PRO	N-CA	7.56	1.60	1.47
1	A	167	CYS	N-CA	-6.73	1.32	1.46
1	A	175	LEU	N-CA	5.69	1.57	1.46
1	A	166	VAL	C-N	-5.41	1.21	1.34

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	172	TYR	CB-CG-CD2	21.57	133.94	121.00
1	A	172	TYR	CB-CG-CD1	-20.94	108.44	121.00
1	A	172	TYR	CA-CB-CG	13.56	139.16	113.40
1	A	166	VAL	N-CA-C	9.40	136.37	111.00
1	A	166	VAL	CB-CA-C	-7.18	97.76	111.40
1	A	172	TYR	N-CA-CB	-6.42	99.04	110.60
1	A	168	PRO	CA-C-N	-6.40	103.11	117.20
1	A	11	PRO	CA-N-CD	-6.02	103.08	111.50
1	A	168	PRO	CA-N-CD	-6.00	103.10	111.50
1	A	172	TYR	CB-CA-C	5.99	122.38	110.40
1	A	4	VAL	N-CA-C	5.75	126.54	111.00
1	A	167	CYS	N-CA-C	-5.70	95.62	111.00
1	A	312	TYR	CB-CG-CD1	-5.41	117.76	121.00
1	A	234	PRO	CA-N-CD	-5.38	103.97	111.50
1	A	176	ALA	N-CA-C	-5.20	96.97	111.00
1	A	34	PRO	CA-N-CD	-5.04	104.45	111.50

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	4770	0	4689	213	0
2	A	78	0	68	1	0
3	A	28	0	25	3	0
4	A	28	0	25	1	0
5	A	1	0	0	0	0
6	A	3	0	0	0	0
7	A	4	0	0	0	0
8	A	6	0	0	1	0
9	A	43	0	30	4	0
10	A	177	0	0	15	0
All	All	5138	0	4837	215	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 22.

All (215) 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:169:THR:HB	1:A:170:PRO:CD	1.72	1.17
1:A:169:THR:HB	1:A:170:PRO:HD2	1.10	1.09
1:A:120:GLY:HA3	1:A:126:LYS:HE3	1.11	1.07
1:A:216:ASN:ND2	8:A:706:IOD:I	2.59	1.05
1:A:82:ILE:HD11	1:A:483:LEU:CD1	1.90	1.00
1:A:504:ARG:HD3	10:A:834:HOH:O	1.60	0.99
1:A:169:THR:CB	1:A:170:PRO:CD	2.40	0.98
1:A:227:LEU:HD23	1:A:270:LEU:HD22	1.49	0.93
1:A:174:SER:O	1:A:175:LEU:HB2	1.68	0.92
1:A:10:VAL:HG21	1:A:41:ARG:NH2	1.85	0.90
1:A:2:TRP:NE1	1:A:35:ALA:HB3	1.86	0.89
1:A:175:LEU:HG	10:A:731:HOH:O	1.72	0.88
1:A:381:PHE:CZ	1:A:424:PRO:HG3	2.08	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:238:GLU:HG2	1:A:245:ARG:O	1.74	0.87
1:A:169:THR:HG22	1:A:170:PRO:HD3	1.57	0.85
1:A:123:GLU:HG2	1:A:125:SER:HB3	1.61	0.83
1:A:169:THR:CG2	1:A:170:PRO:HD3	2.09	0.82
1:A:205:ASN:CG	3:A:599:NAG:C1	2.46	0.82
1:A:82:ILE:HD11	1:A:483:LEU:HD12	1.63	0.80
1:A:2:TRP:HB2	1:A:33:SER:HA	1.64	0.79
1:A:167:CYS:HB2	1:A:168:PRO:HD2	1.65	0.77
1:A:167:CYS:CB	1:A:168:PRO:HD2	2.17	0.75
1:A:167:CYS:CB	1:A:168:PRO:CD	2.66	0.74
1:A:9:PRO:HG2	10:A:766:HOH:O	1.88	0.72
1:A:205:ASN:O	1:A:206:LEU:HD23	1.88	0.72
1:A:169:THR:CB	1:A:170:PRO:HD3	2.18	0.72
1:A:2:TRP:CZ3	1:A:36:LEU:HD13	2.26	0.71
1:A:146:LYS:O	1:A:147:ASN:HB2	1.90	0.71
1:A:377:HIS:HB3	1:A:416:GLU:OE2	1.90	0.71
1:A:494:ILE:O	1:A:494:ILE:HD13	1.94	0.68
1:A:166:VAL:CG1	1:A:180:ILE:HG12	2.24	0.68
1:A:343:PHE:CD1	1:A:518:GLN:HG2	2.29	0.67
1:A:260:ILE:HG21	1:A:379:LEU:HD13	1.76	0.67
1:A:581:THR:HG22	1:A:581:THR:O	1.95	0.67
1:A:333:ASN:HD22	1:A:333:ASN:C	1.96	0.67
1:A:205:ASN:ND2	3:A:599:NAG:C2	2.56	0.67
1:A:82:ILE:HD11	1:A:483:LEU:HD13	1.76	0.67
1:A:166:VAL:HG12	1:A:180:ILE:HG12	1.77	0.67
1:A:4:VAL:HG13	1:A:5:GLY:H	1.60	0.67
1:A:119:LEU:HD21	1:A:170:PRO:HD3	1.76	0.67
1:A:124:HIS:HB3	10:A:824:HOH:O	1.97	0.65
1:A:120:GLY:HA3	1:A:126:LYS:CE	2.07	0.64
1:A:174:SER:O	1:A:175:LEU:CB	2.42	0.64
1:A:213:MET:HG2	1:A:273:HIS:CD2	2.32	0.64
1:A:175:LEU:O	1:A:176:ALA:HB2	1.98	0.64
1:A:370:PRO:HG2	1:A:371:GLU:HG3	1.80	0.64
1:A:463:THR:HB	10:A:880:HOH:O	1.98	0.63
1:A:119:LEU:HD21	1:A:169:THR:CG2	2.29	0.63
1:A:335:VAL:HG22	4:A:604:NAG:H62	1.81	0.63
1:A:272:GLU:O	1:A:276:LEU:HB2	1.99	0.63
1:A:244:ALA:O	1:A:246:VAL:HG23	1.99	0.62
1:A:170:PRO:HB2	1:A:171:PRO:HD2	1.82	0.62
1:A:170:PRO:CB	1:A:171:PRO:HD2	2.30	0.61
1:A:570:ASN:HB3	1:A:575:ASP:CB	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:ASN:HB3	1:A:33:SER:O	2.00	0.61
1:A:167:CYS:HB3	1:A:168:PRO:CD	2.31	0.60
1:A:121:SER:O	1:A:122:ASN:HB2	2.01	0.60
1:A:171:PRO:O	1:A:172:TYR:CB	2.48	0.60
1:A:537:THR:OG1	1:A:540:GLN:HG3	2.02	0.60
1:A:349:PHE:HA	1:A:497:ASN:HD21	1.66	0.59
1:A:119:LEU:HD22	1:A:170:PRO:HG3	1.85	0.59
1:A:588:SER:OG	1:A:589:PRO:HD3	2.03	0.59
1:A:480:LEU:HG	1:A:490:ILE:HD12	1.84	0.58
1:A:303:PHE:HD2	1:A:304:ILE:HD12	1.67	0.58
1:A:475:ILE:HG22	1:A:479:LYS:HE3	1.85	0.58
1:A:166:VAL:HG22	1:A:178:GLU:O	2.02	0.58
1:A:113:PHE:O	1:A:115:PRO:HD3	2.04	0.58
1:A:258:GLU:OE1	1:A:259:GLN:HG2	2.03	0.58
1:A:260:ILE:CG2	1:A:379:LEU:HD13	2.34	0.58
1:A:36:LEU:HG	1:A:337:PRO:HD2	1.85	0.58
1:A:551:ARG:HD3	1:A:583:ASP:O	2.04	0.57
1:A:376:LEU:HD22	1:A:376:LEU:O	2.03	0.57
1:A:119:LEU:HD21	1:A:169:THR:HG22	1.85	0.57
1:A:170:PRO:CB	1:A:171:PRO:CD	2.82	0.57
1:A:348:ARG:HH11	1:A:437:ASN:ND2	2.02	0.57
1:A:363:GLU:C	1:A:365:TYR:H	2.08	0.57
1:A:313:LEU:HB3	1:A:317:LEU:HD23	1.86	0.57
1:A:496:GLY:C	1:A:511:LEU:HD21	2.25	0.56
1:A:407:MET:HB3	1:A:501:MET:HE2	1.88	0.56
1:A:313:LEU:N	1:A:314:PRO:CD	2.69	0.56
1:A:199:LEU:HG	1:A:203:LEU:CD2	2.36	0.56
1:A:449:TYR:CB	1:A:490:ILE:HB	2.36	0.55
9:A:708:HEM:NA	10:A:872:HOH:O	2.33	0.55
1:A:179:GLN:HG2	1:A:444:HIS:CE1	2.41	0.55
1:A:333:ASN:HD22	1:A:334:SER:N	2.04	0.55
1:A:530:TRP:CE2	1:A:531:GLU:HG3	2.41	0.55
1:A:187:LEU:HD22	1:A:304:ILE:CG2	2.36	0.55
1:A:171:PRO:O	1:A:172:TYR:HB3	2.04	0.55
1:A:10:VAL:HG23	1:A:10:VAL:O	2.07	0.55
1:A:259:GLN:HG2	9:A:708:HEM:HBB2	1.87	0.54
1:A:220:TRP:HD1	10:A:746:HOH:O	1.90	0.54
1:A:2:TRP:HE1	1:A:35:ALA:HB3	1.72	0.54
1:A:407:MET:HB3	1:A:501:MET:CE	2.37	0.54
1:A:461:PRO:HG3	1:A:470:VAL:HG21	1.88	0.54
1:A:328:TYR:CD1	1:A:523:ARG:HD3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ASP:HB2	1:A:394:PRO:HD3	1.90	0.53
1:A:175:LEU:O	1:A:176:ALA:CB	2.55	0.53
1:A:335:VAL:O	1:A:337:PRO:HD3	2.08	0.53
1:A:462:LYS:NZ	1:A:488:ASP:OD1	2.41	0.53
1:A:10:VAL:CG2	1:A:10:VAL:O	2.56	0.53
1:A:4:VAL:HG13	1:A:5:GLY:N	2.22	0.52
1:A:187:LEU:HD22	1:A:304:ILE:HG22	1.90	0.52
1:A:106:ILE:HG23	1:A:191:LEU:HD11	1.91	0.52
1:A:199:LEU:O	1:A:203:LEU:HD22	2.09	0.52
1:A:16:ASP:C	1:A:18:ASN:H	2.12	0.52
1:A:544:LEU:O	1:A:547:VAL:HG22	2.09	0.52
1:A:475:ILE:CG2	1:A:479:LYS:HE3	2.39	0.52
1:A:328:TYR:HD1	1:A:523:ARG:HD3	1.75	0.52
1:A:16:ASP:O	1:A:18:ASN:N	2.44	0.51
1:A:272:GLU:HG3	1:A:272:GLU:O	2.10	0.51
1:A:400:LEU:HD13	1:A:563:PRO:HD2	1.94	0.51
1:A:549:PHE:CE2	1:A:553:ILE:HD11	2.46	0.50
1:A:502:VAL:HG13	1:A:508:GLY:HA2	1.93	0.50
1:A:253:ASP:OD2	1:A:255:ARG:HD3	2.12	0.50
1:A:120:GLY:CA	1:A:126:LYS:HE3	2.07	0.50
1:A:572:TYR:CD1	1:A:573:PRO:HA	2.46	0.50
1:A:165:PHE:HZ	1:A:170:PRO:O	1.94	0.49
1:A:63:GLN:CD	1:A:63:GLN:H	2.16	0.49
1:A:232:LYS:HG3	10:A:854:HOH:O	2.13	0.49
1:A:118:GLU:O	1:A:119:LEU:HB2	2.12	0.49
1:A:570:ASN:HB3	1:A:575:ASP:HB2	1.95	0.49
1:A:117:THR:O	1:A:118:GLU:HB2	2.13	0.49
1:A:4:VAL:O	1:A:6:CYS:N	2.46	0.48
1:A:166:VAL:HG13	1:A:180:ILE:HG12	1.95	0.48
2:A:601:NAG:H62	2:A:602:NAG:C1	2.43	0.48
1:A:418:ARG:O	1:A:432:ASP:HB2	2.13	0.48
1:A:67:ARG:NH1	10:A:719:HOH:O	2.45	0.48
1:A:485:LYS:O	1:A:486:THR:HB	2.14	0.48
1:A:449:TYR:HB2	1:A:490:ILE:HB	1.95	0.47
1:A:108:ASP:HB2	1:A:347:PHE:CD2	2.48	0.47
1:A:258:GLU:O	1:A:380:PHE:HA	2.14	0.47
1:A:175:LEU:CG	10:A:731:HOH:O	2.45	0.47
1:A:360:ARG:NH1	1:A:372:ALA:HA	2.29	0.47
1:A:78:VAL:HG13	1:A:82:ILE:HD13	1.97	0.47
1:A:588:SER:N	1:A:589:PRO:HD2	2.29	0.47
1:A:42:ALA:HB2	1:A:166:VAL:HG11	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:ARG:HA	1:A:432:ASP:OD1	2.15	0.47
1:A:432:ASP:O	1:A:436:ILE:HG13	2.15	0.47
1:A:496:GLY:CA	1:A:511:LEU:HD21	2.45	0.47
1:A:588:SER:OG	1:A:589:PRO:CD	2.63	0.46
1:A:35:ALA:O	1:A:36:LEU:C	2.52	0.46
1:A:264:THR:O	1:A:268:LEU:HD13	2.14	0.46
1:A:326:PRO:HB2	1:A:327:PRO:HD2	1.97	0.46
1:A:129:CYS:HB2	10:A:721:HOH:O	2.14	0.46
1:A:76:ARG:NH2	1:A:150:LYS:HD2	2.30	0.46
1:A:93:ASP:O	1:A:403:LYS:HD2	2.16	0.46
1:A:298:LYS:HD3	1:A:536:PHE:CZ	2.51	0.45
1:A:2:TRP:CD1	1:A:35:ALA:HB3	2.49	0.45
1:A:583:ASP:HB2	10:A:823:HOH:O	2.17	0.45
1:A:180:ILE:HG22	1:A:181:ASN:N	2.32	0.45
1:A:421:LEU:HD21	9:A:708:HEM:HMA1	1.98	0.45
1:A:537:THR:O	1:A:540:GLN:N	2.50	0.45
1:A:187:LEU:HB3	1:A:305:GLN:HG2	1.99	0.45
1:A:462:LYS:HD2	10:A:863:HOH:O	2.16	0.45
1:A:140:PHE:CE2	1:A:439:GLN:NE2	2.84	0.45
1:A:175:LEU:CD1	10:A:731:HOH:O	2.65	0.45
1:A:10:VAL:HG21	1:A:41:ARG:CZ	2.45	0.45
1:A:2:TRP:HB2	1:A:33:SER:CA	2.43	0.45
1:A:62:THR:CG2	1:A:64:ARG:HD2	2.47	0.45
1:A:251:ALA:O	1:A:253:ASP:N	2.49	0.45
1:A:350:GLY:O	1:A:353:GLU:N	2.47	0.44
1:A:113:PHE:CE2	1:A:115:PRO:HG3	2.52	0.44
1:A:167:CYS:HB3	1:A:168:PRO:HD3	2.00	0.44
1:A:229:PHE:CD1	1:A:247:PRO:HG2	2.52	0.44
1:A:244:ALA:O	1:A:246:VAL:N	2.50	0.44
1:A:233:LYS:HD3	1:A:233:LYS:HA	1.39	0.44
1:A:240:ILE:HD11	1:A:382:ASN:HA	2.00	0.44
1:A:165:PHE:N	1:A:165:PHE:CD1	2.84	0.44
1:A:579:CYS:O	1:A:581:THR:N	2.51	0.44
1:A:39:ALA:O	1:A:40:ASN:HB2	2.18	0.43
1:A:363:GLU:C	1:A:365:TYR:N	2.71	0.43
1:A:150:LYS:HE2	1:A:419:ASN:OD1	2.19	0.43
1:A:422:PHE:HE1	1:A:427:LYS:O	2.02	0.43
1:A:283:LEU:O	1:A:285:PRO:HD3	2.19	0.43
1:A:343:PHE:CE1	1:A:518:GLN:HG2	2.53	0.42
1:A:246:VAL:HA	1:A:247:PRO:HD2	1.81	0.42
1:A:186:PHE:O	1:A:188:ASP:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:GLU:HG2	10:A:723:HOH:O	2.18	0.42
1:A:169:THR:O	1:A:170:PRO:O	2.37	0.42
1:A:233:LYS:O	1:A:235:SER:N	2.53	0.42
1:A:345:PHE:CZ	1:A:440:ARG:HG3	2.55	0.42
1:A:110:ASP:OD2	1:A:191:LEU:HD22	2.20	0.42
1:A:235:SER:HA	1:A:236:PRO:HD3	1.93	0.42
1:A:154:GLN:NE2	1:A:428:ILE:HD13	2.34	0.42
1:A:449:TYR:HB2	1:A:490:ILE:O	2.19	0.42
1:A:140:PHE:CZ	1:A:439:GLN:NE2	2.88	0.42
1:A:64:ARG:H	1:A:64:ARG:HG3	1.49	0.41
1:A:25:THR:OG1	1:A:27:ASP:OD2	2.23	0.41
1:A:66:THR:HB	1:A:70:PHE:O	2.19	0.41
1:A:257:SER:O	1:A:381:PHE:HA	2.19	0.41
1:A:333:ASN:ND2	1:A:333:ASN:C	2.66	0.41
1:A:300:LEU:O	1:A:303:PHE:HB3	2.20	0.41
1:A:117:THR:O	1:A:118:GLU:CB	2.69	0.41
1:A:119:LEU:HD21	1:A:169:THR:HG21	2.00	0.41
1:A:205:ASN:OD1	3:A:599:NAG:C1	2.67	0.41
1:A:121:SER:O	1:A:122:ASN:CB	2.67	0.41
1:A:579:CYS:C	1:A:581:THR:H	2.23	0.41
1:A:165:PHE:O	1:A:180:ILE:HD11	2.21	0.41
1:A:345:PHE:HZ	1:A:440:ARG:HG3	1.86	0.41
1:A:540:GLN:NE2	1:A:590:TRP:NE1	2.68	0.41
1:A:199:LEU:HG	1:A:203:LEU:HD21	2.02	0.41
1:A:4:VAL:O	1:A:5:GLY:C	2.59	0.41
1:A:191:LEU:H	1:A:191:LEU:HD23	1.86	0.41
1:A:43:LEU:HD12	1:A:179:GLN:HB2	2.04	0.40
1:A:417:LEU:HD21	9:A:708:HEM:CMB	2.50	0.40
1:A:269:LEU:HD23	1:A:269:LEU:HA	1.91	0.40
1:A:101:MET:SD	1:A:101:MET:C	3.00	0.40
1:A:123:GLU:HG2	1:A:125:SER:CB	2.40	0.40
1:A:377:HIS:HA	1:A:380:PHE:CE2	2.56	0.40
1:A:464:LEU:C	1:A:464:LEU:HD22	2.41	0.40
1:A:549:PHE:O	1:A:553:ILE:HG12	2.21	0.40
1:A:312:TYR:O	1:A:316:VAL:HG23	2.21	0.40
1:A:496:GLY:HA3	1:A:511:LEU:HD21	2.03	0.40
1:A:461:PRO:CG	1:A:470:VAL:HG21	2.51	0.40
1:A:594:GLU:CD	1:A:594:GLU:H	2.23	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	593/595 (100%)	513 (86%)	55 (9%)	25 (4%)	3 19

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	5	GLY
1	A	121	SER
1	A	167	CYS
1	A	168	PRO
1	A	169	THR
1	A	170	PRO
1	A	175	LEU
1	A	176	ALA
1	A	245	ARG
1	A	6	CYS
1	A	8	ALA
1	A	17	GLU
1	A	118	GLU
1	A	122	ASN
1	A	252	GLY
1	A	3	GLU
1	A	171	PRO
1	A	256	ALA
1	A	580	SER
1	A	56	ALA
1	A	83	VAL
1	A	351	HIS
1	A	234	PRO
1	A	10	VAL
1	A	84	GLY

5.3.2 Protein sidechains ⓘ

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	518/518 (100%)	471 (91%)	47 (9%)	12	40

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	6	CYS
1	A	10	VAL
1	A	12	LEU
1	A	34	PRO
1	A	64	ARG
1	A	71	ARG
1	A	98	LEU
1	A	108	ASP
1	A	117	THR
1	A	118	GLU
1	A	123	GLU
1	A	124	HIS
1	A	130	GLU
1	A	151	LEU
1	A	171	PRO
1	A	172	TYR
1	A	173	GLN
1	A	174	SER
1	A	175	LEU
1	A	187	LEU
1	A	202	ARG
1	A	203	LEU
1	A	216	ASN
1	A	226	TYR
1	A	232	LYS
1	A	233	LYS
1	A	255	ARG
1	A	261	LEU
1	A	290	GLU

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Mol	Chain	Res	Type
1	A	298	LYS
1	A	322	GLN
1	A	333	ASN
1	A	347	PHE
1	A	360	ARG
1	A	367	PRO
1	A	376	LEU
1	A	377	HIS
1	A	464	LEU
1	A	478	LYS
1	A	494	ILE
1	A	520	GLN
1	A	523	ARG
1	A	564	LEU
1	A	570	ASN
1	A	585	LEU
1	A	592	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	128	GLN
1	A	147	ASN
1	A	216	ASN
1	A	333	ASN
1	A	341	ASN
1	A	437	ASN
1	A	468	GLN
1	A	497	ASN
1	A	520	GLN
1	A	545	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 ⓘ

10 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$
2	NAG	A	596	1,2	14,14,15	0.58	0	15,19,21	0.72	0
2	NAG	A	597	2	14,14,15	0.75	0	15,19,21	0.70	0
2	MAN	A	598	2	11,11,12	0.70	0	14,15,17	0.76	0
3	NAG	A	599	1,3	14,14,15	0.58	0	15,19,21	0.84	1 (6%)
3	NAG	A	600	3	14,14,15	0.67	0	15,19,21	0.88	1 (6%)
2	NAG	A	601	1,2	14,14,15	0.54	0	15,19,21	0.88	1 (6%)
2	NAG	A	602	2	14,14,15	0.69	0	15,19,21	0.94	1 (6%)
2	MAN	A	603	2	11,11,12	0.91	1 (9%)	14,15,17	0.42	0
4	NAG	A	604	1,4	14,14,15	0.60	0	15,19,21	0.80	0
4	NDG	A	605	4	14,14,15	0.65	0	15,19,21	1.71	3 (20%)

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	NAG	A	596	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	597	2	-	0/6/23/26	0/1/1/1
2	MAN	A	598	2	-	0/2/19/22	1/1/1/1
3	NAG	A	599	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	600	3	-	0/6/23/26	0/1/1/1
2	NAG	A	601	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	602	2	-	0/6/23/26	0/1/1/1
2	MAN	A	603	2	-	0/2/19/22	0/1/1/1
4	NAG	A	604	1,4	-	0/6/23/26	0/1/1/1
4	NDG	A	605	4	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	603	MAN	C2-C3	2.21	1.55	1.52

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	599	NAG	C2-N2-C7	-2.42	119.93	123.04
4	A	605	NDG	C2-N2-C7	-2.36	120.00	123.04
2	A	601	NAG	C2-N2-C7	-2.30	120.08	123.04
3	A	600	NAG	C2-N2-C7	-2.22	120.18	123.04
2	A	602	NAG	C1-O5-C5	2.35	115.23	112.25
4	A	605	NDG	C3-C4-C5	3.93	117.05	110.20
4	A	605	NDG	C4-C3-C2	4.19	117.75	111.23

There are no chirality outliers.

There are no torsion outliers.

All (1) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	598	MAN	C1-C2-C3-C4-C5-O5

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	599	NAG	3	0
2	A	601	NAG	1	0
2	A	602	NAG	1	0
4	A	604	NAG	1	0

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 7 are monoatomic - leaving 3 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
7	CO3	A	688	-	0,3,3	0.00	-	0,3,3	0.00	-
6	SCN	A	702	-	2,2,2	2.76	2 (100%)	1,1,1	0.11	0
9	HEM	A	708	1,10	30,50,50	2.88	11 (36%)	24,82,82	2.33	8 (33%)

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	CO3	A	688	-	-	0/0/0/0	0/0/0/0
6	SCN	A	702	-	-	0/0/0/0	0/0/0/0
9	HEM	A	708	1,10	-	0/10/54/54	0/0/8/8

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	708	HEM	C3B-C4B	-11.37	1.41	1.51
9	A	708	HEM	C1A-CHA	-4.66	1.27	1.39
9	A	708	HEM	C2B-C1B	-2.92	1.42	1.51
9	A	708	HEM	C2D-C1D	-2.60	1.43	1.51
9	A	708	HEM	CHC-C4B	-2.15	1.32	1.38
9	A	708	HEM	C3B-CAB	2.01	1.55	1.51
6	A	702	SCN	C-N	2.19	1.30	1.15
9	A	708	HEM	CAA-C2A	2.42	1.56	1.52
9	A	708	HEM	C4C-NC	3.07	1.39	1.36
9	A	708	HEM	CMC-C2C	3.18	1.60	1.53
6	A	702	SCN	C-S	3.23	1.84	1.63
9	A	708	HEM	CAD-C3D	3.39	1.60	1.54
9	A	708	HEM	C3C-CAC	4.03	1.58	1.51

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	708	HEM	C3B-CAB-CBB	-2.94	119.94	124.46
9	A	708	HEM	CAA-C2A-C1A	-2.11	124.71	127.01
9	A	708	HEM	C4B-CHC-C1C	2.06	129.27	125.82
9	A	708	HEM	CAD-C3D-C2D	2.77	121.17	113.22
9	A	708	HEM	CMC-C2C-C3C	3.38	124.96	116.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	708	HEM	C3C-CAC-CBC	3.84	130.35	124.46
9	A	708	HEM	CMB-C2B-C3B	4.32	127.33	116.53
9	A	708	HEM	CAD-C3D-C4D	6.65	135.94	112.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	708	HEM	4	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 ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.