



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 05:07 AM GMT

PDB ID : 1RS8
Title : Bovine endothelial NOS heme domain with D-lysine-D-nitroarginineamide bound
Authors : Flinspach, M.; Li, H.; Jamal, J.; Yang, W.; Huang, H.; Silverman, R.B.; Poulos, T.L.
Deposited on : 2003-12-09
Resolution : 2.30 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

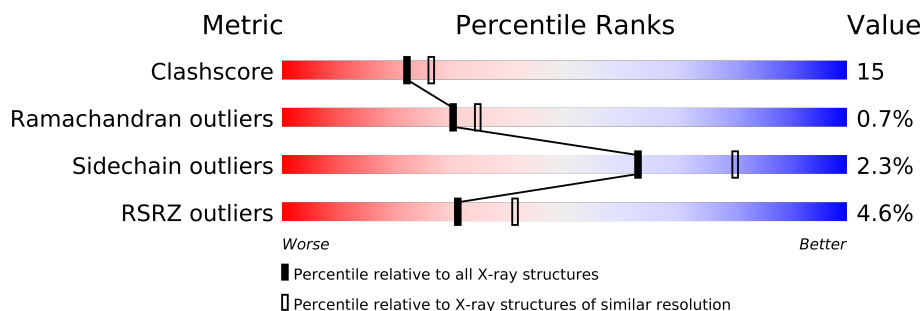
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.30 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	79885	3679 (2.30-2.30)
Ramachandran outliers	78287	3642 (2.30-2.30)
Sidechain outliers	78261	3641 (2.30-2.30)
RSRZ outliers	66119	2930 (2.30-2.30)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	416	
1	B	416	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	ACT	B	861	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 7079 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

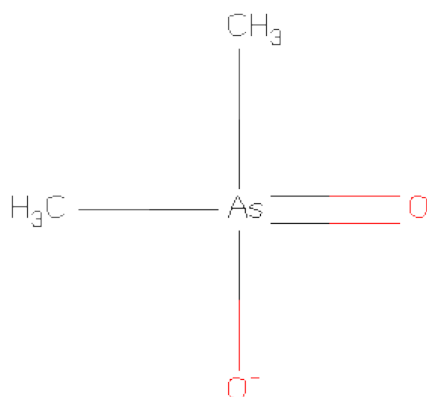
- Molecule 1 is a protein called Nitric-oxide synthase, endothelial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	406	Total	C	N	O	S	0	0	0
			3227	2052	569	590	16			
1	B	404	Total	C	N	O	S	0	0	0
			3216	2045	567	588	16			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	100	ARG	CYS	SEE REMARK 999	UNP P29473
B	100	ARG	CYS	SEE REMARK 999	UNP P29473

- Molecule 2 is CACODYLATE ION (three-letter code: CAC) (formula: C₂H₆AsO₂).



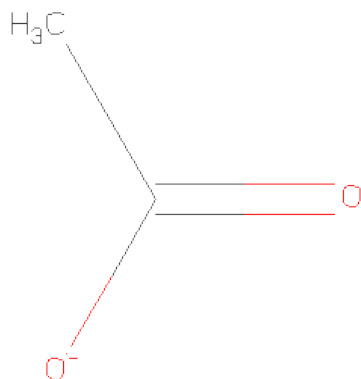
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	As C	0	0
			3	1 2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	As	C	0	0
			3	1	2		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

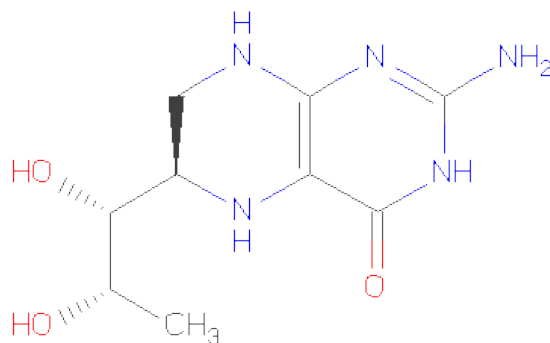
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



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

- Molecule 6 is 5,6,7,8-TETRAHYDROBIOPTERIN (three-letter code: H4B) (formula: $C_9H_{15}N_5O_3$).



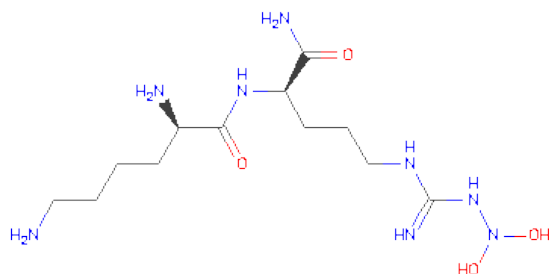
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			17	9	5	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	N	O	0	0
			17	9	5	3		

- Molecule 7 is L-LYSYL-N 5 -[(Z)-(2,2-DIHYDROXYHYDRAZINO)(IMINO)METHYL]-L-ORNITHINAMIDE (three-letter code: DP2) (formula: $C_{12}H_{28}N_8O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			24	12	8	4		
7	B	1	Total	C	N	O	0	0
			24	12	8	4		

- Molecule 8 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 9 is water.

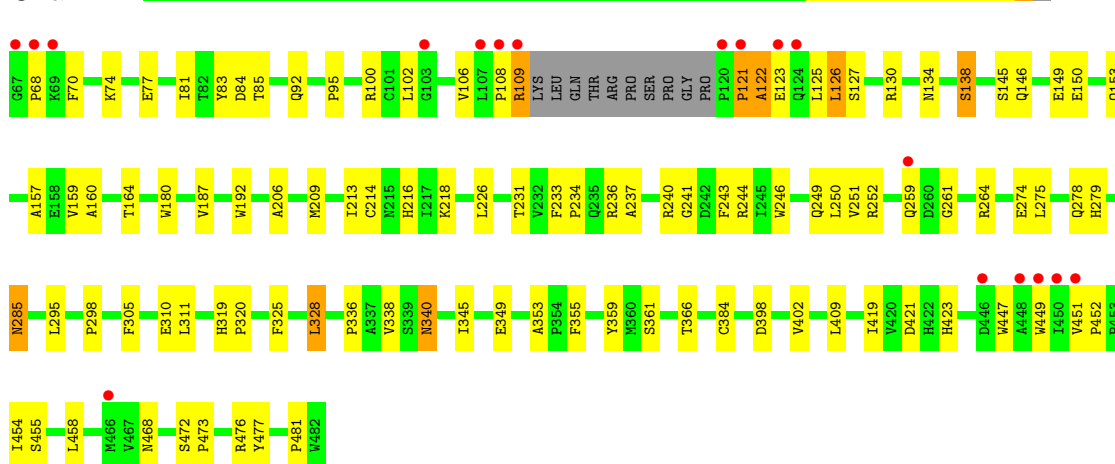
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	231	Total	O	0	0
			231	231		
9	B	210	Total	O	0	0
			210	210		

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.

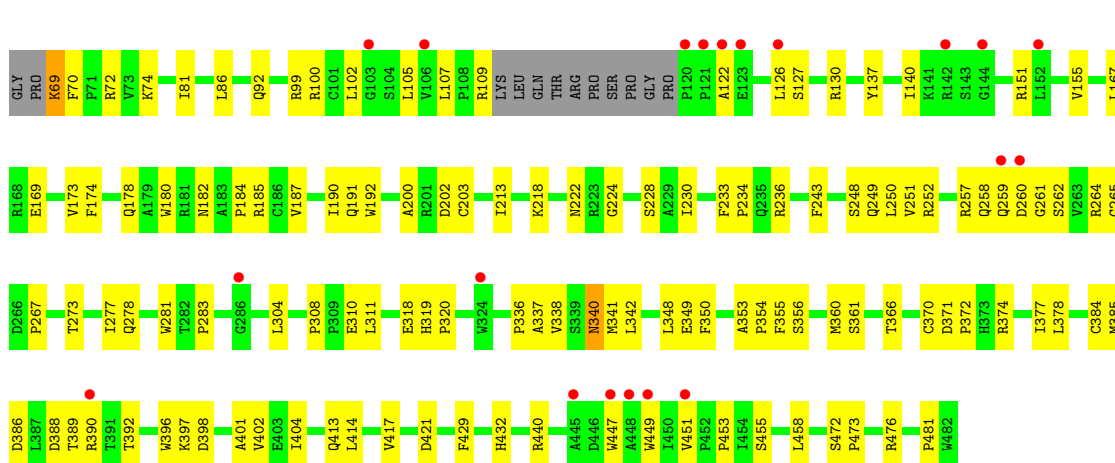
- Molecule 1: Nitric-oxide synthase, endothelial

Chain A:



- Molecule 1: Nitric-oxide synthase, endothelial

Chain B:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.01Å 106.22Å 156.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.83 – 2.30 46.83 – 2.19	Depositor EDS
% Data completeness (in resolution range)	97.1 (46.83-2.30) 82.2 (46.83-2.19)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.222 , 0.276 0.221 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	34.2	Xtriage
Anisotropy	0.502	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	2 of 48100 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7079	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.84% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, H4B, ACT, CAC, HEM, DP2

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	0.42	0/3318	0.65	0/4520
1	B	0.40	0/3306	0.65	1/4503 (0.0%)
All	All	0.41	0/6624	0.65	1/9023 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	360	MET	N-CA-C	-5.46	96.25	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3227	0	3135	93	0
1	B	3216	0	3125	103	0
2	A	3	0	0	3	0
2	B	3	0	0	1	0
3	A	4	0	3	0	0
3	B	4	0	3	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
5	A	43	0	30	0	0
5	B	43	0	30	2	0
6	A	17	0	15	1	0
6	B	17	0	15	1	0
7	A	24	0	27	1	0
7	B	24	0	27	2	0
8	A	6	0	8	0	0
8	B	6	0	8	2	0
9	A	231	0	0	5	0
9	B	210	0	0	14	0
All	All	7079	0	6426	196	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 15.

All (196) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:384:CYS:SG	2:A:850:CAC:AS	2.84	0.95
1:B:350:PHE:HB3	9:B:1071:HOH:O	1.76	0.85
1:B:249:GLN:HB2	1:B:252:ARG:HD2	1.60	0.84
1:B:388:ASP:OD1	1:B:390:ARG:HB3	1.79	0.82
1:A:149:GLU:O	1:A:153:GLN:HG2	1.79	0.81
1:B:384:CYS:SG	2:B:852:CAC:AS	3.01	0.79
1:B:259:GLN:HG2	1:B:260:ASP:H	1.47	0.79
1:B:277:ILE:HG12	1:B:283:PRO:HG3	1.66	0.77
1:B:190:ILE:HB	9:B:1059:HOH:O	1.84	0.77
1:A:109:ARG:HG2	1:A:109:ARG:HH11	1.50	0.76
1:A:146:GLN:O	1:A:150:GLU:HG3	1.85	0.75
1:A:108:PRO:HD3	9:A:1118:HOH:O	1.86	0.74
1:B:259:GLN:HG2	1:B:260:ASP:N	2.03	0.73
1:A:240:ARG:HD3	1:A:298:PRO:HB3	1.71	0.72
1:B:432:HIS:HB2	9:B:1059:HOH:O	1.89	0.71
1:A:274:GLU:O	1:A:278:GLN:HG3	1.91	0.71
1:A:77:GLU:HG3	1:B:372:PRO:HG2	1.73	0.70
1:B:429:PHE:HA	9:B:1059:HOH:O	1.91	0.70
1:B:248:SER:HA	1:B:340:ASN:HB3	1.73	0.70
1:A:244:ARG:NH2	1:A:481:PRO:HD3	2.06	0.69
1:A:122:ALA:O	1:A:126:LEU:HB2	1.95	0.67
1:B:69:LYS:HE2	1:B:70:PHE:H	1.60	0.66
1:B:281:TRP:O	1:B:283:PRO:HD3	1.97	0.65
1:B:398:ASP:O	1:B:402:VAL:HG23	1.97	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:265:GLY:O	1:B:267:PRO:HD3	1.96	0.64
1:B:260:ASP:C	1:B:262:SER:H	2.01	0.64
1:B:340:ASN:HD22	1:B:340:ASN:H	1.44	0.64
1:A:127:SER:HB3	9:A:1106:HOH:O	1.97	0.64
1:B:258:GLN:NE2	1:B:264:ARG:HB2	2.12	0.64
1:A:134:ASN:O	1:A:138:SER:HB2	1.98	0.64
1:B:178:GLN:HB3	9:B:1078:HOH:O	1.97	0.63
1:A:92:GLN:HE22	1:A:476:ARG:HH22	1.46	0.63
1:B:182:ASN:O	1:B:184:PRO:HD3	1.98	0.63
1:A:126:LEU:O	1:A:130:ARG:HG3	1.98	0.62
1:A:285:ASN:HD22	1:A:285:ASN:H	1.46	0.62
1:A:366:THR:HG21	1:A:454:ILE:HG23	1.81	0.62
1:A:237:ALA:HB3	1:A:240:ARG:HB3	1.82	0.62
1:A:285:ASN:N	1:A:285:ASN:HD22	1.98	0.62
1:B:249:GLN:HB2	1:B:252:ARG:CD	2.30	0.61
1:B:361:SER:OG	1:B:421:ASP:HA	2.03	0.59
1:B:251:VAL:O	1:B:252:ARG:HG2	2.02	0.59
1:B:319:HIS:CG	1:B:320:PRO:HD2	2.38	0.58
1:A:218:LYS:HG2	1:A:311:LEU:HD22	1.85	0.58
1:B:378:LEU:HB2	9:B:887:HOH:O	2.03	0.58
1:A:145:SER:O	1:A:149:GLU:HG2	2.03	0.58
1:B:224:GLY:O	1:B:417:VAL:HA	2.04	0.57
1:B:69:LYS:HE2	1:B:70:PHE:N	2.20	0.57
1:A:121:PRO:O	1:A:123:GLU:N	2.38	0.57
1:A:74:LYS:HB2	1:A:81:ILE:HD13	1.86	0.57
1:A:109:ARG:HG2	1:A:109:ARG:NH1	2.20	0.57
1:A:214:CYS:O	1:A:218:LYS:HG3	2.05	0.57
1:B:257:ARG:HG3	1:B:257:ARG:HH11	1.69	0.56
1:B:250:LEU:N	9:B:1070:HOH:O	2.39	0.55
1:B:371:ASP:HB2	1:B:374:ARG:HG2	1.89	0.55
1:B:340:ASN:N	1:B:340:ASN:HD22	2.03	0.54
1:B:338:VAL:HB	1:B:355:PHE:CZ	2.42	0.54
1:B:371:ASP:HB2	1:B:374:ARG:CG	2.37	0.53
1:B:218:LYS:CG	1:B:311:LEU:HD11	2.38	0.53
1:B:258:GLN:HE22	1:B:264:ARG:HD2	1.74	0.52
1:B:102:LEU:HB3	1:B:105:LEU:HD22	1.92	0.52
1:B:388:ASP:C	1:B:390:ARG:H	2.12	0.52
1:B:257:ARG:HG3	1:B:257:ARG:NH1	2.25	0.52
1:A:340:ASN:HD22	1:A:340:ASN:H	1.57	0.52
1:A:249:GLN:HB2	1:A:252:ARG:CG	2.38	0.52
1:B:260:ASP:O	1:B:262:SER:N	2.43	0.52
1:A:361:SER:CB	1:A:421:ASP:HA	2.41	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:310:GLU:N	1:B:310:GLU:OE2	2.32	0.51
1:A:361:SER:OG	1:A:409:LEU:HG	2.10	0.51
1:B:337:ALA:HA	1:B:355:PHE:O	2.10	0.51
1:A:249:GLN:HB2	1:A:252:ARG:HG2	1.93	0.51
1:A:70:PHE:CD1	1:A:85:THR:HG22	2.46	0.51
1:B:151:ARG:O	1:B:155:VAL:HG23	2.11	0.51
1:B:281:TRP:HB2	1:B:304:LEU:HD21	1.93	0.50
1:B:353:ALA:HB2	9:B:1071:HOH:O	2.10	0.50
1:B:228:SER:HA	1:B:356:SER:O	2.11	0.50
1:A:213:ILE:HG23	1:A:250:LEU:HD13	1.94	0.50
1:A:455:SER:HB3	1:A:458:LEU:HD12	1.94	0.49
1:B:366:THR:O	1:B:370:CYS:HB2	2.13	0.49
1:A:476:ARG:HH11	1:A:476:ARG:HG2	1.77	0.49
1:B:218:LYS:HG2	1:B:311:LEU:HD11	1.93	0.49
1:B:107:LEU:HD21	7:B:793:DP2:HE'1	1.94	0.49
1:A:240:ARG:HD3	1:A:298:PRO:CB	2.41	0.49
1:B:273:THR:O	1:B:277:ILE:HG13	2.12	0.49
1:B:340:ASN:H	1:B:340:ASN:ND2	2.09	0.49
1:A:384:CYS:CB	2:A:850:CAC:AS	3.21	0.49
1:A:236:ARG:HG3	1:A:349:GLU:O	2.13	0.49
1:B:180:TRP:CE3	1:B:192:TRP:HA	2.48	0.49
1:A:449:TRP:HA	6:A:760:H4B:N1	2.28	0.49
1:A:92:GLN:HE22	1:A:476:ARG:NH2	2.09	0.48
1:A:409:LEU:HD11	1:A:421:ASP:HB3	1.95	0.48
1:B:260:ASP:C	1:B:262:SER:N	2.64	0.48
1:A:240:ARG:HD2	1:A:241:GLY:O	2.14	0.48
1:A:361:SER:HB2	1:A:421:ASP:HA	1.96	0.48
1:A:398:ASP:O	1:A:402:VAL:HG23	2.13	0.48
1:B:72:ARG:HH21	1:B:74:LYS:HD2	1.78	0.48
1:B:191:GLN:HB3	9:B:892:HOH:O	2.13	0.48
1:A:423:HIS:HB2	1:B:392:THR:HB	1.96	0.47
1:B:126:LEU:O	1:B:130:ARG:HG3	2.13	0.47
1:A:476:ARG:NH1	1:A:476:ARG:HG2	2.29	0.47
1:A:340:ASN:N	1:A:340:ASN:HD22	2.12	0.47
1:A:95:PRO:O	1:A:102:LEU:HD12	2.15	0.47
1:A:251:VAL:O	1:A:252:ARG:HG2	2.15	0.47
1:A:275:LEU:O	1:A:279:HIS:HD2	1.97	0.47
1:B:200:ALA:O	1:B:203:CYS:HB2	2.15	0.47
1:B:233:PHE:HB3	1:B:234:PRO:CD	2.45	0.47
1:A:231:THR:O	1:A:353:ALA:HA	2.15	0.47
1:A:234:PRO:HB2	1:A:243:PHE:CE1	2.50	0.47
1:B:234:PRO:HB2	1:B:243:PHE:CE1	2.50	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:137:TYR:HA	1:B:140:ILE:HG12	1.96	0.46
1:B:233:PHE:HB3	1:B:234:PRO:HD2	1.96	0.46
1:A:264:ARG:HG3	1:A:264:ARG:HH11	1.81	0.46
1:A:319:HIS:CG	1:A:320:PRO:HD2	2.50	0.46
1:A:472:SER:HA	1:A:473:PRO:C	2.36	0.46
1:A:246:TRP:CD1	1:A:481:PRO:HG3	2.50	0.46
1:A:106:VAL:HG11	9:A:931:HOH:O	2.16	0.46
1:B:455:SER:HB3	1:B:458:LEU:HD12	1.96	0.46
1:A:226:LEU:CD1	1:A:226:LEU:N	2.78	0.46
1:A:240:ARG:NH2	9:A:955:HOH:O	2.48	0.46
1:B:236:ARG:HG3	1:B:349:GLU:O	2.15	0.45
1:A:477:TYR:CE1	7:A:792:DP2:HG'1	2.52	0.45
1:B:213:ILE:HG23	1:B:250:LEU:HD13	1.97	0.45
1:A:249:GLN:HB3	9:A:934:HOH:O	2.15	0.45
1:A:421:ASP:OD2	1:A:423:HIS:HB2	2.17	0.45
1:A:338:VAL:HB	1:A:355:PHE:CZ	2.52	0.45
1:B:258:GLN:HE21	1:B:264:ARG:HB2	1.81	0.45
1:A:366:THR:CG2	1:A:454:ILE:HG23	2.44	0.45
1:B:185:ARG:HB3	1:B:449:TRP:CE3	2.51	0.45
1:B:169:GLU:O	1:B:173:VAL:HG23	2.16	0.45
1:B:122:ALA:O	1:B:126:LEU:HB2	2.17	0.45
1:B:81:ILE:HD11	9:B:954:HOH:O	2.17	0.45
1:B:69:LYS:CE	1:B:70:PHE:H	2.28	0.44
1:A:361:SER:HA	1:A:419:ILE:HD11	1.99	0.44
5:B:500:HEM:HBA2	7:B:793:DP2:HD1	1.99	0.44
1:B:342:LEU:HD23	1:B:342:LEU:C	2.37	0.44
8:B:882:GOL:H32	9:B:1046:HOH:O	2.16	0.44
1:A:384:CYS:HB3	2:A:850:CAC:AS	2.77	0.44
1:A:325:PHE:O	1:A:328:LEU:HB2	2.17	0.44
1:A:150:GLU:O	1:A:153:GLN:HB2	2.18	0.44
1:B:218:LYS:HG2	1:B:311:LEU:CD1	2.48	0.44
1:A:187:VAL:O	1:A:187:VAL:HG22	2.17	0.44
1:A:295:LEU:HD12	1:A:305:PHE:CD1	2.53	0.44
1:A:244:ARG:CZ	1:A:481:PRO:HD3	2.46	0.44
1:B:174:PHE:O	1:B:178:GLN:HG2	2.17	0.44
1:A:159:VAL:HA	1:A:164:THR:O	2.17	0.44
1:B:385:MET:O	1:B:386:ASP:HB3	2.17	0.44
1:A:70:PHE:HB3	1:A:84:ASP:O	2.18	0.43
8:B:882:GOL:C3	9:B:1046:HOH:O	2.66	0.43
1:A:121:PRO:O	1:A:122:ALA:C	2.56	0.43
1:A:157:ALA:O	1:A:160:ALA:HB3	2.19	0.43
1:B:69:LYS:N	1:B:69:LYS:HZ3	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:472:SER:HA	1:B:473:PRO:C	2.39	0.43
1:B:366:THR:HG21	1:B:453:PRO:HB2	2.00	0.43
1:A:206:ALA:O	1:A:209:MET:HB2	2.19	0.43
1:B:230:ILE:HG13	1:B:354:PRO:O	2.18	0.43
1:B:447:TRP:CZ2	1:B:451:VAL:HG21	2.54	0.43
1:A:310:GLU:N	1:A:310:GLU:OE1	2.47	0.43
5:B:500:HEM:HBB2	5:B:500:HEM:HHC	2.01	0.42
1:B:318:GLU:OE1	1:B:414:LEU:HD22	2.18	0.42
1:B:86:LEU:HD13	1:B:440:ARG:HB3	2.01	0.42
1:B:476:ARG:HD2	9:B:898:HOH:O	2.18	0.42
1:A:458:LEU:HD22	1:B:378:LEU:HD21	2.01	0.42
1:A:340:ASN:ND2	1:A:340:ASN:H	2.17	0.42
1:B:99:ARG:HD3	9:B:1061:HOH:O	2.18	0.42
1:A:125:LEU:HD12	1:A:125:LEU:O	2.18	0.42
1:A:216:HIS:CD2	1:A:216:HIS:C	2.93	0.42
1:B:167:LEU:HG	1:B:348:LEU:HD12	2.02	0.42
1:A:74:LYS:HD2	1:A:81:ILE:HD11	2.02	0.42
1:A:458:LEU:HD11	1:B:401:ALA:CB	2.50	0.42
1:B:377:ILE:HD11	1:B:404:ILE:HD13	2.00	0.42
1:A:451:VAL:HA	1:A:452:PRO:HD3	1.87	0.41
1:A:180:TRP:CE3	1:A:192:TRP:HA	2.55	0.41
1:B:449:TRP:HA	6:B:761:H4B:N1	2.35	0.41
1:B:385:MET:O	1:B:386:ASP:CB	2.68	0.41
1:B:202:ASP:CG	1:B:202:ASP:O	2.59	0.41
1:B:234:PRO:HB2	1:B:243:PHE:CD1	2.55	0.41
1:B:396:TRP:CH2	1:B:397:LYS:HG2	2.55	0.41
1:B:109:ARG:HH11	1:B:109:ARG:HG2	1.86	0.41
1:B:137:TYR:CD2	1:B:140:ILE:HD11	2.56	0.41
1:B:182:ASN:O	1:B:184:PRO:CD	2.68	0.41
1:A:285:ASN:N	1:A:285:ASN:ND2	2.65	0.41
1:B:187:VAL:O	1:B:187:VAL:HG22	2.21	0.41
1:A:259:GLN:C	1:A:261:GLY:H	2.24	0.41
1:A:345:ILE:HG12	1:A:473:PRO:HB3	2.03	0.41
1:A:447:TRP:CZ2	1:A:451:VAL:HG21	2.56	0.41
1:B:258:GLN:HE21	1:B:264:ARG:CB	2.34	0.40
1:A:361:SER:HB3	1:A:421:ASP:HA	2.03	0.40
1:A:259:GLN:CD	1:A:259:GLN:H	2.25	0.40
1:B:249:GLN:HB2	1:B:252:ARG:CG	2.51	0.40
1:A:340:ASN:N	1:A:340:ASN:ND2	2.68	0.40
1:B:388:ASP:O	1:B:390:ARG:N	2.53	0.40
1:B:396:TRP:CZ3	1:B:397:LYS:HG2	2.55	0.40
1:B:340:ASN:ND2	1:B:341:MET:HG3	2.36	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:308:PRO:HB2	1:B:311:LEU:HB2	2.03	0.40
1:A:68:PRO:HB2	1:A:83:TYR:CD2	2.57	0.40
1:A:233:PHE:HB3	1:A:234:PRO:HD2	2.03	0.40
1:A:336:PRO:HB3	1:A:359:TYR:CZ	2.57	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	402/416 (97%)	375 (93%)	25 (6%)	2 (0%)	38	45
1	B	400/416 (96%)	367 (92%)	29 (7%)	4 (1%)	22	23
All	All	802/832 (96%)	742 (92%)	54 (7%)	6 (1%)	30	34

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	ALA
1	B	261	GLY
1	B	389	THR
1	A	121	PRO
1	B	336	PRO
1	B	481	PRO

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	345/354 (98%)	337 (98%)	8 (2%)	63	80
1	B	344/354 (97%)	336 (98%)	8 (2%)	63	80
All	All	689/708 (97%)	673 (98%)	16 (2%)	63	80

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	ARG
1	A	109	ARG
1	A	126	LEU
1	A	138	SER
1	A	285	ASN
1	A	328	LEU
1	A	340	ASN
1	A	468	ASN
1	B	69	LYS
1	B	92	GLN
1	B	100	ARG
1	B	127	SER
1	B	222	ASN
1	B	278	GLN
1	B	340	ASN
1	B	413	GLN

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

Mol	Chain	Res	Type
1	A	92	GLN
1	A	124	GLN
1	A	191	GLN
1	A	278	GLN
1	A	279	HIS
1	A	285	ASN
1	A	340	ASN
1	A	376	ASN
1	A	468	ASN
1	B	178	GLN
1	B	222	ASN

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Mol	Chain	Res	Type
1	B	225	ASN
1	B	258	GLN
1	B	278	GLN
1	B	340	ASN
1	B	405	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 13 ligands modelled in this entry, 1 is monoatomic - leaving 12 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	HEM	A	500	1	49,50,50	2.41	16 (32%)	46,82,82	1.67	9 (19%)
6	H4B	A	760	-	18,18,18	1.69	4 (22%)	24,26,26	2.61	9 (37%)
7	DP2	A	792	-	20,23,23	0.82	0	24,28,28	1.20	2 (8%)
2	CAC	A	850	-	2,2,4	0.44	0	0,1,6	0.00	-
3	ACT	A	860	-	1,3,3	3.70	1 (100%)	0,3,3	0.00	-
8	GOL	A	880	-	5,5,5	0.07	0	5,5,5	0.26	0
5	HEM	B	500	1	49,50,50	2.33	10 (20%)	46,82,82	1.66	10 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	H4B	B	761	-	18,18,18	1.39	5 (27%)	24,26,26	2.62	11 (45%)
7	DP2	B	793	-	20,23,23	0.76	0	24,28,28	1.20	2 (8%)
2	CAC	B	852	-	2,2,4	0.46	0	0,1,6	0.00	-
3	ACT	B	861	-	1,3,3	4.30	1 (100%)	0,3,3	0.00	-
8	GOL	B	882	-	5,5,5	0.15	0	5,5,5	0.20	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
5	HEM	A	500	1	-	0/14/114/114	0/0/8/8
6	H4B	A	760	-	-	0/8/17/17	0/0/2/2
7	DP2	A	792	-	-	0/24/28/28	0/0/0/0
2	CAC	A	850	-	-	0/0/0/0	0/0/0/0
3	ACT	A	860	-	-	0/0/0/0	0/0/0/0
8	GOL	A	880	-	-	0/4/4/4	0/0/0/0
5	HEM	B	500	1	-	0/14/114/114	0/0/8/8
6	H4B	B	761	-	-	0/8/17/17	0/0/2/2
7	DP2	B	793	-	-	0/24/28/28	0/0/0/0
2	CAC	B	852	-	-	0/0/0/0	0/0/0/0
3	ACT	B	861	-	-	0/0/0/0	0/0/0/0
8	GOL	B	882	-	-	0/4/4/4	0/0/0/0

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	500	HEM	C3D-C4D	11.17	1.47	1.44
5	A	500	HEM	C2D-C1D	9.30	1.46	1.44
5	A	500	HEM	C4A-C3A	5.70	1.47	1.40
5	A	500	HEM	C3D-C2D	-4.91	1.35	1.43
3	B	861	ACT	CH3-C	4.30	1.54	1.48
5	B	500	HEM	C4A-C3A	4.25	1.45	1.40
6	A	760	H4B	C6-N5	4.02	1.54	1.46
5	A	500	HEM	C4A-NA	3.79	1.44	1.36
5	A	500	HEM	C3C-C2C	-3.75	1.37	1.43
3	A	860	ACT	CH3-C	3.70	1.54	1.48
5	B	500	HEM	C3C-C2C	-3.55	1.37	1.43
5	A	500	HEM	C3B-C2B	-3.52	1.37	1.43
5	B	500	HEM	C3B-C2B	-3.19	1.38	1.43
6	A	760	H4B	C4-N3	3.17	1.42	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	B	761	H4B	C6-N5	3.11	1.52	1.46
5	B	500	HEM	C4A-NA	3.03	1.42	1.36
5	B	500	HEM	C3D-C2D	-3.02	1.38	1.43
5	B	500	HEM	CHD-C4C	2.96	1.41	1.36
5	B	500	HEM	CHB-C1B	2.84	1.39	1.35
5	A	500	HEM	C4C-NC	2.81	1.42	1.38
5	A	500	HEM	C1C-NC	2.76	1.41	1.38
5	A	500	HEM	CHB-C1B	2.70	1.39	1.35
5	A	500	HEM	C3B-C4B	2.56	1.47	1.44
5	A	500	HEM	C1A-NA	2.40	1.41	1.36
5	A	500	HEM	CMD-C2D	2.36	1.54	1.47
5	A	500	HEM	CMB-C2B	2.33	1.54	1.47
5	B	500	HEM	C1A-NA	2.32	1.41	1.36
5	A	500	HEM	C2B-C1B	2.32	1.45	1.44
6	A	760	H4B	C4A-N5	2.31	1.46	1.38
6	A	760	H4B	C8A-N1	2.29	1.39	1.34
6	B	761	H4B	C4A-N5	2.28	1.46	1.38
6	B	761	H4B	C8A-N1	2.28	1.39	1.34
5	A	500	HEM	CHC-C1C	2.09	1.40	1.36
5	A	500	HEM	CHD-C4C	2.07	1.40	1.36
5	B	500	HEM	C3B-C4B	2.07	1.46	1.44
6	B	761	H4B	C4-N3	2.06	1.40	1.37
6	B	761	H4B	C2-N1	2.00	1.36	1.33

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	761	H4B	C4-C4A-C8A	9.08	122.97	114.56
6	A	760	H4B	C4-C4A-C8A	8.99	122.89	114.56
5	A	500	HEM	C3B-C4B-NB	-5.87	109.80	114.00
5	B	500	HEM	CBA-CAA-C2A	-5.11	103.69	112.69
5	B	500	HEM	C3B-C4B-NB	-4.72	110.62	114.00
5	A	500	HEM	CBD-CAD-C3D	-4.34	104.91	114.37
7	A	792	DP2	O-C-N2	-3.48	117.14	123.03
6	A	760	H4B	C4-N3-C2	3.46	125.56	119.51
5	A	500	HEM	C3A-C4A-NA	3.43	112.00	109.41
6	A	760	H4B	C2-N1-C8A	3.32	122.33	117.61
7	B	793	DP2	O-C-N2	-3.24	117.54	123.03
6	A	760	H4B	N3-C2-N1	-3.21	117.28	121.78
5	B	500	HEM	C4A-NA-C1A	-3.21	102.54	106.76
6	B	761	H4B	C4-N3-C2	3.12	124.97	119.51
5	A	500	HEM	C1A-CHA-C4D	-3.01	123.52	127.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	760	H4B	C4A-N5-C6	-2.91	113.25	121.16
5	A	500	HEM	C4A-NA-C1A	-2.91	102.94	106.76
5	B	500	HEM	C4A-CHB-C1B	-2.88	123.68	127.47
6	B	761	H4B	C2-N1-C8A	2.84	121.64	117.61
6	B	761	H4B	C9-C6-N5	-2.79	104.49	109.69
5	B	500	HEM	C4C-NC-C1C	-2.73	102.70	105.53
6	B	761	H4B	C4A-N5-C6	-2.69	113.83	121.16
6	B	761	H4B	N3-C2-N1	-2.68	118.02	121.78
5	B	500	HEM	C4D-ND-C1D	-2.60	102.50	105.16
5	B	500	HEM	C3A-C4A-NA	2.46	111.27	109.41
6	B	761	H4B	N8-C8A-N1	2.44	119.40	115.82
6	B	761	H4B	C4A-C8A-N8	2.38	122.49	119.23
6	A	760	H4B	N8-C8A-N1	2.37	119.29	115.82
5	A	500	HEM	C4C-NC-C1C	-2.28	103.16	105.53
5	A	500	HEM	C4A-C3A-C2A	-2.23	105.44	107.00
6	A	760	H4B	C4A-C8A-N8	2.23	122.29	119.23
7	A	792	DP2	CA-C-N2	2.22	121.08	116.78
5	B	500	HEM	CBD-CAD-C3D	-2.22	109.53	114.37
6	B	761	H4B	O9-C9-C6	2.20	114.39	109.07
5	B	500	HEM	CHD-C1D-ND	-2.18	122.77	124.58
6	A	760	H4B	N2-C2-N1	2.16	123.23	120.31
7	B	793	DP2	CA-C-N2	2.12	120.89	116.78
6	B	761	H4B	C4A-C8A-N1	-2.12	118.11	121.50
6	A	760	H4B	C9-C6-N5	-2.10	105.77	109.69
5	B	500	HEM	C2A-C1A-CHA	-2.10	122.02	126.00
6	B	761	H4B	C4-C4A-N5	-2.08	116.06	119.10
5	A	500	HEM	C4D-ND-C1D	-2.04	103.08	105.16
5	A	500	HEM	C4A-CHB-C1B	-2.01	124.82	127.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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, 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	406/416 (97%)	0.33	18 (4%) 33 43	29, 46, 71, 104	0
1	B	404/416 (97%)	0.33	20 (4%) 28 38	30, 48, 74, 102	0
All	All	810/832 (97%)	0.33	38 (4%) 31 40	29, 47, 74, 104	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	120	PRO	7.4
1	A	67	GLY	7.1
1	B	120	PRO	5.1
1	A	123	GLU	4.4
1	A	121	PRO	3.8
1	B	259	GLN	3.6
1	A	259	GLN	3.5
1	A	69	LYS	3.5
1	B	121	PRO	3.5
1	B	324	TRP	3.2
1	B	122	ALA	3.2
1	A	448	ALA	3.1
1	A	109	ARG	3.1
1	B	106	VAL	2.8
1	B	142	ARG	2.8
1	B	448	ALA	2.7
1	A	449	TRP	2.6
1	B	286	GLY	2.4
1	B	152	LEU	2.4
1	B	144	GLY	2.4
1	A	450	ILE	2.4
1	A	68	PRO	2.4
1	A	108	PRO	2.4
1	B	447	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	126	LEU	2.3
1	B	103	GLY	2.3
1	A	103	GLY	2.2
1	B	260	ASP	2.2
1	B	451	VAL	2.2
1	A	124	GLN	2.2
1	A	446	ASP	2.1
1	A	107	LEU	2.1
1	B	445	ALA	2.1
1	B	390	ARG	2.0
1	B	449	TRP	2.0
1	B	123	GLU	2.0
1	A	466	MET	2.0
1	A	451	VAL	2.0

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	ACT	B	861	4/4	0.23	9.06	49,50,56,57	0
7	DP2	B	793	24/24	0.21	1.43	40,55,63,72	0
8	GOL	A	880	6/6	0.21	0.93	45,47,50,51	0
5	HEM	A	500	43/43	0.18	0.38	25,34,41,45	0
5	HEM	B	500	43/43	0.17	0.29	28,34,39,44	0
8	GOL	B	882	6/6	0.19	0.25	35,40,44,50	0
3	ACT	A	860	4/4	0.17	0.22	49,51,51,53	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	H4B	A	760	17/17	0.21	0.04	29,38,41,45	0
7	DP2	A	792	24/24	0.17	0.00	37,45,56,60	0
6	H4B	B	761	17/17	0.20	-0.09	31,34,40,42	0
2	CAC	B	852	3/5	0.15	-0.46	86,86,88,89	0
2	CAC	A	850	3/5	0.10	-0.85	76,76,77,78	0
4	ZN	A	900	1/1	0.10	-1.49	46,46,46,46	0

6.5 Other polymers ⓘ

There are no such residues in this entry.