



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:22 AM UTC

PDB ID : 1SJ2 / pdb_00001sj2
Title : Crystal structure of Mycobacterium tuberculosis catalase-peroxidase
Authors : Bertrand, T.; Eady, N.A.J.; Jones, J.N.; Bodiguel, J.; Jesmin; Nagy, J.M.;
Raven, E.L.; Jamart-Gregoire, B.; Brown, K.A.
Deposited on : 2004-03-02
Resolution : 2.41 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

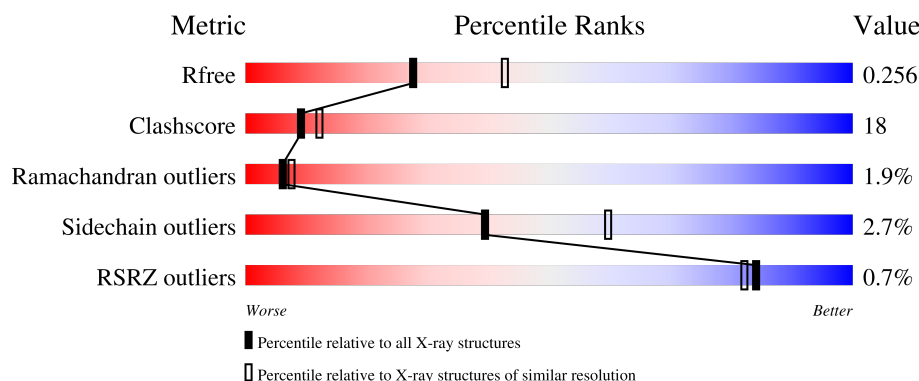
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.41 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}	180053	6062 (2.44-2.40)
Clashscore	190562	6562 (2.44-2.40)
Ramachandran outliers	187476	6481 (2.44-2.40)
Sidechain outliers	187428	6482 (2.44-2.40)
RSRZ outliers	180081	6066 (2.44-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	743	% 65% 28% • •
1	B	743	% 61% 32% • •

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	A	1194	-	X	-	-
3	GOL	A	1195	-	X	-	-
3	GOL	A	1196	-	X	-	-
3	GOL	B	2194	-	X	-	-
3	GOL	B	2195	-	X	-	-
3	GOL	B	2196	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11883 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 Peroxidase/catalase T.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	717	Total	C	N	O	S	0	0	0
			5529	3515	953	1042	19			
1	B	717	Total	C	N	O	S	0	0	0
			5529	3515	953	1042	19			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	MET	-	initiating methionine	UNP Q08129
A	-1	GLU	-	cloning artifact	UNP Q08129
A	0	PHE	-	cloning artifact	UNP Q08129
A	1	VAL	-	cloning artifact	UNP Q08129
B	-2	MET	-	initiating methionine	UNP Q08129
B	-1	GLU	-	cloning artifact	UNP Q08129
B	0	PHE	-	cloning artifact	UNP Q08129
B	1	VAL	-	cloning artifact	UNP Q08129

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



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

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

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

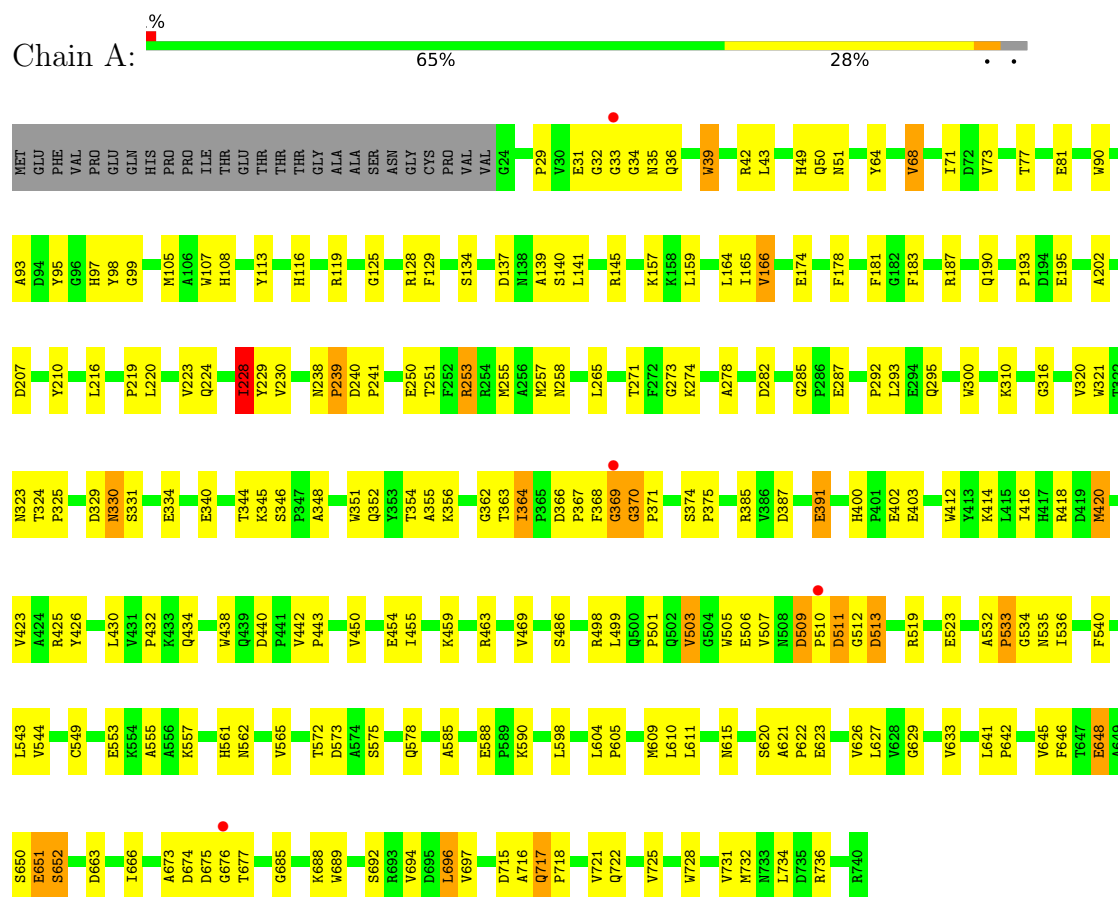
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	381	Total	O	0	0
			381	381		
4	B	322	Total	O	0	0
			322	322		

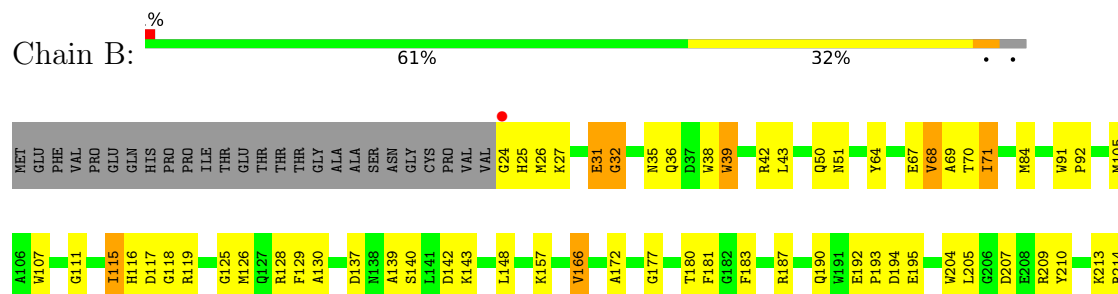
3 Residue-property plots

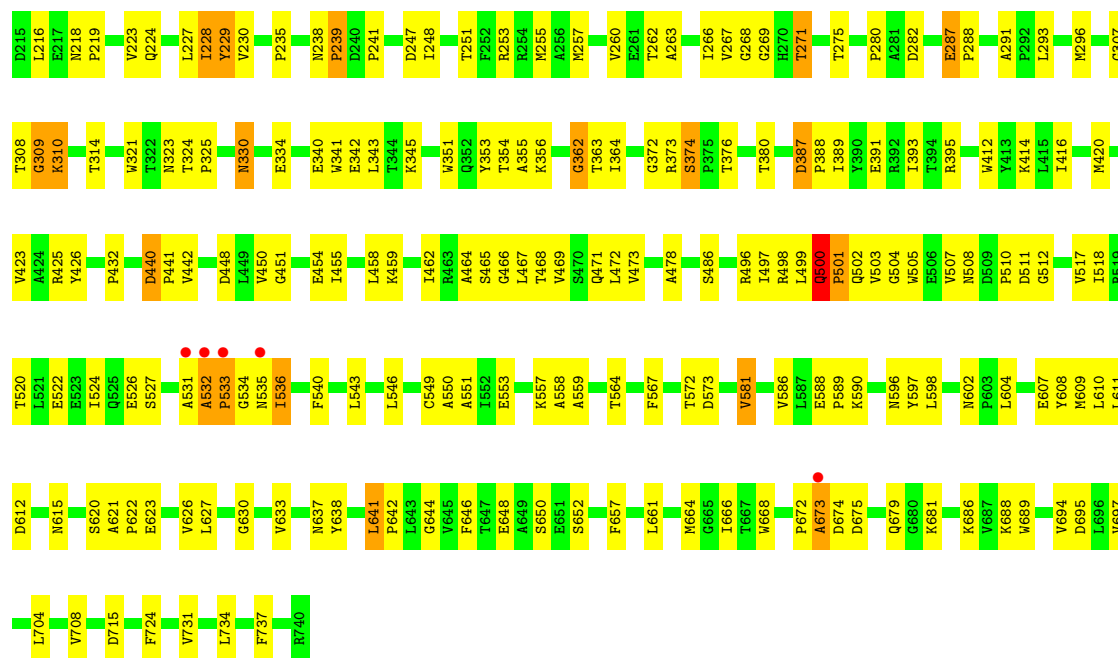
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Peroxidase/catalase T



• Molecule 1: Peroxidase/catalase T





4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	150.33Å 150.33Å 154.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	23.71 – 2.41 23.71 – 2.41	Depositor EDS
% Data completeness (in resolution range)	90.3 (23.71-2.41) 90.2 (23.71-2.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.16	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 2.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.211 , 0.268 0.197 , 0.256	Depositor DCC
R_{free} test set	6260 reflections (10.13%)	wwPDB-VP
Wilson B-factor (Å ²)	27.6	Xtriage
Anisotropy	1.346	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 47.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,l,k 0.007 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	11883	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.72% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, 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	0.57	2/5680 (0.0%)	0.97	27/7732 (0.3%)
1	B	0.65	2/5680 (0.0%)	1.11	31/7732 (0.4%)
All	All	0.61	4/11360 (0.0%)	1.04	58/15464 (0.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
All	All	0	2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	228	ILE	C-N	-30.11	0.91	1.33
1	B	229	TYR	C-N	-22.73	1.04	1.33
1	A	229	TYR	C-N	-20.31	1.06	1.33
1	A	228	ILE	C-N	-19.95	1.05	1.33

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	228	ILE	O-C-N	-46.71	61.39	122.11
1	B	321	TRP	N-CA-C	8.99	120.69	111.07
1	A	229	TYR	CA-C-N	8.45	134.53	123.03
1	A	229	TYR	C-N-CA	8.45	134.53	123.03
1	B	39	TRP	CA-C-N	8.26	128.73	119.32

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	39	TRP	C-N-CA	8.26	128.73	119.32
1	A	590	LYS	N-CA-C	-7.79	103.78	113.28
1	B	229	TYR	CA-C-N	7.71	134.02	122.92
1	B	229	TYR	C-N-CA	7.71	134.02	122.92
1	A	271	THR	N-CA-C	-7.61	104.00	113.28
1	A	39	TRP	CA-C-N	7.58	129.32	119.84
1	A	39	TRP	C-N-CA	7.58	129.32	119.84
1	A	228	ILE	O-C-N	-7.44	112.02	121.84
1	B	35	ASN	N-CA-C	7.42	121.25	111.75
1	B	271	THR	N-CA-C	-7.19	104.48	113.18
1	B	31	GLU	N-CA-C	-7.15	101.88	108.75
1	B	440	ASP	CA-C-N	7.08	127.13	119.90
1	B	440	ASP	C-N-CA	7.08	127.13	119.90
1	B	500	GLN	N-CA-C	6.66	124.53	109.81
1	B	602	ASN	CA-C-N	6.51	126.44	119.28
1	B	602	ASN	C-N-CA	6.51	126.44	119.28
1	A	716	ALA	N-CA-C	6.48	121.26	113.23
1	A	400	HIS	CA-C-N	6.39	126.88	119.47
1	A	400	HIS	C-N-CA	6.39	126.88	119.47
1	B	364	ILE	CA-C-N	6.35	126.30	119.76
1	B	364	ILE	C-N-CA	6.35	126.30	119.76
1	B	590	LYS	N-CA-C	-6.27	105.38	113.16
1	B	341	TRP	N-CA-C	6.26	119.67	109.59
1	B	581	VAL	N-CA-C	6.15	116.82	110.36
1	A	321	TRP	N-CA-C	5.87	118.15	111.11
1	A	440	ASP	CA-C-N	5.75	125.77	119.90
1	A	440	ASP	C-N-CA	5.75	125.77	119.90
1	B	648	GLU	N-CA-C	-5.66	106.54	113.50
1	B	387	ASP	CA-C-N	5.64	126.89	119.84
1	B	387	ASP	C-N-CA	5.64	126.89	119.84
1	B	641	LEU	CA-C-N	5.62	125.71	119.87
1	B	641	LEU	C-N-CA	5.62	125.71	119.87
1	A	652	SER	N-CA-C	5.57	118.04	109.07
1	B	287	GLU	CA-C-N	5.55	126.78	119.84
1	B	287	GLU	C-N-CA	5.55	126.78	119.84
1	A	273	GLY	N-CA-C	5.52	122.28	112.02
1	A	71	ILE	N-CA-C	5.51	117.57	109.63
1	B	71	ILE	N-CA-C	5.42	116.58	109.21
1	A	387	ASP	CA-C-N	5.38	124.83	119.24
1	A	387	ASP	C-N-CA	5.38	124.83	119.24
1	B	177	GLY	N-CA-C	5.29	122.05	114.64
1	B	291	ALA	CA-C-N	5.29	125.22	119.78

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	291	ALA	C-N-CA	5.29	125.22	119.78
1	A	696	LEU	N-CA-C	5.28	117.94	111.82
1	A	331	SER	N-CA-C	5.14	116.88	111.28
1	B	673	ALA	N-CA-C	-5.14	101.75	109.15
1	A	229	TYR	O-C-N	-5.06	115.86	122.59
1	A	285	GLY	CA-C-N	5.06	124.96	119.85
1	A	285	GLY	C-N-CA	5.06	124.96	119.85
1	A	364	ILE	CA-C-N	5.04	124.94	119.85
1	A	364	ILE	C-N-CA	5.04	124.94	119.85
1	A	736	ARG	N-CA-C	5.04	118.51	110.70
1	A	685	GLY	N-CA-C	-5.01	108.17	115.63

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	228	ILE	Mainchain
1	B	228	ILE	Mainchain

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	5529	0	5353	189	0
1	B	5529	0	5353	218	0
2	A	43	0	30	1	0
2	B	43	0	30	4	0
3	A	18	0	12	1	0
3	B	18	0	12	0	0
4	A	381	0	0	18	0
4	B	322	0	0	30	0
All	All	11883	0	10790	401	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 18.

All (401) 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:51:ASN:HD21	1:A:190:GLN:HB3	1.28	0.98
1:A:366:ASP:HB3	1:A:370:GLY:HA2	1.51	0.93
1:B:51:ASN:HD21	1:B:190:GLN:HB3	1.38	0.88
1:A:253:ARG:HB3	1:A:253:ARG:HH11	1.36	0.88
1:A:450:VAL:HG13	1:A:454:GLU:HB2	1.56	0.88
1:A:443:PRO:HB2	1:A:572:THR:HG21	1.54	0.88
1:A:166:VAL:HG22	1:A:416:ILE:HD13	1.56	0.87
1:A:450:VAL:HG12	1:A:455:ILE:HG13	1.58	0.85
1:A:257:MET:HE3	1:A:265:LEU:HD11	1.57	0.85
1:A:50:GLN:NE2	1:A:195:GLU:HG2	1.90	0.85
1:B:115:ILE:HG23	1:B:586:VAL:HG11	1.59	0.84
1:B:119:ARG:HH21	1:B:615:ASN:ND2	1.76	0.83
1:B:310:LYS:HD3	1:B:310:LYS:H	1.41	0.83
1:A:43:LEU:H	3:A:1195:GOL:H12	1.44	0.81
1:A:51:ASN:ND2	1:A:190:GLN:HB3	1.95	0.81
1:A:499:LEU:O	1:A:503:VAL:HG23	1.82	0.80
1:B:92:PRO:HD2	1:B:308:THR:HG22	1.64	0.79
1:A:575:SER:OG	1:A:578:GLN:HG3	1.82	0.79
1:A:370:GLY:H	1:A:371:PRO:HD3	1.44	0.79
1:B:342:GLU:HG3	1:B:356:LYS:HG2	1.66	0.77
1:B:166:VAL:HG22	1:B:416:ILE:HD13	1.67	0.77
1:A:498:ARG:HG2	1:A:498:ARG:HH11	1.50	0.76
1:B:500:GLN:HB3	1:B:501:PRO:HD3	1.67	0.75
1:A:129:PHE:HB3	1:A:193:PRO:HG3	1.69	0.75
1:A:450:VAL:HG13	1:A:454:GLU:CB	2.18	0.74
1:B:610:LEU:HD22	1:B:694:VAL:HG13	1.69	0.74
1:B:499:LEU:O	1:B:503:VAL:HG23	1.88	0.72
1:A:50:GLN:HE21	1:A:195:GLU:HG2	1.50	0.72
1:A:557:LYS:HA	4:A:1820:HOH:O	1.89	0.72
1:B:68:VAL:O	1:B:71:ILE:HG22	1.90	0.72
1:A:330:ASN:O	1:A:334:GLU:HG3	1.89	0.71
1:B:51:ASN:HD21	1:B:190:GLN:CB	2.03	0.71
1:A:166:VAL:HG21	1:A:416:ILE:HG23	1.71	0.71
1:B:621:ALA:HB3	1:B:622:PRO:HD3	1.71	0.71
1:A:253:ARG:HB3	1:A:253:ARG:NH1	2.04	0.71
1:B:559:ALA:HB2	1:B:652:SER:OG	1.90	0.71
1:B:308:THR:HG22	1:B:309:GLY:H	1.56	0.70
1:B:557:LYS:C	1:B:559:ALA:H	2.00	0.70
1:B:442:VAL:HG22	1:B:572:THR:OG1	1.92	0.70
1:A:363:THR:HG21	4:A:1513:HOH:O	1.91	0.70
1:A:696:LEU:HG	1:B:296:MET:HE1	1.73	0.69
1:A:519:ARG:HD2	4:A:1822:HOH:O	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:ASP:OD1	1:A:511:ASP:HB3	1.92	0.69
1:A:519:ARG:O	1:A:523:GLU:HG3	1.92	0.69
1:B:412:TRP:CZ2	1:B:416:ILE:HD11	2.28	0.68
1:A:718:PRO:HG2	4:A:1515:HOH:O	1.92	0.68
1:A:412:TRP:CZ2	1:A:416:ILE:HD11	2.29	0.68
1:A:604:LEU:HB2	1:A:609:MET:HE3	1.75	0.68
1:B:24:GLY:HA3	4:B:2307:HOH:O	1.93	0.68
1:B:420:MET:HA	1:B:420:MET:HE2	1.73	0.68
1:B:119:ARG:HH21	1:B:615:ASN:HD22	1.39	0.68
1:A:324:THR:HG21	1:A:329:ASP:OD2	1.94	0.68
1:B:450:VAL:HG13	1:B:454:GLU:HB2	1.75	0.68
1:A:239:PRO:O	1:A:241:PRO:HD3	1.94	0.68
1:B:450:VAL:HG13	1:B:454:GLU:CB	2.25	0.68
1:B:187:ARG:HG2	1:B:420:MET:HE1	1.76	0.67
1:A:450:VAL:CG1	1:A:455:ILE:HG13	2.24	0.67
1:B:116:HIS:CD2	1:B:219:PRO:HB3	2.29	0.67
1:B:51:ASN:ND2	1:B:190:GLN:HB3	2.08	0.67
1:B:69:ALA:HB2	4:B:2421:HOH:O	1.93	0.67
1:B:549:CYS:O	1:B:553:GLU:HG3	1.94	0.67
1:B:166:VAL:HG21	1:B:416:ILE:HG23	1.77	0.66
1:B:308:THR:HG22	1:B:309:GLY:N	2.12	0.65
1:B:91:TRP:HA	1:B:308:THR:CG2	2.26	0.65
1:B:644:GLY:HA3	1:B:695:ASP:OD1	1.96	0.65
1:B:451:GLY:O	1:B:455:ILE:HG13	1.97	0.65
1:A:503:VAL:O	1:A:510:PRO:HG3	1.98	0.64
1:B:310:LYS:H	1:B:310:LYS:CD	2.03	0.63
1:A:187:ARG:HG2	1:A:420:MET:HE3	1.81	0.63
1:B:64:TYR:O	1:B:68:VAL:HG23	1.97	0.63
1:B:91:TRP:HA	1:B:308:THR:HG21	1.79	0.63
1:B:129:PHE:HB3	1:B:193:PRO:HG3	1.78	0.63
1:B:468:THR:OG1	1:B:471:GLN:HG3	1.99	0.63
1:B:533:PRO:HD3	4:B:2491:HOH:O	1.98	0.62
1:B:557:LYS:HG3	4:B:2256:HOH:O	1.98	0.62
1:A:469:VAL:HG21	1:A:651:GLU:HG3	1.81	0.62
1:B:92:PRO:HD2	1:B:308:THR:CG2	2.29	0.62
1:B:253:ARG:HB3	1:B:253:ARG:NH1	2.14	0.62
1:A:675:ASP:CG	1:A:676:GLY:H	2.06	0.62
1:A:676:GLY:O	1:A:692:SER:HA	1.99	0.62
1:B:472:LEU:HB2	1:B:551:ALA:HB2	1.82	0.61
1:A:510:PRO:O	1:A:512:GLY:N	2.34	0.61
1:B:310:LYS:HD3	1:B:310:LYS:N	2.13	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:688:LYS:HE3	1:B:689:TRP:CZ2	2.36	0.61
1:B:498:ARG:HG2	1:B:498:ARG:HH11	1.66	0.61
1:A:346:SER:HB3	1:A:352:GLN:OE1	2.01	0.60
1:B:214:ARG:N	4:B:2203:HOH:O	2.32	0.60
1:B:604:LEU:HB2	1:B:609:MET:HE3	1.83	0.60
1:A:443:PRO:HB2	1:A:572:THR:CG2	2.30	0.60
1:A:119:ARG:HH21	1:A:615:ASN:ND2	2.00	0.60
1:B:666:ILE:HD13	1:B:689:TRP:CD1	2.36	0.60
1:B:91:TRP:CE3	1:B:308:THR:HG23	2.36	0.60
1:A:572:THR:HG22	1:A:573:ASP:N	2.17	0.60
1:B:119:ARG:NH2	1:B:615:ASN:HD22	1.99	0.59
1:A:139:ALA:HA	1:A:300:TRP:CH2	2.38	0.59
1:B:50:GLN:HE21	1:B:195:GLU:HG2	1.67	0.59
1:B:111:GLY:O	1:B:255:MET:HE1	2.02	0.59
1:B:50:GLN:NE2	1:B:195:GLU:HG2	2.18	0.59
1:B:224:GLN:HB2	1:B:227:LEU:HD12	1.83	0.59
1:B:239:PRO:O	1:B:241:PRO:HD3	2.03	0.59
1:B:520:THR:O	1:B:524:ILE:HG13	2.02	0.59
1:A:561:HIS:HE2	1:A:717:GLN:HG2	1.67	0.59
1:B:269:GLY:HA3	2:B:1500:HEM:HAC	1.83	0.59
1:A:535:ASN:ND2	4:A:1608:HOH:O	2.35	0.58
1:B:450:VAL:HG12	1:B:455:ILE:HG13	1.85	0.58
1:B:39:TRP:O	1:B:42:ARG:HB2	2.02	0.58
1:B:448:ASP:OD2	1:B:535:ASN:HB3	2.04	0.58
1:A:207:ASP:OD2	1:A:207:ASP:C	2.47	0.58
1:A:715:ASP:OD2	1:B:157:LYS:HG2	2.04	0.58
1:B:459:LYS:HG2	1:B:550:ALA:HB2	1.85	0.58
1:A:416:ILE:O	1:A:416:ILE:HG22	2.02	0.57
1:A:442:VAL:CG1	1:A:572:THR:HB	2.34	0.57
1:A:402:GLU:HG2	1:A:403:GLU:N	2.19	0.57
1:A:621:ALA:HB3	1:A:622:PRO:HD3	1.85	0.57
1:A:105:MET:HE3	1:A:165:ILE:O	2.03	0.57
1:B:323:ASN:OD1	1:B:324:THR:HG23	2.04	0.57
1:B:478:ALA:HB1	1:B:508:ASN:OD1	2.05	0.57
1:B:166:VAL:CG2	1:B:416:ILE:HG23	2.35	0.57
1:A:31:GLU:O	1:A:31:GLU:HG2	2.04	0.57
1:A:366:ASP:CG	1:A:367:PRO:HD2	2.30	0.57
1:A:119:ARG:HH21	1:A:615:ASN:HD22	1.52	0.56
1:A:107:TRP:HB2	2:A:1500:HEM:HBC2	1.87	0.56
1:A:499:LEU:C	1:A:503:VAL:HG23	2.29	0.56
1:B:307:GLY:HA2	4:B:2206:HOH:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:GLU:O	1:B:32:GLY:O	2.22	0.56
1:B:166:VAL:HG13	1:B:183:PHE:HE1	1.71	0.56
1:B:187:ARG:HG2	1:B:420:MET:CE	2.36	0.56
1:A:503:VAL:O	1:A:510:PRO:CG	2.54	0.56
1:B:26:MET:HE3	1:B:38:TRP:CE2	2.41	0.56
1:B:533:PRO:HD2	4:B:2464:HOH:O	2.04	0.56
1:B:467:LEU:HD22	1:B:517:VAL:HG22	1.88	0.56
1:A:562:ASN:N	4:A:1820:HOH:O	2.39	0.56
1:B:248:ILE:HD11	1:B:380:THR:HG22	1.88	0.55
1:B:502:GLN:HG2	1:B:505:TRP:CZ3	2.41	0.55
1:B:125:GLY:O	1:B:128:ARG:HG2	2.05	0.55
1:B:395:ARG:HD3	4:B:2251:HOH:O	2.06	0.55
1:B:260:VAL:HG23	4:B:2359:HOH:O	2.05	0.55
1:B:518:ILE:O	1:B:522:GLU:HG3	2.07	0.55
1:B:623:GLU:O	1:B:626:VAL:HG12	2.07	0.55
1:A:43:LEU:HG	1:A:611:LEU:HD12	1.89	0.55
1:A:278:ALA:HB1	4:A:1648:HOH:O	2.05	0.55
1:B:253:ARG:HB3	1:B:253:ARG:HH11	1.72	0.55
1:A:292:PRO:HD2	1:A:295:GLN:NE2	2.21	0.54
1:A:43:LEU:HG	1:A:611:LEU:CD1	2.38	0.54
1:A:511:ASP:CG	1:A:512:GLY:N	2.64	0.54
1:B:531:ALA:O	1:B:532:ALA:HB2	2.07	0.54
1:B:596:ASN:HB2	1:B:637:ASN:ND2	2.22	0.54
1:A:535:ASN:HA	4:A:1747:HOH:O	2.07	0.54
1:B:31:GLU:O	1:B:32:GLY:C	2.51	0.54
1:A:29:PRO:HA	1:A:33:GLY:HA2	1.88	0.54
1:B:207:ASP:OD2	1:B:207:ASP:C	2.50	0.54
1:A:506:GLU:O	1:A:509:ASP:HB2	2.07	0.54
1:B:293:LEU:O	1:B:296:MET:HE2	2.07	0.54
1:B:213:LYS:HA	4:B:2203:HOH:O	2.08	0.53
1:B:116:HIS:HD2	1:B:219:PRO:HB3	1.70	0.53
1:B:373:ARG:C	4:B:2454:HOH:O	2.51	0.53
1:A:561:HIS:NE2	1:A:717:GLN:HG2	2.23	0.53
1:B:498:ARG:HD3	1:B:540:PHE:CE2	2.43	0.53
1:B:557:LYS:O	1:B:559:ALA:N	2.41	0.53
1:A:620:SER:OG	1:A:623:GLU:HG3	2.09	0.53
1:B:126:MET:HE3	1:B:194:ASP:OD2	2.08	0.53
1:B:620:SER:OG	1:B:623:GLU:HG3	2.09	0.53
1:A:553:GLU:HG2	1:A:565:VAL:HG23	1.90	0.53
1:B:630:GLY:O	1:B:633:VAL:HG22	2.08	0.53
1:A:355:ALA:HB2	1:A:375:PRO:HG2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:370:GLY:H	1:A:371:PRO:CD	2.19	0.52
1:B:673:ALA:O	1:B:675:ASP:N	2.38	0.52
1:B:694:VAL:O	1:B:697:VAL:HG12	2.08	0.52
1:B:340:GLU:HB3	1:B:356:LYS:HD2	1.90	0.52
1:A:49:HIS:O	1:A:49:HIS:CD2	2.62	0.52
1:B:287:GLU:HB2	1:B:288:PRO:HD2	1.91	0.52
1:B:557:LYS:C	1:B:559:ALA:N	2.67	0.52
1:B:354:THR:HG22	1:B:355:ALA:N	2.24	0.52
1:A:181:PHE:CE2	1:A:432:PRO:HG2	2.44	0.52
1:A:416:ILE:O	1:A:416:ILE:CG2	2.58	0.52
1:B:345:LYS:HE3	1:B:351:TRP:CE3	2.44	0.52
1:A:443:PRO:HG2	1:A:573:ASP:O	2.10	0.51
1:A:555:ALA:HA	1:A:651:GLU:O	2.10	0.51
1:A:536:ILE:HB	4:A:1831:HOH:O	2.10	0.51
1:A:420:MET:HE2	1:A:425:ARG:HH12	1.76	0.51
1:B:43:LEU:HG	1:B:611:LEU:HD11	1.92	0.51
1:A:534:GLY:N	4:A:1831:HOH:O	2.42	0.51
1:B:224:GLN:HB2	1:B:227:LEU:CD1	2.41	0.51
1:B:342:GLU:HG2	4:B:2258:HOH:O	2.11	0.51
1:B:442:VAL:HG12	4:B:2218:HOH:O	2.11	0.51
1:A:374:SER:HB2	1:A:375:PRO:HD2	1.93	0.50
1:B:502:GLN:HG2	1:B:505:TRP:CH2	2.46	0.50
1:B:668:TRP:HA	1:B:679:GLN:O	2.10	0.50
1:B:210:TYR:OH	1:B:223:VAL:HG12	2.11	0.50
1:B:496:ARG:HB2	4:B:2259:HOH:O	2.11	0.50
1:A:385:ARG:O	1:A:391:GLU:HG3	2.11	0.50
1:B:416:ILE:CG2	1:B:416:ILE:O	2.59	0.50
1:B:604:LEU:HB2	1:B:609:MET:CE	2.41	0.50
1:B:67:GLU:O	1:B:70:THR:HB	2.11	0.50
1:B:180:THR:HB	4:B:2340:HOH:O	2.11	0.50
1:A:324:THR:N	1:A:325:PRO:HD3	2.26	0.50
1:A:469:VAL:CG2	1:A:651:GLU:HG3	2.41	0.50
1:B:115:ILE:HG23	1:B:586:VAL:CG1	2.37	0.50
1:B:533:PRO:O	1:B:535:ASN:N	2.44	0.49
1:B:607:GLU:HG2	1:B:608:TYR:CD1	2.47	0.49
1:B:666:ILE:HD13	1:B:689:TRP:HD1	1.77	0.49
1:A:51:ASN:HD21	1:A:190:GLN:CB	2.11	0.49
1:A:585:ALA:HA	4:A:1697:HOH:O	2.11	0.49
1:B:440:ASP:N	1:B:441:PRO:HD3	2.27	0.49
1:B:500:GLN:O	1:B:501:PRO:C	2.55	0.49
1:A:694:VAL:O	1:A:697:VAL:HG12	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:731:VAL:HA	1:A:734:LEU:HG	1.93	0.49
1:A:125:GLY:O	1:A:128:ARG:HG2	2.13	0.49
1:A:533:PRO:C	4:A:1831:HOH:O	2.56	0.49
1:A:340:GLU:CB	1:A:356:LYS:HD2	2.42	0.49
1:B:458:LEU:O	1:B:462:ILE:HG13	2.12	0.49
1:B:507:VAL:HG22	1:B:597:TYR:CE2	2.47	0.49
1:B:533:PRO:C	1:B:535:ASN:H	2.21	0.49
1:A:510:PRO:O	1:A:511:ASP:C	2.55	0.49
1:A:223:VAL:HG22	1:A:230:VAL:HA	1.94	0.49
1:B:142:ASP:CG	1:B:143:LYS:HZ2	2.21	0.49
1:A:159:LEU:HD21	1:A:164:LEU:HD13	1.94	0.48
1:A:293:LEU:HD13	4:B:2363:HOH:O	2.12	0.48
1:A:549:CYS:O	1:A:553:GLU:HG3	2.12	0.48
1:B:374:SER:N	4:B:2454:HOH:O	2.46	0.48
1:B:263:ALA:O	1:B:267:VAL:HG23	2.13	0.48
1:A:90:TRP:CZ2	1:B:664:MET:HG2	2.48	0.48
1:A:674:ASP:OD2	1:A:675:ASP:O	2.31	0.48
1:A:463:ARG:NH2	1:A:553:GLU:OE1	2.47	0.48
1:B:501:PRO:HG3	1:B:581:VAL:HG13	1.94	0.48
1:A:540:PHE:O	1:A:544:VAL:HG23	2.14	0.48
1:B:450:VAL:HG13	1:B:454:GLU:HB3	1.96	0.48
1:A:33:GLY:HA3	4:B:2294:HOH:O	2.14	0.47
1:A:202:ALA:HB2	1:B:25:HIS:HB2	1.95	0.47
1:B:637:ASN:HB2	4:B:2431:HOH:O	2.13	0.47
1:A:629:GLY:O	1:A:633:VAL:HG22	2.15	0.47
1:B:166:VAL:HG13	1:B:183:PHE:CE1	2.48	0.47
1:B:546:LEU:HD13	1:B:567:PHE:CG	2.49	0.47
1:B:557:LYS:HE3	4:B:2256:HOH:O	2.14	0.47
1:B:630:GLY:HA3	1:B:724:PHE:CE1	2.50	0.47
1:B:510:PRO:O	1:B:512:GLY:N	2.48	0.47
1:A:364:ILE:CD1	1:A:375:PRO:HA	2.45	0.47
1:A:97:HIS:CE1	1:A:99:GLY:HA3	2.49	0.47
1:A:113:TYR:O	1:A:255:MET:HG2	2.14	0.47
1:B:116:HIS:HB3	1:B:219:PRO:CB	2.45	0.47
1:B:526:GLU:O	1:B:527:SER:C	2.57	0.47
1:A:157:LYS:HG2	1:B:715:ASP:OD2	2.14	0.47
1:B:507:VAL:HG21	1:B:589:PRO:HB2	1.97	0.47
1:A:251:THR:O	1:A:255:MET:HG3	2.15	0.47
1:A:420:MET:O	1:A:425:ARG:HD3	2.15	0.47
1:B:118:GLY:O	1:B:486:SER:HB2	2.15	0.47
1:B:192:GLU:HG2	4:B:2512:HOH:O	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:TRP:CG	1:A:588:GLU:HG3	2.50	0.47
1:B:373:ARG:O	4:B:2242:HOH:O	2.21	0.47
1:B:540:PHE:HB3	1:B:573:ASP:OD1	2.14	0.47
1:A:323:ASN:C	1:A:325:PRO:HD3	2.40	0.47
1:A:420:MET:HE2	1:A:425:ARG:NH1	2.30	0.47
1:B:260:VAL:HG22	1:B:393:ILE:HD12	1.97	0.47
1:B:450:VAL:HG23	4:B:2357:HOH:O	2.13	0.47
1:A:345:LYS:HE3	1:A:351:TRP:CE3	2.50	0.46
1:B:497:ILE:O	1:B:503:VAL:HG22	2.16	0.46
1:A:49:HIS:O	1:A:49:HIS:HD2	1.97	0.46
1:A:166:VAL:CG2	1:A:416:ILE:HG23	2.42	0.46
1:A:368:PHE:O	1:A:369:GLY:O	2.33	0.46
1:B:389:ILE:O	1:B:393:ILE:HG12	2.14	0.46
1:A:355:ALA:CB	1:A:375:PRO:HG2	2.45	0.46
1:B:465:SER:OG	1:B:466:GLY:N	2.48	0.46
1:A:42:ARG:NH1	4:A:1845:HOH:O	2.49	0.46
1:A:620:SER:HG	1:A:623:GLU:HG3	1.81	0.46
1:A:675:ASP:CG	1:A:676:GLY:N	2.74	0.46
1:B:416:ILE:O	1:B:416:ILE:HG22	2.14	0.46
1:B:223:VAL:HG22	1:B:230:VAL:HA	1.97	0.46
1:B:257:MET:HE1	1:B:414:LYS:HD3	1.97	0.46
1:B:343:LEU:HD13	1:B:353:TYR:CZ	2.50	0.46
1:A:498:ARG:HH11	1:A:498:ARG:CG	2.22	0.46
1:B:31:GLU:HG2	1:B:32:GLY:H	1.81	0.46
1:A:93:ALA:HB2	1:A:98:TYR:CZ	2.50	0.46
1:B:373:ARG:N	4:B:2454:HOH:O	2.48	0.46
1:A:116:HIS:ND1	1:A:219:PRO:HB3	2.31	0.46
1:A:181:PHE:CD2	1:A:432:PRO:HG2	2.51	0.46
1:B:314:THR:HB	2:B:1500:HEM:O1A	2.16	0.46
1:A:459:LYS:O	1:A:463:ARG:HG3	2.15	0.46
1:A:108:HIS:HE1	1:A:137:ASP:O	1.99	0.45
1:B:373:ARG:NH2	4:B:2479:HOH:O	2.46	0.45
1:A:223:VAL:O	1:A:224:GLN:HG3	2.16	0.45
1:A:610:LEU:HD22	1:A:694:VAL:HG13	1.99	0.45
1:A:675:ASP:C	1:A:677:THR:H	2.24	0.45
1:A:253:ARG:HH11	1:A:253:ARG:CB	2.20	0.45
1:B:218:ASN:ND2	4:B:2224:HOH:O	2.49	0.45
1:B:262:THR:O	1:B:266:ILE:HG13	2.17	0.45
1:A:97:HIS:ND1	1:A:99:GLY:N	2.60	0.45
1:B:118:GLY:C	1:B:486:SER:HB2	2.41	0.45
1:A:73:VAL:HG11	1:A:430:LEU:HD11	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:108:HIS:CE1	1:A:137:ASP:O	2.70	0.45
1:B:38:TRP:HB2	1:B:39:TRP:CE3	2.52	0.45
1:A:434:GLN:H	1:A:434:GLN:NE2	2.16	0.45
1:A:728:TRP:O	1:A:732:MET:HG2	2.17	0.45
1:B:533:PRO:HB2	4:B:2464:HOH:O	2.18	0.44
1:B:130:ALA:O	1:B:193:PRO:HB3	2.17	0.44
1:B:423:VAL:HA	1:B:426:TYR:CD1	2.53	0.44
1:B:500:GLN:HB3	1:B:501:PRO:CD	2.41	0.44
1:A:108:HIS:CD2	1:A:228:ILE:HG13	2.53	0.44
1:A:572:THR:HG23	4:A:1581:HOH:O	2.17	0.44
1:A:250:GLU:OE2	1:A:253:ARG:NH1	2.50	0.44
1:A:134:SER:HB3	1:A:287:GLU:HG3	1.99	0.44
1:A:455:ILE:O	1:A:459:LYS:HG3	2.17	0.44
1:B:166:VAL:HG22	1:B:416:ILE:CD1	2.42	0.44
1:B:181:PHE:CE2	1:B:432:PRO:HG2	2.52	0.44
1:B:235:PRO:HG3	1:B:247:ASP:OD2	2.17	0.44
1:A:609:MET:HE2	1:A:609:MET:HA	2.00	0.44
1:B:473:VAL:HG23	1:B:551:ALA:CB	2.48	0.44
1:B:498:ARG:NH2	4:B:2343:HOH:O	2.51	0.44
1:B:330:ASN:O	1:B:334:GLU:HG3	2.18	0.43
1:B:704:LEU:O	1:B:708:VAL:HG23	2.18	0.43
1:A:139:ALA:HA	1:A:300:TRP:CZ3	2.53	0.43
1:A:258:ASN:HB2	4:A:1550:HOH:O	2.17	0.43
1:A:646:PHE:HA	1:A:689:TRP:CZ3	2.53	0.43
1:A:340:GLU:HB2	1:A:356:LYS:HD2	2.01	0.43
1:A:344:THR:HG21	1:A:354:THR:OG1	2.18	0.43
1:A:650:SER:C	1:A:652:SER:N	2.76	0.43
1:B:105:MET:HE1	1:B:148:LEU:HD11	1.99	0.43
1:B:363:THR:HG21	4:B:2197:HOH:O	2.17	0.43
1:A:64:TYR:O	1:A:68:VAL:HG23	2.18	0.43
1:B:469:VAL:HG13	1:B:551:ALA:HB1	2.00	0.43
1:B:672:PRO:HD2	1:B:679:GLN:HE21	1.83	0.43
1:B:731:VAL:HA	1:B:734:LEU:HG	2.01	0.43
1:B:238:ASN:C	1:B:238:ASN:HD22	2.25	0.43
1:B:362:GLY:HA2	1:B:372:GLY:C	2.44	0.43
1:A:93:ALA:HB2	1:A:98:TYR:CE1	2.54	0.43
1:A:648:GLU:HB2	4:A:1587:HOH:O	2.18	0.43
1:B:504:GLY:O	1:B:510:PRO:HG2	2.19	0.43
1:B:681:LYS:HA	1:B:686:LYS:O	2.18	0.43
1:A:364:ILE:HD12	1:A:375:PRO:HA	2.00	0.43
1:A:663:ASP:OD2	1:A:666:ILE:HD13	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:GLY:HA2	1:B:36:GLN:CD	2.44	0.42
1:A:187:ARG:HG2	1:A:420:MET:CE	2.47	0.42
1:A:423:VAL:HA	1:A:426:TYR:CD1	2.54	0.42
1:A:721:VAL:O	1:A:725:VAL:HG23	2.19	0.42
1:B:423:VAL:HA	1:B:426:TYR:CE1	2.54	0.42
1:A:174:GLU:HA	1:A:178:PHE:O	2.19	0.42
1:A:572:THR:CG2	1:A:573:ASP:N	2.82	0.42
1:A:418:ARG:HD2	1:A:418:ARG:HA	1.84	0.42
1:B:210:TYR:CZ	1:B:216:LEU:HD13	2.54	0.42
1:B:275:THR:HG22	2:B:1500:HEM:HAA1	2.01	0.42
1:A:39:TRP:O	1:A:42:ARG:HB2	2.20	0.42
1:A:316:GLY:O	1:A:348:ALA:HB3	2.19	0.42
1:B:116:HIS:HB3	1:B:219:PRO:HB2	2.01	0.42
1:B:209:ARG:HD2	1:B:223:VAL:O	2.19	0.42
1:B:268:GLY:O	1:B:271:THR:HB	2.19	0.42
1:B:324:THR:N	1:B:325:PRO:HD3	2.35	0.42
1:B:501:PRO:HD3	1:B:581:VAL:HG22	2.01	0.42
1:A:166:VAL:HG13	1:A:183:PHE:HE1	1.85	0.42
1:B:27:LYS:HG2	4:B:2505:HOH:O	2.18	0.42
1:B:425:ARG:HD2	1:B:737:PHE:CD2	2.55	0.42
1:B:536:ILE:O	1:B:536:ILE:HG22	2.20	0.42
1:A:717:GLN:HE21	1:A:717:GLN:HB2	1.58	0.42
1:B:546:LEU:HD13	1:B:567:PHE:CD2	2.55	0.42
1:A:239:PRO:HG3	1:A:351:TRP:CD1	2.54	0.42
1:A:139:ALA:O	1:A:140:SER:HB2	2.20	0.42
1:A:572:THR:HG22	1:A:573:ASP:H	1.84	0.42
1:A:641:LEU:HA	1:A:642:PRO:HD3	1.86	0.42
1:A:645:VAL:O	1:A:645:VAL:HG12	2.20	0.42
1:B:251:THR:O	1:B:255:MET:HG3	2.20	0.42
1:B:503:VAL:O	1:B:503:VAL:HG12	2.20	0.42
1:B:553:GLU:OE2	1:B:564:THR:HA	2.19	0.42
1:A:250:GLU:CD	1:A:253:ARG:NH1	2.78	0.41
1:A:340:GLU:HB3	1:A:356:LYS:HD2	2.00	0.41
1:A:623:GLU:O	1:A:626:VAL:HG12	2.20	0.41
1:A:666:ILE:HG12	1:A:689:TRP:CD1	2.55	0.41
1:A:34:GLY:O	1:A:36:GLN:N	2.53	0.41
1:A:604:LEU:HB3	1:A:605:PRO:CD	2.50	0.41
1:B:51:ASN:ND2	1:B:190:GLN:OE1	2.51	0.41
1:A:77:THR:O	1:A:81:GLU:HG3	2.20	0.41
1:A:532:ALA:HA	1:A:533:PRO:HD3	1.85	0.41
1:A:650:SER:C	1:A:652:SER:H	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:666:ILE:HD11	1:A:688:LYS:HE2	2.01	0.41
1:B:533:PRO:C	1:B:535:ASN:N	2.77	0.41
1:B:641:LEU:HA	1:B:642:PRO:HD3	1.78	0.41
1:A:274:LYS:HB2	1:A:320:VAL:HG22	2.02	0.41
1:B:498:ARG:C	1:B:503:VAL:CG2	2.93	0.41
1:B:673:ALA:O	1:B:675:ASP:OD1	2.38	0.41
1:A:575:SER:HG	1:A:578:GLN:HG3	1.81	0.41
1:B:280:PRO:HB2	1:B:282:ASP:OD1	2.19	0.41
1:B:505:TRP:CE2	1:B:588:GLU:HB2	2.55	0.41
1:B:646:PHE:HB2	1:B:657:PHE:HA	2.03	0.41
1:B:661:LEU:HD23	1:B:708:VAL:HG11	2.02	0.41
1:A:718:PRO:O	1:A:722:GLN:HG3	2.21	0.41
1:B:387:ASP:HA	1:B:388:PRO:HD3	1.91	0.41
1:B:672:PRO:HD2	1:B:679:GLN:NE2	2.36	0.41
1:B:275:THR:HA	2:B:1500:HEM:HAA1	2.02	0.41
1:A:141:LEU:O	1:A:145:ARG:HG3	2.20	0.41
1:A:310:LYS:HG2	4:A:1514:HOH:O	2.20	0.41
1:A:414:LYS:HA	1:A:438:TRP:CZ2	2.56	0.41
1:A:533:PRO:HB2	4:A:1831:HOH:O	2.20	0.41
1:B:204:TRP:O	1:B:205:LEU:HB2	2.20	0.41
1:B:84:MET:SD	1:B:172:ALA:HA	2.61	0.41
1:B:612:ASP:O	1:B:615:ASN:HB3	2.21	0.41
1:B:638:TYR:O	1:B:641:LEU:HG	2.21	0.40
1:A:210:TYR:CZ	1:A:216:LEU:HD13	2.56	0.40
1:B:117:ASP:OD2	1:B:119:ARG:HD2	2.21	0.40
1:B:473:VAL:HG23	1:B:551:ALA:HB3	2.03	0.40
1:A:238:ASN:C	1:A:240:ASP:H	2.30	0.40
1:A:498:ARG:HG2	1:A:498:ARG:NH1	2.28	0.40
1:B:139:ALA:O	1:B:140:SER:HB2	2.21	0.40
1:B:464:ALA:O	1:B:465:SER:C	2.65	0.40
1:B:353:TYR:O	1:B:376:THR:HA	2.21	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	715/743 (96%)	663 (93%)	39 (6%)	13 (2%)	6	8
1	B	715/743 (96%)	656 (92%)	45 (6%)	14 (2%)	6	7
All	All	1430/1486 (96%)	1319 (92%)	84 (6%)	27 (2%)	6	7

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	511	ASP
1	A	533	PRO
1	B	32	GLY
1	B	229	TYR
1	B	500	GLN
1	B	532	ALA
1	B	533	PRO
1	B	650	SER
1	A	369	GLY
1	A	673	ALA
1	B	511	ASP
1	B	534	GLY
1	B	558	ALA
1	A	370	GLY
1	A	509	ASP
1	A	513	ASP
1	A	95	TYR
1	A	239	PRO
1	A	362	GLY
1	A	486	SER
1	B	309	GLY
1	B	674	ASP
1	A	220	LEU
1	B	501	PRO
1	B	239	PRO
1	B	362	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	565/587 (96%)	548 (97%)	17 (3%)	36	56
1	B	565/587 (96%)	552 (98%)	13 (2%)	44	64
All	All	1130/1174 (96%)	1100 (97%)	30 (3%)	39	60

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	VAL
1	A	166	VAL
1	A	253	ARG
1	A	282	ASP
1	A	330	ASN
1	A	391	GLU
1	A	420	MET
1	A	501	PRO
1	A	503	VAL
1	A	507	VAL
1	A	513	ASP
1	A	543	LEU
1	A	598	LEU
1	A	627	LEU
1	A	648	GLU
1	A	651	GLU
1	A	717	GLN
1	B	68	VAL
1	B	107	TRP
1	B	115	ILE
1	B	137	ASP
1	B	166	VAL
1	B	310	LYS
1	B	330	ASN
1	B	374	SER
1	B	391	GLU
1	B	536	ILE
1	B	543	LEU
1	B	598	LEU
1	B	627	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	25	HIS
1	A	50	GLN
1	A	51	ASN
1	A	190	GLN
1	A	218	ASN
1	A	238	ASN
1	A	295	GLN
1	A	330	ASN
1	A	434	GLN
1	A	615	ASN
1	A	679	GLN
1	A	717	GLN
1	A	733	ASN
1	B	36	GLN
1	B	49	HIS
1	B	51	ASN
1	B	88	GLN
1	B	116	HIS
1	B	190	GLN
1	B	238	ASN
1	B	330	ASN
1	B	461	GLN
1	B	596	ASN
1	B	602	ASN
1	B	615	ASN
1	B	679	GLN
1	B	722	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 oligosaccharides in this entry.

5.6 Ligand geometry

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
3	GOL	A	1195	-	5,5,5	4.79	5 (100%)	5,5,5	6.15	3 (60%)
3	GOL	B	2196	-	5,5,5	4.63	5 (100%)	5,5,5	6.13	3 (60%)
3	GOL	B	2194	-	5,5,5	4.82	5 (100%)	5,5,5	6.08	3 (60%)
3	GOL	B	2195	-	5,5,5	4.74	5 (100%)	5,5,5	6.10	3 (60%)
3	GOL	A	1196	-	5,5,5	4.73	5 (100%)	5,5,5	6.16	3 (60%)
2	HEM	B	1500	1	50,50,50	1.36	6 (12%)	67,82,82	0.78	3 (4%)
3	GOL	A	1194	-	5,5,5	4.76	5 (100%)	5,5,5	6.12	3 (60%)
2	HEM	A	1500	1	50,50,50	1.34	5 (10%)	67,82,82	0.83	3 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	1195	-	-	2/4/4/4	-
3	GOL	B	2196	-	-	2/4/4/4	-
3	GOL	B	2194	-	-	3/4/4/4	-
3	GOL	B	2195	-	-	2/4/4/4	-
3	GOL	A	1196	-	-	2/4/4/4	-
2	HEM	B	1500	1	-	8/14/54/54	-
3	GOL	A	1194	-	-	3/4/4/4	-
2	HEM	A	1500	1	-	6/14/54/54	-

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2194	GOL	C3-C2	-8.44	1.19	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1194	GOL	C3-C2	-8.10	1.20	1.51
3	A	1195	GOL	C3-C2	-8.04	1.21	1.51
3	B	2195	GOL	C3-C2	-8.00	1.21	1.51
3	A	1196	GOL	C3-C2	-7.95	1.21	1.51
3	B	2196	GOL	C3-C2	-7.85	1.21	1.51
3	A	1195	GOL	O1-C1	4.94	1.63	1.42
3	A	1196	GOL	O1-C1	4.72	1.62	1.42
3	B	2196	GOL	O1-C1	4.52	1.61	1.42
3	B	2195	GOL	O1-C1	4.48	1.61	1.42
2	A	1500	HEM	FE-NB	4.44	2.08	1.94
3	A	1194	GOL	O1-C1	4.34	1.60	1.42
3	B	2194	GOL	O1-C1	4.33	1.60	1.42
2	B	1500	HEM	FE-NB	4.31	2.08	1.94
2	A	1500	HEM	FE-NC	3.69	2.07	1.95
3	A	1196	GOL	O3-C3	3.46	1.57	1.42
2	B	1500	HEM	FE-NC	3.41	2.06	1.95
3	B	2196	GOL	O3-C3	3.41	1.56	1.42
3	B	2195	GOL	O3-C3	3.36	1.56	1.42
3	A	1194	GOL	C1-C2	-3.31	1.39	1.51
3	A	1195	GOL	O3-C3	3.28	1.56	1.42
3	A	1194	GOL	O3-C3	3.28	1.56	1.42
2	B	1500	HEM	FE-NA	3.28	2.06	1.95
2	B	1500	HEM	FE-ND	3.23	2.04	1.94
2	A	1500	HEM	FE-ND	3.10	2.04	1.94
3	B	2194	GOL	C1-C2	-3.08	1.40	1.51
3	B	2194	GOL	O3-C3	3.04	1.55	1.42
3	B	2195	GOL	C1-C2	-3.01	1.40	1.51
2	A	1500	HEM	FE-NA	2.94	2.04	1.95
3	B	2195	GOL	O2-C2	-2.84	1.35	1.43
3	A	1196	GOL	C1-C2	-2.83	1.41	1.51
3	B	2194	GOL	O2-C2	-2.76	1.35	1.43
3	A	1195	GOL	C1-C2	-2.74	1.41	1.51
3	A	1195	GOL	O2-C2	-2.67	1.35	1.43
3	B	2196	GOL	C1-C2	-2.67	1.41	1.51
3	A	1194	GOL	O2-C2	-2.67	1.35	1.43
3	B	2196	GOL	O2-C2	-2.57	1.35	1.43
3	A	1196	GOL	O2-C2	-2.54	1.36	1.43
2	B	1500	HEM	CBD-CGD	2.20	1.55	1.50
2	A	1500	HEM	C4D-ND	-2.19	1.36	1.40
2	B	1500	HEM	C4D-ND	-2.08	1.36	1.40

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1196	GOL	O3-C3-C2	11.31	161.28	110.38
3	A	1195	GOL	O3-C3-C2	11.26	161.06	110.38
3	B	2196	GOL	O3-C3-C2	11.19	160.73	110.38
3	A	1194	GOL	O3-C3-C2	11.09	160.32	110.38
3	B	2195	GOL	O3-C3-C2	11.01	159.95	110.38
3	B	2194	GOL	O3-C3-C2	10.97	159.75	110.38
3	A	1194	GOL	O2-C2-C3	7.26	139.26	109.18
3	B	2195	GOL	O2-C2-C3	7.26	139.23	109.18
3	B	2194	GOL	O2-C2-C3	7.22	139.09	109.18
3	B	2196	GOL	O2-C2-C3	7.07	138.44	109.18
3	A	1195	GOL	O2-C2-C3	7.06	138.43	109.18
3	A	1196	GOL	O2-C2-C3	7.00	138.18	109.18
3	B	2196	GOL	O1-C1-C2	3.47	125.99	110.38
3	A	1196	GOL	O1-C1-C2	3.43	125.81	110.38
3	B	2195	GOL	O1-C1-C2	3.41	125.73	110.38
3	A	1195	GOL	O1-C1-C2	3.39	125.66	110.38
3	B	2194	GOL	O1-C1-C2	3.31	125.26	110.38
3	A	1194	GOL	O1-C1-C2	3.21	124.83	110.38
2	B	1500	HEM	CBD-CAD-C3D	2.56	119.61	112.53
2	B	1500	HEM	CAD-CBD-CGD	-2.33	107.49	113.67
2	A	1500	HEM	CAD-C3D-C4D	2.31	128.73	124.70
2	B	1500	HEM	C4D-ND-C1D	2.22	107.83	105.21
2	A	1500	HEM	C4D-ND-C1D	2.17	107.78	105.21
2	A	1500	HEM	CBD-CAD-C3D	2.16	118.50	112.53

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1500	HEM	C2B-C3B-CAB-CBB
2	A	1500	HEM	C2C-C3C-CAC-CBC
2	B	1500	HEM	C2B-C3B-CAB-CBB
3	A	1194	GOL	C1-C2-C3-O3
3	A	1195	GOL	C1-C2-C3-O3
3	A	1196	GOL	C1-C2-C3-O3
3	B	2194	GOL	C1-C2-C3-O3
3	B	2195	GOL	C1-C2-C3-O3
3	A	1194	GOL	O1-C1-C2-C3
3	B	2194	GOL	O1-C1-C2-C3
3	B	2196	GOL	C1-C2-C3-O3
3	A	1196	GOL	O1-C1-C2-O2
3	B	2195	GOL	O1-C1-C2-O2
3	B	2196	GOL	O1-C1-C2-O2

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Mol	Chain	Res	Type	Atoms
2	A	1500	HEM	C4B-C3B-CAB-CBB
2	B	1500	HEM	C4B-C3B-CAB-CBB
3	A	1195	GOL	O1-C1-C2-O2
3	B	2194	GOL	O1-C1-C2-O2
2	B	1500	HEM	C2C-C3C-CAC-CBC
2	A	1500	HEM	C4C-C3C-CAC-CBC
2	A	1500	HEM	CAA-CBA-CGA-O2A
2	B	1500	HEM	CAA-CBA-CGA-O1A
3	A	1194	GOL	O1-C1-C2-O2
2	B	1500	HEM	CAA-CBA-CGA-O2A
2	A	1500	HEM	CAA-CBA-CGA-O1A
2	B	1500	HEM	C4C-C3C-CAC-CBC
2	B	1500	HEM	CAD-CBD-CGD-O1D
2	B	1500	HEM	CAD-CBD-CGD-O2D

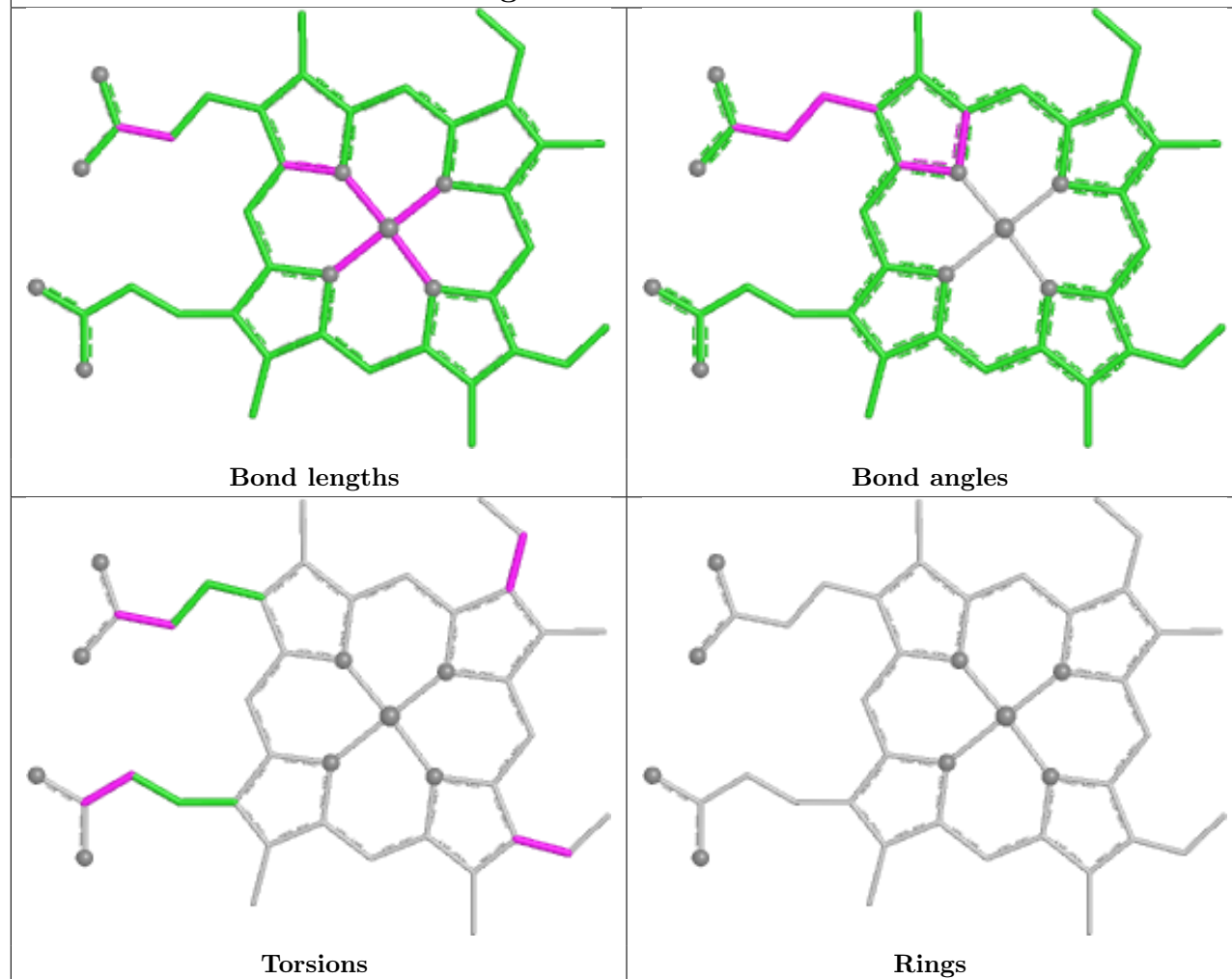
There are no ring outliers.

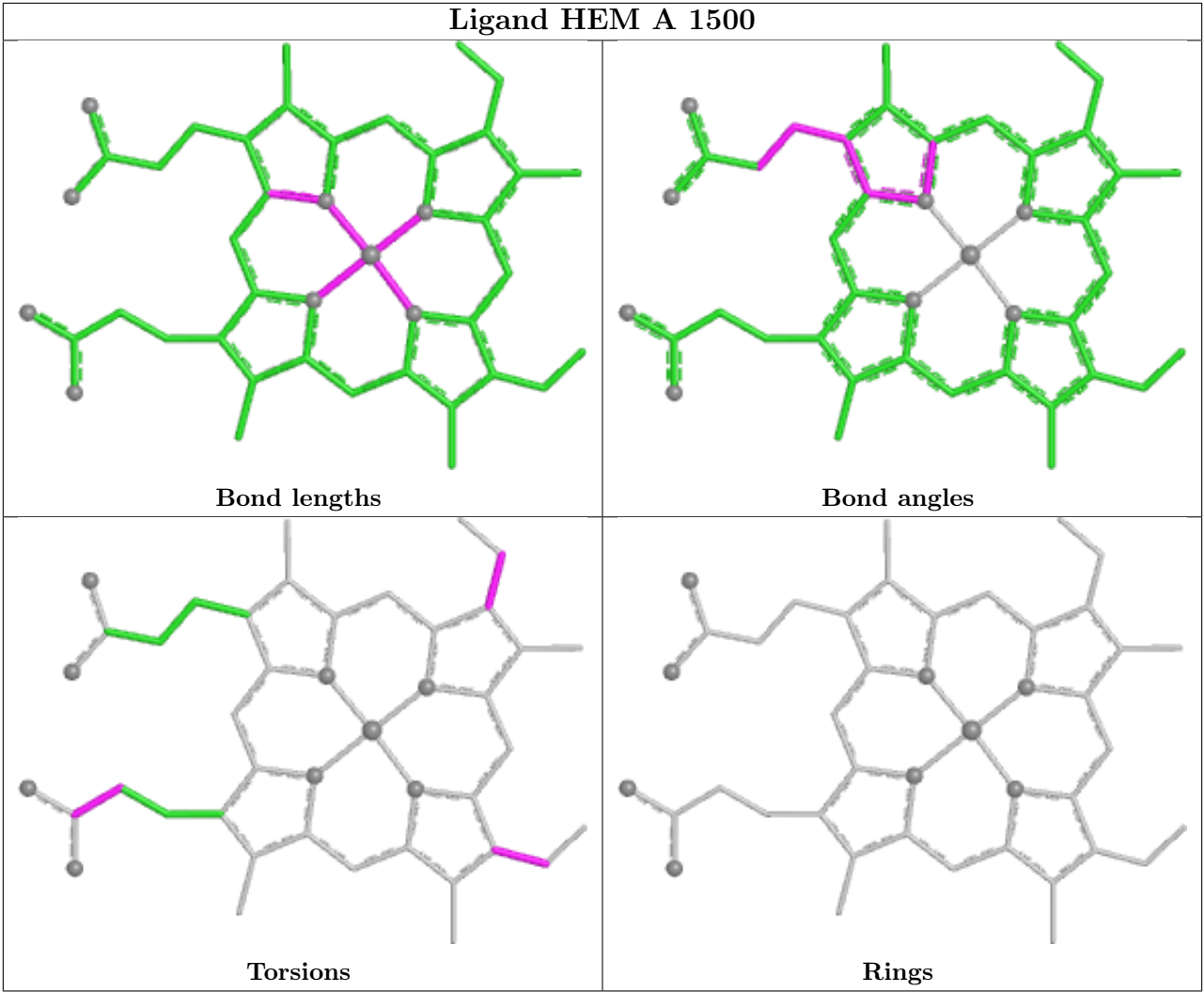
3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1195	GOL	1	0
2	B	1500	HEM	4	0
2	A	1500	HEM	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand HEM B 1500





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	2
1	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	229:TYR	C	230:VAL	N	1.06

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	228:ILE	C	229:TYR	N	1.05
1	B	229:TYR	C	230:VAL	N	1.04
1	B	228:ILE	C	229:TYR	N	0.91

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	717/743 (96%)	-0.29	4 (0%) 85 84	21, 34, 50, 72	0
1	B	717/743 (96%)	-0.09	6 (0%) 82 80	24, 39, 63, 89	0
All	All	1434/1486 (96%)	-0.19	10 (0%) 84 82	21, 36, 59, 89	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	531	ALA	3.4
1	B	673	ALA	3.0
1	B	24	GLY	2.8
1	A	369	GLY	2.6
1	A	510	PRO	2.6
1	B	535	ASN	2.6
1	B	533	PRO	2.5
1	A	676	GLY	2.4
1	B	532	ALA	2.3
1	A	33	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 oligosaccharides in this entry.

6.4 Ligands ⓘ

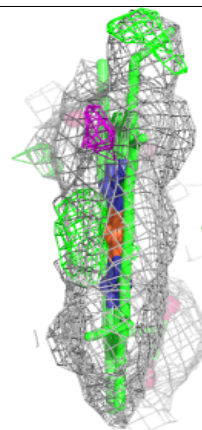
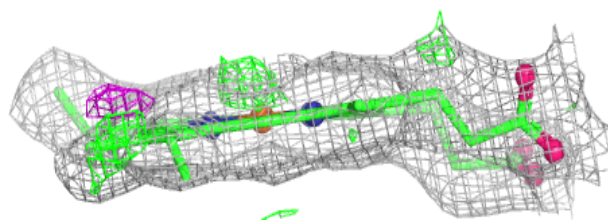
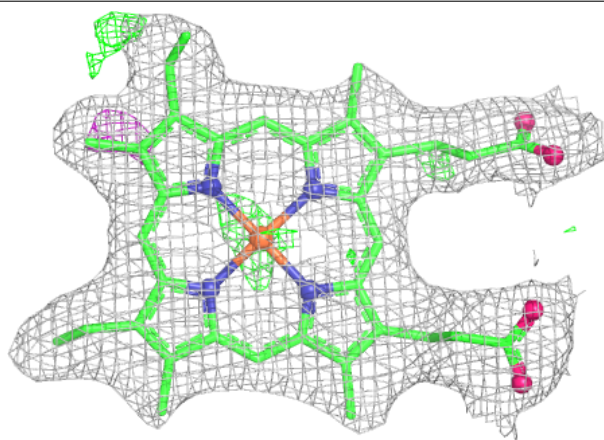
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	GOL	B	2196	6/6	0.75	0.15	49,52,53,53	0
3	GOL	A	1195	6/6	0.79	0.14	38,39,42,42	0
3	GOL	B	2194	6/6	0.89	0.10	27,31,34,38	0
3	GOL	A	1196	6/6	0.90	0.11	48,50,52,52	0
3	GOL	B	2195	6/6	0.92	0.08	41,43,43,44	0
3	GOL	A	1194	6/6	0.96	0.06	31,33,35,35	0
2	HEM	A	1500	43/43	0.96	0.09	24,29,32,34	0
2	HEM	B	1500	43/43	0.96	0.09	25,32,34,39	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

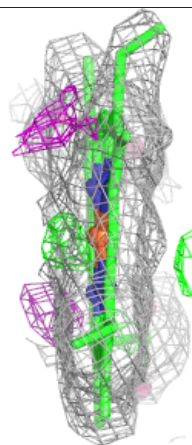
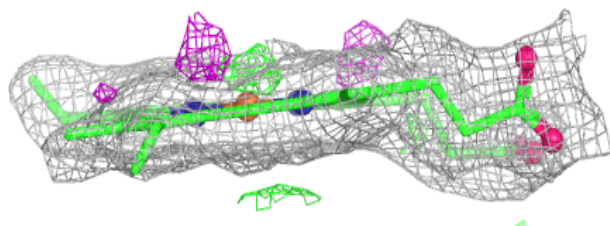
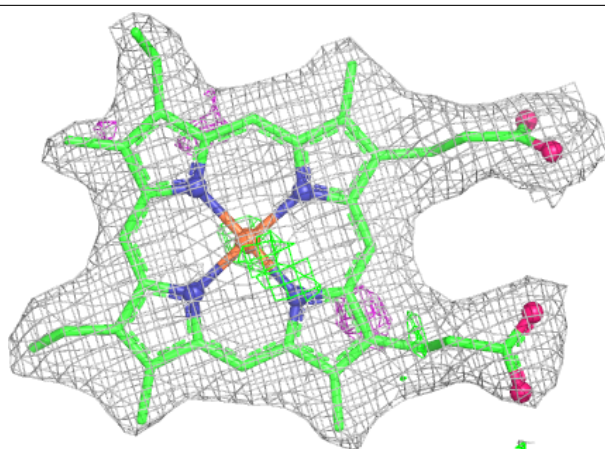
Electron density around HEM A 1500:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around HEM B 1500:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers ⓘ

There are no such residues in this entry.