



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 3, 2026 – 12:09 AM EDT

PDB ID : 5WHQ / pdb_00005whq
Title : Crystal structure of the catalase-peroxidase from *Neurospora crassa* at 2.9 Å
Authors : Diaz-Vilchis, A.; Vega-Garcia, V.; Rudino-Pinera, E.; Hansberg, W.
Deposited on : 2017-07-18
Resolution : 2.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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 : 9.0.015 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

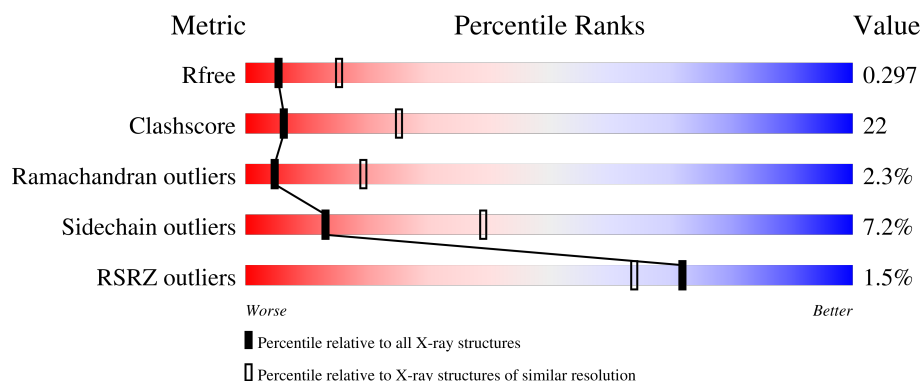
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

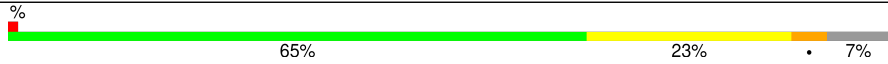
The reported resolution of this entry is 2.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	768	
1	B	768	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11326 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 Catalase-peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	711	Total	C	N	O	S	0	0	0
			5579	3545	975	1047	12			
1	B	711	Total	C	N	O	S	0	0	0
			5579	3545	975	1047	12			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	initiating methionine	UNP Q8X182
A	-13	ARG	-	expression tag	UNP Q8X182
A	-12	GLY	-	expression tag	UNP Q8X182
A	-11	SER	-	expression tag	UNP Q8X182
A	-10	HIS	-	expression tag	UNP Q8X182
A	-9	HIS	-	expression tag	UNP Q8X182
A	-8	HIS	-	expression tag	UNP Q8X182
A	-7	HIS	-	expression tag	UNP Q8X182
A	-6	HIS	-	expression tag	UNP Q8X182
A	-5	HIS	-	expression tag	UNP Q8X182
A	-4	GLY	-	expression tag	UNP Q8X182
A	-3	SER	-	expression tag	UNP Q8X182
A	-2	ALA	-	expression tag	UNP Q8X182
A	-1	CYS	-	expression tag	UNP Q8X182
A	0	GLU	-	expression tag	UNP Q8X182
A	1	LEU	-	expression tag	UNP Q8X182
B	-14	MET	-	initiating methionine	UNP Q8X182
B	-13	ARG	-	expression tag	UNP Q8X182
B	-12	GLY	-	expression tag	UNP Q8X182
B	-11	SER	-	expression tag	UNP Q8X182
B	-10	HIS	-	expression tag	UNP Q8X182
B	-9	HIS	-	expression tag	UNP Q8X182
B	-8	HIS	-	expression tag	UNP Q8X182
B	-7	HIS	-	expression tag	UNP Q8X182
B	-6	HIS	-	expression tag	UNP Q8X182

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	expression tag	UNP Q8X182
B	-4	GLY	-	expression tag	UNP Q8X182
B	-3	SER	-	expression tag	UNP Q8X182
B	-2	ALA	-	expression tag	UNP Q8X182
B	-1	CYS	-	expression tag	UNP Q8X182
B	0	GLU	-	expression tag	UNP Q8X182
B	1	LEU	-	expression tag	UNP Q8X182

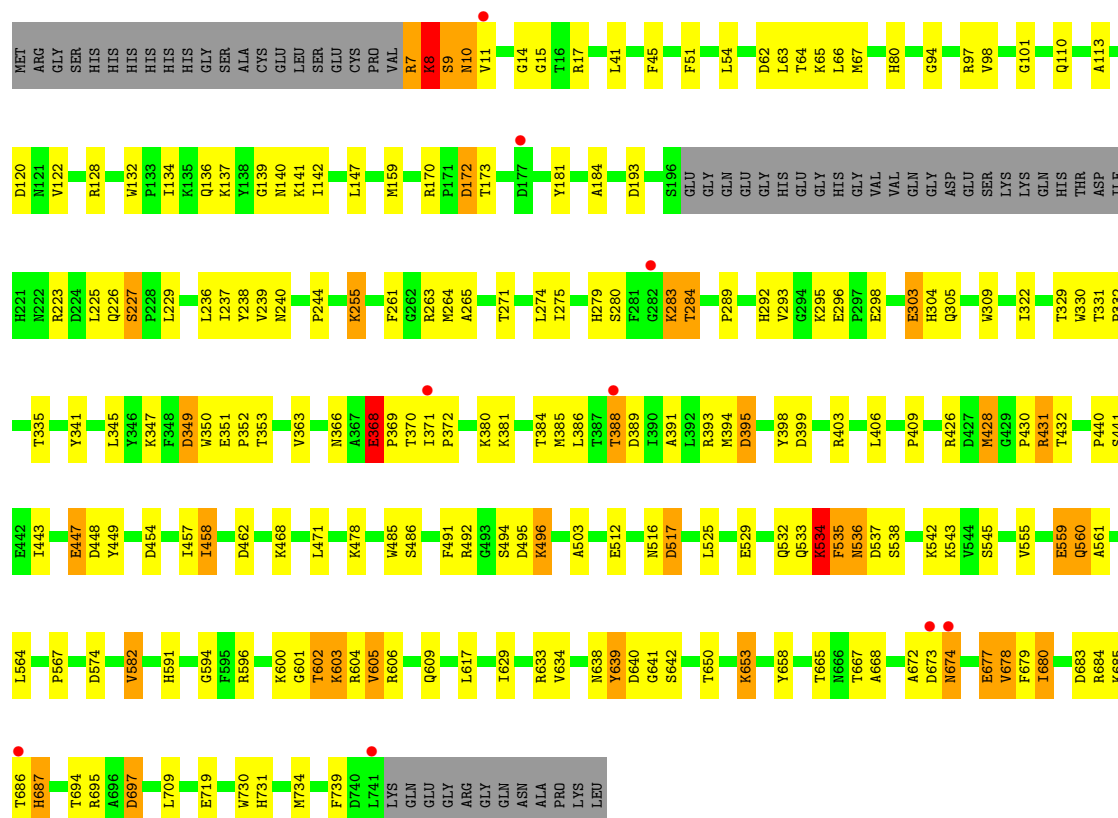
- # HEM

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

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 3 | A | 1 | Total K
1 1 | 0 | 0 |
| 3 | B | 1 | Total K
1 1 | 0 | 0 |

- 
- WORLD WIDE
PDB
PROTEIN DATA BANK

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	32	Total 32	O 32	0	0
4	B	48	Total 48	O 48	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	104.31Å 115.65Å 123.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	84.27 – 2.90 84.27 – 2.90	Depositor EDS
% Data completeness (in resolution range)	96.2 (84.27-2.90) 96.2 (84.27-2.90)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.38 (at 2.91Å)	Xtrriage
Refinement program	REFMAC 5.8.0107	Depositor
R, R_{free}	0.224 , 0.297 0.226 , 0.297	Depositor DCC
R_{free} test set	1652 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtrriage
Anisotropy	0.036	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11326	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 34.27 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.0111e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: HEM, K

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.13	6/5735 (0.1%)	1.10	26/7795 (0.3%)
1	B	1.14	3/5735 (0.1%)	1.12	26/7795 (0.3%)
All	All	1.14	9/11470 (0.1%)	1.11	52/15590 (0.3%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	677	GLU	N-CA	-5.55	1.39	1.46
1	A	98	VAL	C-O	-5.43	1.17	1.24
1	A	523	GLU	C-O	-5.38	1.17	1.24
1	A	153	ASN	C-O	-5.36	1.17	1.24
1	A	134	ILE	C-O	-5.34	1.18	1.24
1	A	731	HIS	C-O	-5.22	1.17	1.24
1	B	559	GLU	N-CA	-5.21	1.41	1.46
1	A	719	GLU	C-O	-5.04	1.18	1.24
1	B	141	LYS	C-O	-5.03	1.17	1.24

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	330	TRP	N-CA-C	10.58	123.81	111.11
1	A	349	ASP	N-CA-C	-10.58	93.13	109.95
1	B	591	HIS	N-CA-C	-9.57	99.95	112.68
1	B	295	LYS	N-CA-C	8.98	123.23	108.96
1	A	282	GLY	N-CA-C	8.94	128.94	112.77
1	A	447	GLU	N-CA-C	7.78	119.76	111.28
1	B	677	GLU	N-CA-C	-7.58	101.27	111.96
1	B	409	PRO	N-CA-C	7.50	123.60	113.84
1	B	94	GLY	N-CA-C	7.48	122.70	114.40
1	A	186	THR	N-CA-C	-7.14	101.49	112.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	349	ASP	N-CA-C	-6.97	98.49	109.50
1	B	350	TRP	N-CA-C	6.86	120.86	109.95
1	A	559	GLU	N-CA-C	-6.74	103.55	111.03
1	A	495	ASP	CB-CA-C	6.69	120.61	109.38
1	A	636	GLU	N-CA-C	6.57	120.87	112.86
1	A	591	HIS	N-CA-C	-6.50	103.41	112.45
1	B	113	ALA	C-N-CD	6.50	134.90	120.60
1	A	711	GLU	N-CA-C	6.43	118.29	111.28
1	A	719	GLU	N-CA-C	6.42	118.85	111.02
1	A	385	MET	N-CA-C	6.30	116.89	108.38
1	B	227	SER	CA-C-O	-6.16	114.30	120.64
1	A	348	PHE	CA-C-N	-6.14	112.98	122.87
1	A	348	PHE	C-N-CA	-6.14	112.98	122.87
1	B	280	SER	N-CA-C	-6.10	105.88	113.38
1	A	305	GLN	N-CA-C	6.07	119.72	111.17
1	A	460	ASP	N-CA-C	6.05	117.95	111.36
1	B	255	LYS	N-CA-C	-6.00	104.66	111.07
1	A	16	THR	N-CA-C	-5.98	102.07	110.50
1	B	458	ILE	N-CA-C	5.95	116.73	109.30
1	B	304	HIS	CA-C-N	-5.94	114.07	122.63
1	B	304	HIS	C-N-CA	-5.94	114.07	122.63
1	B	227	SER	C-N-CD	5.89	133.55	120.60
1	B	14	GLY	N-CA-C	5.85	122.14	112.66
1	A	413	ALA	N-CA-C	-5.75	104.61	111.69
1	B	226	GLN	N-CA-C	5.74	118.78	110.28
1	B	305	GLN	N-CA-C	5.74	119.02	111.28
1	A	106	GLY	N-CA-C	5.68	120.70	114.40
1	B	17	ARG	N-CA-C	5.63	118.42	110.14
1	A	367	ALA	N-CA-C	5.54	122.60	110.80
1	A	495	ASP	N-CA-C	-5.52	106.44	114.12
1	A	185	GLU	N-CA-C	-5.48	99.14	110.80
1	A	447	GLU	CB-CA-C	-5.47	101.71	110.79
1	B	605	VAL	N-CA-C	5.41	115.84	107.78
1	B	559	GLU	N-CA-C	-5.40	102.67	111.04
1	A	650	THR	CA-C-N	-5.18	114.38	119.92
1	A	650	THR	C-N-CA	-5.18	114.38	119.92
1	B	368	GLU	CB-CA-C	5.17	116.52	108.61
1	B	395	ASP	CA-C-N	-5.08	114.43	119.56
1	B	395	ASP	C-N-CA	-5.08	114.43	119.56
1	A	280	SER	N-CA-C	-5.06	106.61	112.89
1	B	478	LYS	CB-CA-C	-5.01	102.16	110.68
1	A	438	GLU	N-CA-C	5.00	118.22	112.57

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	5579	0	5397	317	1
1	B	5579	0	5397	177	1
2	A	43	0	30	15	0
2	B	43	0	30	13	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	32	0	0	1	0
4	B	48	0	0	5	0
All	All	11326	0	10854	490	1

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 (490) 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:B:284:THR:HG22	2:B:801:HEM:CAA	1.54	1.38
1:A:511:ASN:OD1	1:A:512:GLU:HG2	1.35	1.24
1:A:288:GLY:O	1:A:357:ALA:HB2	1.31	1.24
1:A:221:HIS:ND1	1:A:222:ASN:N	1.91	1.19
1:A:717:ASP:OD2	1:B:139:GLY:HA3	1.39	1.18
1:B:284:THR:CG2	2:B:801:HEM:HAA1	1.76	1.16
1:A:362:TRP:O	1:A:384:THR:OG1	1.64	1.14
1:B:639:TYR:O	1:B:640:ASP:CG	1.91	1.14
1:B:668:ALA:HB2	1:B:684:ARG:HH21	1.02	1.14
1:A:345:LEU:O	1:A:393:ARG:NH1	1.86	1.09
1:B:331:THR:OG1	1:B:332:PRO:HD2	1.51	1.08
1:A:288:GLY:O	1:A:357:ALA:CB	2.04	1.06
1:B:673:ASP:OD1	1:B:674:ASN:OD1	1.73	1.05
1:A:506:ARG:NH2	1:A:575:ALA:O	1.91	1.03
1:A:457:ILE:O	1:A:542:LYS:NZ	1.94	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:TYR:O	1:A:264:MET:HG2	1.62	0.98
1:A:194:ARG:NH2	1:A:231:SER:O	1.95	0.98
1:B:8:LYS:HA	1:B:15:GLY:H	1.27	0.98
1:A:7:ARG:O	1:A:9:SER:N	1.97	0.98
1:A:604:ARG:O	1:B:9:SER:HB3	1.64	0.97
1:A:191:ASN:HB3	1:A:233:HIS:HD2	1.28	0.95
1:A:639:TYR:O	1:A:641:GLY:N	2.00	0.95
1:B:668:ALA:HB2	1:B:684:ARG:NH2	1.80	0.95
1:B:532:GLN:O	1:B:536:ASN:HB2	1.67	0.94
1:B:368:GLU:O	1:B:370:THR:HG23	1.67	0.94
1:B:193:ASP:OD1	1:B:604:ARG:NH2	1.99	0.94
1:B:668:ALA:CB	1:B:684:ARG:HH21	1.81	0.93
1:B:345:LEU:HD13	1:B:385:MET:HE2	1.50	0.93
1:A:384:THR:O	1:A:385:MET:HG2	1.68	0.92
1:A:335:THR:O	1:A:336:LYS:HD3	1.70	0.91
1:A:369:PRO:HB3	1:A:380:LYS:C	1.97	0.90
1:A:239:VAL:HG22	1:A:240:ASN:H	1.37	0.89
1:A:385:MET:HE1	1:A:389:ASP:HB3	1.54	0.87
1:A:385:MET:CE	1:A:389:ASP:HB3	2.05	0.87
1:A:537:ASP:O	1:A:539:SER:N	2.07	0.87
1:B:639:TYR:O	1:B:640:ASP:OD1	1.93	0.85
1:A:349:ASP:CB	1:A:365:LYS:HE2	2.07	0.84
1:B:673:ASP:HB2	1:B:678:VAL:HG22	1.60	0.84
1:B:264:MET:O	1:B:426:ARG:NH1	2.11	0.84
1:A:194:ARG:HH21	1:A:231:SER:C	1.86	0.83
1:B:331:THR:OG1	1:B:332:PRO:CD	2.27	0.82
1:A:159:MET:HE2	1:A:335:THR:HA	1.62	0.81
1:A:349:ASP:HB3	1:A:365:LYS:HE2	1.61	0.81
1:A:511:ASN:OD1	1:A:512:GLU:CG	2.26	0.81
1:A:115:LEU:O	1:A:121:ASN:ND2	2.12	0.81
1:A:353:THR:CG2	1:A:363:VAL:CG2	2.58	0.81
1:A:639:TYR:C	1:A:641:GLY:H	1.88	0.80
1:B:533:GLN:O	1:B:534:LYS:O	1.98	0.80
1:B:677:GLU:OE2	4:B:901:HOH:O	2.00	0.80
1:B:284:THR:HG22	2:B:801:HEM:HAA1	0.81	0.80
1:A:311:ASN:HD21	1:A:322:ILE:HD12	1.46	0.80
1:A:184:ALA:C	1:A:185:GLU:O	2.20	0.79
1:A:343:GLU:O	1:A:347:LYS:HG2	1.82	0.79
1:A:349:ASP:HB3	1:A:365:LYS:CE	2.12	0.79
1:A:492:ARG:NH1	1:A:588:LEU:HD12	1.98	0.78
1:A:349:ASP:CB	1:A:365:LYS:CE	2.61	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:284:THR:CG2	2:B:801:HEM:CAA	2.49	0.78
1:A:239:VAL:HG22	1:A:240:ASN:N	1.99	0.78
1:A:385:MET:CE	1:A:389:ASP:CB	2.61	0.77
2:A:801:HEM:HBC2	2:A:801:HEM:HMC2	1.67	0.77
1:B:633:ARG:NH1	1:B:697:ASP:OD1	2.18	0.77
1:A:283:LYS:NZ	1:A:374:ALA:HB2	1.99	0.77
1:A:343:GLU:O	1:A:347:LYS:CG	2.33	0.77
1:A:296:GLU:N	1:A:296:GLU:OE1	2.18	0.77
1:A:353:THR:HG21	1:A:363:VAL:CG2	2.15	0.77
1:B:7:ARG:O	1:B:9:SER:OG	2.03	0.76
1:A:717:ASP:CG	1:B:139:GLY:HA3	2.09	0.76
1:A:283:LYS:NZ	1:A:374:ALA:CB	2.49	0.75
1:A:384:THR:C	1:A:385:MET:HG2	2.11	0.75
1:A:673:ASP:OD2	1:A:678:VAL:HG22	1.87	0.75
1:A:284:THR:HG22	2:A:801:HEM:HAA1	1.69	0.74
1:A:533:GLN:O	1:A:537:ASP:HB2	1.87	0.74
1:A:311:ASN:HD21	1:A:322:ILE:CD1	2.01	0.74
1:B:542:LYS:C	1:B:543:LYS:HG3	2.12	0.73
2:A:801:HEM:HBB2	2:A:801:HEM:HMB2	1.71	0.73
1:A:194:ARG:NH2	1:A:231:SER:C	2.47	0.73
1:A:311:ASN:HD21	1:A:322:ILE:CG1	2.02	0.72
1:B:147:LEU:HD12	1:B:147:LEU:O	1.90	0.71
1:A:418:ARG:NH2	1:A:442:GLU:OE2	2.23	0.71
1:A:633:ARG:HH12	1:A:697:ASP:CG	1.98	0.71
1:A:311:ASN:ND2	1:A:322:ILE:HB	2.05	0.71
1:A:366:ASN:O	1:A:367:ALA:HB2	1.90	0.71
1:B:393:ARG:HG2	1:B:394:MET:HE2	1.72	0.70
1:A:153:ASN:O	1:A:157:GLU:HG3	1.92	0.70
1:A:339:MET:HE3	1:A:409:PRO:HB3	1.73	0.70
1:A:385:MET:HE3	1:A:389:ASP:CB	2.22	0.69
1:A:275:ILE:HD13	2:A:801:HEM:HHC	1.74	0.69
1:A:311:ASN:ND2	1:A:322:ILE:HD12	2.06	0.69
1:A:386:LEU:O	1:A:389:ASP:N	2.25	0.69
1:A:9:SER:HB2	1:B:605:VAL:HG22	1.75	0.69
1:A:266:MET:HE1	1:A:422:LYS:HG2	1.75	0.69
1:B:534:LYS:O	1:B:535:PHE:C	2.36	0.69
1:A:385:MET:HE3	1:A:389:ASP:HB2	1.75	0.69
1:B:8:LYS:HA	1:B:15:GLY:N	2.06	0.69
1:B:683:ASP:HB3	1:B:687:HIS:H	1.56	0.69
1:A:492:ARG:NH1	1:A:588:LEU:CD1	2.55	0.68
1:A:283:LYS:CE	1:A:374:ALA:HB2	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:369:PRO:HB3	1:A:381:LYS:N	2.08	0.68
1:A:604:ARG:O	1:B:9:SER:CB	2.40	0.68
1:A:349:ASP:HB2	1:A:365:LYS:CE	2.24	0.68
1:B:172:ASP:OD1	4:B:902:HOH:O	2.11	0.67
1:B:677:GLU:O	1:B:679:PHE:CE1	2.46	0.67
1:A:191:ASN:HB3	1:A:233:HIS:CD2	2.20	0.67
1:B:640:ASP:OD1	1:B:641:GLY:N	2.28	0.67
2:B:801:HEM:HMC1	2:B:801:HEM:HBC2	1.77	0.66
1:B:184:ALA:HB3	1:B:193:ASP:OD2	1.96	0.66
1:A:353:THR:CG2	1:A:363:VAL:HG23	2.25	0.66
1:A:7:ARG:CB	1:A:7:ARG:HH21	2.08	0.66
1:A:239:VAL:HG12	2:A:801:HEM:HBB2	1.76	0.66
1:A:431:ARG:NH2	1:A:440:PRO:O	2.29	0.66
1:B:533:GLN:O	1:B:534:LYS:C	2.38	0.66
1:A:365:LYS:C	1:A:366:ASN:OD1	2.39	0.65
1:A:248:PRO:HG3	1:A:360:ASN:HB3	1.77	0.65
2:B:801:HEM:HMB1	2:B:801:HEM:HBB2	1.77	0.65
1:A:221:HIS:CG	1:A:222:ASN:H	2.10	0.65
1:A:184:ALA:O	1:A:185:GLU:O	2.15	0.65
1:A:633:ARG:NH1	1:A:697:ASP:OD1	2.30	0.65
1:A:656:ASN:OD1	1:A:719:GLU:HG2	1.97	0.65
1:A:376:ASP:HB3	1:A:379:LYS:HB3	1.79	0.65
1:A:386:LEU:O	1:A:387:THR:C	2.40	0.65
1:A:477:PRO:HA	1:A:480:LEU:HD12	1.79	0.65
1:B:7:ARG:CG	1:B:7:ARG:HH21	2.09	0.65
1:B:516:ASN:O	1:B:517:ASP:O	2.15	0.65
1:B:683:ASP:HB3	1:B:687:HIS:N	2.12	0.65
1:A:244:PRO:O	1:A:246:GLY:N	2.30	0.64
1:A:489:SER:OG	1:A:614:ARG:NH2	2.29	0.64
1:B:431:ARG:NH2	1:B:440:PRO:O	2.30	0.64
1:A:32:ARG:NH1	1:A:705:GLU:OE2	2.30	0.64
1:A:349:ASP:HB2	1:A:365:LYS:HE3	1.80	0.64
1:A:353:THR:HG22	1:A:363:VAL:HG23	1.80	0.64
1:B:395:ASP:O	1:B:399:ASP:HB2	1.98	0.63
1:A:348:PHE:CE1	1:A:366:ASN:O	2.52	0.63
1:B:239:VAL:HG12	1:B:240:ASN:N	2.13	0.63
1:A:598:TYR:HD1	1:A:639:TYR:CE2	2.16	0.63
1:B:329:THR:HB	1:B:371:ILE:HD12	1.81	0.63
1:B:447:GLU:OE2	1:B:449:TYR:HB2	1.98	0.63
1:A:194:ARG:HD2	1:A:232:SER:O	1.98	0.63
1:B:399:ASP:OD2	1:B:403:ARG:NH1	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:559:GLU:O	1:B:560:GLN:C	2.42	0.62
1:A:239:VAL:CG2	1:A:240:ASN:H	2.12	0.62
1:B:683:ASP:OD2	1:B:686:THR:HB	1.99	0.62
1:A:193:ASP:OD2	1:A:604:ARG:NH2	2.32	0.61
1:B:371:ILE:HD11	1:B:381:LYS:HG3	1.80	0.61
1:B:516:ASN:O	1:B:517:ASP:C	2.42	0.61
1:B:137:LYS:O	1:B:137:LYS:HG2	2.00	0.61
1:B:284:THR:HG22	2:B:801:HEM:HAA2	1.70	0.61
1:B:495:ASP:C	1:B:496:LYS:HG2	2.23	0.61
1:A:423:LEU:HD12	1:A:426:ARG:CZ	2.31	0.61
1:A:606:ARG:CZ	1:A:609:GLN:OE1	2.49	0.61
1:A:339:MET:CE	1:A:409:PRO:HB3	2.30	0.61
1:B:7:ARG:O	1:B:9:SER:N	2.33	0.61
1:A:188:TRP:O	1:A:189:LEU:HB2	2.01	0.61
1:A:9:SER:O	1:A:11:VAL:N	2.33	0.60
1:A:194:ARG:HD2	1:A:232:SER:C	2.27	0.60
1:B:237:ILE:HG22	1:B:238:TYR:CD2	2.37	0.60
1:B:694:THR:HG22	1:B:695:ARG:N	2.16	0.60
1:A:239:VAL:HG12	2:A:801:HEM:CBB	2.30	0.60
1:B:353:THR:HG21	1:B:363:VAL:CG2	2.31	0.60
2:A:801:HEM:HBC2	2:A:801:HEM:CMC	2.32	0.60
1:A:353:THR:HG23	1:A:354:LYS:N	2.17	0.59
1:B:559:GLU:HG2	1:B:564:LEU:O	2.01	0.59
1:A:7:ARG:HG3	1:A:8:LYS:N	2.17	0.59
1:A:364:ALA:O	1:A:366:ASN:N	2.35	0.59
1:B:672:ALA:HB2	1:B:680:ILE:HG13	1.84	0.59
1:A:290:THR:O	1:A:292:HIS:N	2.36	0.59
1:A:313:PHE:CB	1:A:322:ILE:HD11	2.33	0.59
1:A:537:ASP:C	1:A:539:SER:H	2.06	0.59
1:A:366:ASN:OD1	1:A:366:ASN:N	2.35	0.59
2:B:801:HEM:HBC2	2:B:801:HEM:CMC	2.33	0.59
1:A:7:ARG:HH21	1:A:7:ARG:HB3	1.67	0.59
1:A:264:MET:HB3	1:A:426:ARG:HH12	1.66	0.59
1:A:275:ILE:CD1	2:A:801:HEM:HAB	2.33	0.59
1:A:279:HIS:CE1	2:A:801:HEM:C4B	2.90	0.59
1:A:633:ARG:HG3	1:A:645:GLY:O	2.03	0.58
1:B:371:ILE:CD1	1:B:381:LYS:HG3	2.33	0.58
1:A:116:ASN:OD1	1:A:117:SER:N	2.36	0.58
1:B:674:ASN:OD1	1:B:674:ASN:N	2.32	0.58
1:B:525:LEU:O	1:B:529:GLU:HG3	2.03	0.58
1:A:343:GLU:O	1:A:347:LYS:HG3	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:364:ALA:C	1:A:366:ASN:H	2.11	0.58
1:B:7:ARG:HH21	1:B:7:ARG:HG3	1.67	0.58
1:A:404:ASP:OD2	1:A:411:LYS:HE2	2.04	0.58
1:A:125:ASP:N	1:A:125:ASP:OD1	2.37	0.58
1:A:188:TRP:C	1:A:190:GLY:H	2.10	0.57
1:A:457:ILE:C	1:A:542:LYS:HZ1	2.12	0.57
1:B:9:SER:O	1:B:11:VAL:N	2.36	0.57
1:A:636:GLU:O	1:A:638:ASN:N	2.36	0.57
1:B:142:ILE:HG23	1:B:142:ILE:O	2.04	0.57
1:A:227:SER:OG	1:A:228:PRO:HA	2.05	0.57
1:A:672:ALA:HB2	1:A:680:ILE:HG13	1.87	0.57
1:A:673:ASP:OD1	1:A:676:GLY:N	2.35	0.56
1:B:399:ASP:CG	1:B:403:ARG:NH1	2.63	0.56
1:A:422:LYS:HD2	1:A:446:TRP:CD1	2.40	0.56
1:B:264:MET:HB3	1:B:426:ARG:HH12	1.68	0.56
1:B:686:THR:O	1:B:687:HIS:HB2	2.04	0.56
1:A:283:LYS:HZ3	1:A:374:ALA:CB	2.17	0.56
1:A:193:ASP:C	1:A:195:TYR:H	2.14	0.56
1:A:40:PRO:HG3	1:B:709:LEU:HD22	1.87	0.56
1:A:344:TYR:OH	1:A:370:THR:HG21	2.05	0.56
1:B:606:ARG:H	1:B:609:GLN:NE2	2.04	0.56
1:B:639:TYR:C	1:B:640:ASP:CG	2.71	0.56
1:B:353:THR:CG2	1:B:363:VAL:HG23	2.36	0.56
1:A:313:PHE:HB3	1:A:322:ILE:HD11	1.88	0.56
1:B:458:ILE:HB	1:B:462:ASP:HB2	1.88	0.56
1:A:362:TRP:N	1:A:362:TRP:CD1	2.73	0.56
1:A:545:SER:HB2	1:A:574:ASP:OD1	2.06	0.56
1:A:639:TYR:C	1:A:641:GLY:N	2.53	0.55
1:A:408:ASN:C	1:A:410:ASP:H	2.14	0.55
1:B:371:ILE:CG1	1:B:381:LYS:HG3	2.36	0.55
2:B:801:HEM:HBB2	2:B:801:HEM:CMB	2.36	0.55
1:A:193:ASP:CG	1:A:604:ARG:HH22	2.14	0.55
1:A:283:LYS:HZ1	1:A:374:ALA:CB	2.17	0.55
1:A:167:ALA:O	1:A:170:ARG:NH2	2.39	0.55
1:B:371:ILE:HG13	1:B:381:LYS:HG3	1.88	0.55
1:A:194:ARG:HD3	1:A:231:SER:O	2.04	0.55
1:A:398:TYR:O	1:A:399:ASP:C	2.50	0.54
1:A:269:GLU:OE2	4:A:901:HOH:O	2.18	0.54
1:B:62:ASP:OD1	1:B:65:LYS:NZ	2.37	0.54
1:B:602:THR:HG22	1:B:604:ARG:H	1.72	0.54
1:A:283:LYS:NZ	1:A:374:ALA:HB3	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:349:ASP:CB	1:A:365:LYS:HE3	2.35	0.54
1:B:45:PHE:CE1	1:B:140:ASN:ND2	2.76	0.54
1:B:341:TYR:CE1	1:B:385:MET:HE1	2.43	0.54
1:A:73:TRP:CH2	1:A:130:LEU:CD1	2.91	0.54
1:A:279:HIS:HE1	2:A:801:HEM:C4B	2.25	0.54
1:B:457:ILE:HG22	1:B:458:ILE:N	2.22	0.54
1:B:181:TYR:CE2	1:B:229:LEU:HD21	2.43	0.54
1:B:535:PHE:O	1:B:536:ASN:O	2.24	0.54
1:A:9:SER:HB3	1:B:604:ARG:O	2.07	0.54
1:B:640:ASP:OD1	1:B:642:SER:N	2.38	0.54
1:A:283:LYS:HZ3	1:A:374:ALA:HB2	1.69	0.53
1:A:326:LEU:HD23	1:A:361:GLN:HB3	1.89	0.53
1:B:542:LYS:HB3	1:B:542:LYS:HZ2	1.73	0.53
1:B:239:VAL:CG1	1:B:240:ASN:N	2.71	0.53
1:B:486:SER:OG	1:B:596:ARG:NH1	2.41	0.53
1:B:602:THR:CG2	1:B:603:LYS:N	2.71	0.53
2:A:801:HEM:HBB2	2:A:801:HEM:CMB	2.37	0.53
1:B:430:PRO:O	1:B:431:ARG:C	2.51	0.53
1:A:7:ARG:HG3	1:A:8:LYS:H	1.73	0.53
1:A:349:ASP:HB2	1:A:365:LYS:HE2	1.87	0.53
1:A:605:VAL:HG22	1:B:9:SER:HB2	1.91	0.53
1:A:672:ALA:HB3	1:A:678:VAL:HG23	1.91	0.53
1:B:494:SER:OG	1:B:617:LEU:CD2	2.56	0.53
1:A:7:ARG:HH21	1:A:7:ARG:CG	2.20	0.53
1:A:396:PRO:O	1:A:399:ASP:HB3	2.09	0.53
1:A:462:ASP:OD2	1:A:542:LYS:HE2	2.09	0.53
1:B:170:ARG:NH1	1:B:428:MET:SD	2.82	0.53
1:A:573:ASN:OD1	1:A:574:ASP:N	2.42	0.53
1:A:244:PRO:C	1:A:246:GLY:H	2.16	0.52
1:A:530:SER:O	1:A:534:LYS:HG3	2.09	0.52
1:B:399:ASP:OD1	1:B:403:ARG:NH1	2.42	0.52
1:A:491:PHE:CD2	1:A:736:LEU:HD13	2.44	0.52
1:A:264:MET:HB3	1:A:426:ARG:NH1	2.24	0.52
1:A:411:LYS:O	1:A:411:LYS:HG2	2.08	0.52
1:B:7:ARG:NH2	1:B:7:ARG:HB2	2.23	0.52
1:B:542:LYS:O	1:B:543:LYS:HG3	2.09	0.52
1:A:290:THR:C	1:A:292:HIS:N	2.67	0.52
1:B:535:PHE:O	1:B:536:ASN:C	2.46	0.52
1:A:633:ARG:HG3	1:A:645:GLY:C	2.35	0.52
1:A:98:VAL:CG2	1:A:265:ALA:HB2	2.40	0.52
1:A:348:PHE:CE1	1:A:367:ALA:HB2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:630:GLY:HA3	1:A:659:PHE:CZ	2.45	0.52
1:B:7:ARG:NH2	1:B:7:ARG:CB	2.73	0.52
1:A:335:THR:O	1:A:336:LYS:CD	2.53	0.52
1:B:639:TYR:O	1:B:641:GLY:N	2.43	0.52
1:A:73:TRP:CH2	1:A:130:LEU:HD12	2.44	0.52
1:B:602:THR:HG22	1:B:604:ARG:N	2.24	0.52
1:A:366:ASN:O	1:A:367:ALA:CB	2.57	0.51
1:A:369:PRO:HB3	1:A:381:LYS:CA	2.40	0.51
1:A:492:ARG:O	1:A:492:ARG:HG2	2.10	0.51
1:B:432:THR:OG1	1:B:739:PHE:HB2	2.10	0.51
1:A:328:VAL:HG13	1:A:384:THR:HG23	1.91	0.51
1:A:633:ARG:HD2	1:A:644:TYR:O	2.11	0.51
1:B:261:PHE:CD2	1:B:271:THR:HG23	2.45	0.51
1:A:448:ASP:OD2	1:A:497:ARG:NH1	2.43	0.51
1:B:559:GLU:O	1:B:561:ALA:N	2.43	0.51
1:A:7:ARG:CG	1:A:7:ARG:NH2	2.73	0.50
1:A:276:ALA:HA	1:A:341:TYR:CE1	2.46	0.50
1:A:315:GLN:HB2	1:A:320:ASP:OD2	2.11	0.50
1:A:371:ILE:HD13	1:A:383:PRO:HA	1.93	0.50
1:A:636:GLU:C	1:A:638:ASN:H	2.18	0.50
1:B:694:THR:CG2	4:B:901:HOH:O	2.58	0.50
1:B:385:MET:HE3	1:B:389:ASP:HB3	1.93	0.50
1:A:346:TYR:C	1:A:347:LYS:HG2	2.36	0.50
1:A:313:PHE:HB3	1:A:322:ILE:CD1	2.41	0.50
1:A:361:GLN:C	1:A:362:TRP:HD1	2.19	0.50
1:B:66:LEU:HD22	1:B:134:ILE:HD12	1.94	0.50
1:A:311:ASN:ND2	1:A:322:ILE:CB	2.75	0.50
1:B:650:THR:O	1:B:650:THR:OG1	2.29	0.50
1:A:8:LYS:HA	1:A:15:GLY:H	1.77	0.50
1:A:258:ARG:NH2	1:A:398:TYR:CE1	2.79	0.50
1:A:458:ILE:HA	1:A:542:LYS:NZ	2.25	0.50
1:B:730:TRP:O	1:B:734:MET:HG2	2.11	0.50
1:A:25:GLN:NE2	1:B:298:GLU:OE1	2.41	0.50
1:B:388:THR:O	1:B:391:ALA:HB3	2.12	0.50
1:A:225:LEU:HD11	1:A:231:SER:O	2.12	0.50
1:A:225:LEU:O	1:A:263:ARG:NH2	2.44	0.50
1:A:290:THR:C	1:A:292:HIS:H	2.20	0.50
1:A:284:THR:OG1	1:A:326:LEU:O	2.19	0.50
1:A:542:LYS:O	1:A:543:LYS:HG2	2.11	0.50
1:A:386:LEU:O	1:A:388:THR:N	2.45	0.49
1:A:7:ARG:C	1:A:9:SER:N	2.69	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:TRP:HZ3	1:A:238:TYR:HH	1.54	0.49
1:B:159:MET:HE2	1:B:335:THR:HA	1.93	0.49
1:B:639:TYR:C	1:B:641:GLY:H	2.21	0.49
1:A:363:VAL:HG12	1:A:364:ALA:N	2.27	0.49
1:B:120:ASP:HB2	1:B:236:LEU:HA	1.95	0.49
1:A:194:ARG:O	1:A:225:LEU:HA	2.13	0.49
1:B:371:ILE:O	1:B:380:LYS:HD3	2.13	0.49
1:B:447:GLU:O	1:B:448:ASP:HB2	2.13	0.49
1:B:45:PHE:CZ	1:B:140:ASN:ND2	2.81	0.48
1:B:431:ARG:NH1	1:B:447:GLU:OE1	2.45	0.48
1:A:184:ALA:O	1:A:185:GLU:C	2.53	0.48
1:B:98:VAL:CG2	1:B:265:ALA:HB2	2.44	0.48
1:A:73:TRP:HB3	1:B:684:ARG:HD3	1.95	0.48
1:A:361:GLN:C	1:A:362:TRP:CD1	2.91	0.48
1:A:552:LEU:HD12	1:A:555:VAL:CG2	2.43	0.48
1:B:51:PHE:CE1	1:B:54:LEU:HD22	2.47	0.48
1:B:542:LYS:O	1:B:543:LYS:CG	2.62	0.48
1:A:285:HIS:O	1:A:323:THR:N	2.33	0.48
1:A:339:MET:O	1:A:339:MET:HG3	2.13	0.48
1:A:364:ALA:C	1:A:366:ASN:N	2.71	0.48
1:B:274:LEU:C	2:B:801:HEM:HMC3	2.39	0.48
1:A:353:THR:HG21	1:A:363:VAL:HG21	1.96	0.47
1:A:458:ILE:HA	1:A:542:LYS:HZ3	1.78	0.47
1:A:644:TYR:N	1:A:644:TYR:CD1	2.79	0.47
1:B:132:TRP:CZ2	1:B:136:GLN:HG3	2.49	0.47
1:A:239:VAL:CG2	1:A:240:ASN:N	2.70	0.47
1:A:638:ASN:O	1:A:639:TYR:C	2.54	0.47
1:B:67:MET:HB3	1:B:80:HIS:CE1	2.50	0.47
1:A:683:ASP:O	1:A:687:HIS:HA	2.14	0.47
1:A:188:TRP:C	1:A:190:GLY:N	2.73	0.47
1:B:110:GLN:HG2	1:B:128:ARG:NH1	2.29	0.47
1:B:694:THR:CG2	1:B:695:ARG:N	2.78	0.47
1:A:75:PRO:HD3	1:A:317:LYS:HD2	1.96	0.47
1:A:244:PRO:C	1:A:246:GLY:N	2.70	0.47
1:A:284:THR:CG2	2:A:801:HEM:HAA1	2.43	0.47
1:A:369:PRO:HB3	1:A:380:LYS:O	2.13	0.47
1:A:369:PRO:HB2	1:A:380:LYS:HB2	1.97	0.47
1:B:454:ASP:OD1	1:B:454:ASP:N	2.41	0.47
1:B:457:ILE:CG2	1:B:458:ILE:N	2.77	0.47
1:B:542:LYS:C	1:B:543:LYS:CG	2.84	0.47
1:A:122:VAL:HG22	1:A:309:TRP:CE2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:VAL:HG21	1:B:265:ALA:HB2	1.97	0.47
1:B:225:LEU:O	1:B:263:ARG:NH2	2.47	0.47
1:B:431:ARG:O	1:B:432:THR:C	2.55	0.47
1:A:126:LYS:O	1:A:130:LEU:HD13	2.15	0.46
1:A:479:LYS:O	1:A:480:LEU:C	2.57	0.46
1:A:283:LYS:HZ1	1:A:374:ALA:HB3	1.80	0.46
1:A:633:ARG:NH1	1:A:697:ASP:OD2	2.48	0.46
1:A:633:ARG:CG	1:A:645:GLY:O	2.64	0.46
1:B:63:LEU:HD23	1:B:134:ILE:HD13	1.97	0.46
1:A:232:SER:O	1:A:233:HIS:CD2	2.68	0.46
1:A:348:PHE:HE1	1:A:366:ASN:O	1.98	0.46
1:A:537:ASP:C	1:A:539:SER:N	2.68	0.46
1:B:7:ARG:CG	1:B:7:ARG:NH2	2.72	0.46
1:B:485:TRP:HA	1:B:734:MET:HE1	1.96	0.46
1:A:264:MET:O	1:A:265:ALA:HB3	2.16	0.45
1:B:443:ILE:HG23	1:B:447:GLU:OE2	2.16	0.45
1:A:296:GLU:HB2	1:A:297:PRO:HD2	1.97	0.45
1:A:408:ASN:O	1:A:410:ASP:N	2.42	0.45
1:A:551:VAL:HG13	1:A:734:MET:SD	2.56	0.45
1:A:639:TYR:CD1	1:A:640:ASP:N	2.85	0.45
1:A:194:ARG:HH22	1:A:231:SER:CB	2.29	0.45
1:A:581:ASP:HB3	1:A:584:SER:HB2	1.98	0.45
1:A:193:ASP:C	1:A:195:TYR:N	2.74	0.45
1:A:346:TYR:O	1:A:347:LYS:HG2	2.15	0.45
1:A:707:ARG:O	1:A:711:GLU:HG3	2.16	0.45
1:A:535:PHE:CD1	1:A:535:PHE:C	2.95	0.45
1:A:606:ARG:NH2	1:A:606:ARG:HG3	2.31	0.45
1:A:730:TRP:CE2	1:A:734:MET:HE3	2.52	0.45
1:B:685:LYS:HD2	1:B:685:LYS:HA	1.63	0.45
1:A:367:ALA:O	1:A:368:GLU:C	2.59	0.45
1:A:397:ALA:O	1:A:398:TYR:C	2.57	0.45
1:A:447:GLU:O	1:A:448:ASP:HB2	2.17	0.45
1:B:283:LYS:HG3	1:B:284:THR:O	2.17	0.45
1:A:730:TRP:CZ2	1:A:734:MET:HE3	2.52	0.45
1:B:686:THR:O	1:B:687:HIS:CB	2.65	0.45
1:A:41:LEU:HD13	1:A:45:PHE:CE2	2.52	0.44
1:A:495:ASP:C	1:A:496:LYS:HG2	2.42	0.44
1:B:683:ASP:O	1:B:687:HIS:N	2.46	0.44
1:A:132:TRP:HB3	1:A:133:PRO:HD3	1.98	0.44
1:B:353:THR:HG22	1:B:363:VAL:HG23	2.00	0.44
1:A:371:ILE:HG12	1:A:381:LYS:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:633:ARG:HA	1:A:633:ARG:HD3	1.64	0.44
1:B:279:HIS:CE1	2:B:801:HEM:C4B	3.06	0.44
1:A:147:LEU:O	1:A:147:LEU:HG	2.17	0.44
1:A:353:THR:HG21	1:A:363:VAL:HG22	1.97	0.44
1:B:101:GLY:C	1:B:494:SER:HB3	2.42	0.44
1:A:243:GLY:O	1:A:244:PRO:C	2.61	0.44
1:A:395:ASP:O	1:A:399:ASP:HB2	2.17	0.44
1:B:494:SER:OG	1:B:617:LEU:HD22	2.17	0.44
1:A:98:VAL:HG21	1:A:265:ALA:HB2	1.98	0.44
1:A:363:VAL:HG12	1:A:364:ALA:H	1.82	0.44
1:A:644:TYR:N	1:A:644:TYR:HD1	2.16	0.44
1:A:221:HIS:O	1:A:222:ASN:C	2.61	0.43
1:B:602:THR:HG22	1:B:603:LYS:N	2.33	0.43
1:B:667:THR:O	1:B:684:ARG:NH2	2.51	0.43
1:B:672:ALA:HB2	1:B:680:ILE:CG1	2.46	0.43
1:B:10:ASN:OD1	1:B:10:ASN:N	2.51	0.43
1:A:279:HIS:CE1	2:A:801:HEM:CHC	3.01	0.43
1:A:577:GLN:O	1:A:578:GLU:C	2.59	0.43
1:A:608:GLU:CB	1:A:699:ILE:HD13	2.49	0.43
1:A:48:ALA:O	1:A:52:LYS:HE3	2.17	0.43
1:A:254:ALA:HB1	1:A:395:ASP:OD1	2.18	0.43
1:A:400:LYS:O	1:A:403:ARG:N	2.49	0.43
1:A:290:THR:O	1:A:291:HIS:C	2.60	0.43
1:A:400:LYS:O	1:A:401:ILE:C	2.61	0.43
1:A:638:ASN:C	1:A:639:TYR:O	2.59	0.43
1:A:311:ASN:HD21	1:A:322:ILE:HG13	1.81	0.43
1:A:410:ASP:C	1:A:412:PHE:N	2.73	0.43
1:A:519:SER:O	1:A:522:ARG:HG2	2.18	0.43
1:B:351:GLU:HG2	1:B:352:PRO:HD2	2.00	0.43
2:B:801:HEM:HMB1	2:B:801:HEM:CBB	2.47	0.43
1:A:362:TRP:N	1:A:362:TRP:HD1	2.16	0.43
1:A:396:PRO:O	1:A:399:ASP:CB	2.66	0.43
1:B:122:VAL:HG22	1:B:309:TRP:CE2	2.54	0.43
1:B:639:TYR:CE1	1:B:640:ASP:OD2	2.72	0.43
1:A:439:VAL:HA	1:A:440:PRO:HD2	1.87	0.43
1:A:656:ASN:CG	1:A:719:GLU:HG2	2.44	0.43
1:A:11:VAL:HG13	1:A:12:GLY:O	2.19	0.43
1:A:386:LEU:HB2	1:A:389:ASP:OD2	2.19	0.43
1:A:191:ASN:O	1:A:193:ASP:N	2.50	0.42
1:A:283:LYS:HE2	1:A:374:ALA:HB2	2.01	0.42
1:A:287:ALA:O	1:A:313:PHE:CE2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:620:LEU:HA	1:A:624:GLU:OE2	2.19	0.42
1:B:537:ASP:O	1:B:538:SER:C	2.62	0.42
1:A:7:ARG:CG	1:A:8:LYS:N	2.82	0.42
1:A:388:THR:O	1:A:391:ALA:HB3	2.19	0.42
1:A:511:ASN:OD1	1:A:512:GLU:N	2.52	0.42
1:B:41:LEU:HD13	1:B:45:PHE:CD2	2.54	0.42
1:A:717:ASP:CG	1:B:139:GLY:CA	2.87	0.42
1:B:594:GLY:O	1:B:633:ARG:NH2	2.48	0.42
1:A:149:LEU:HD23	1:A:424:LEU:HB3	2.00	0.42
1:A:248:PRO:HG3	1:A:360:ASN:CB	2.46	0.42
1:A:527:ALA:O	1:A:531:VAL:HG23	2.19	0.42
1:A:264:MET:O	1:A:426:ARG:NH1	2.53	0.42
1:B:223:ARG:H	1:B:223:ARG:HG2	1.70	0.42
1:B:503:ALA:HA	4:B:905:HOH:O	2.18	0.42
1:A:679:PHE:CE2	1:B:303:GLU:HG3	2.55	0.42
1:A:401:ILE:CG2	1:A:405:TYR:CE2	3.02	0.42
1:B:638:ASN:OD1	4:B:903:HOH:O	2.21	0.42
1:A:606:ARG:HG3	1:A:606:ARG:HH21	1.85	0.42
1:A:663:LEU:HD12	1:A:714:ALA:CB	2.50	0.42
1:B:393:ARG:HG2	1:B:394:MET:CE	2.46	0.42
1:B:430:PRO:O	1:B:432:THR:N	2.53	0.42
1:A:275:ILE:CD1	2:A:801:HEM:HHC	2.48	0.42
1:A:535:PHE:CD1	1:A:535:PHE:O	2.73	0.42
1:A:501:ASN:HB2	1:A:737:ASP:OD2	2.21	0.41
1:A:240:ASN:OD1	1:A:241:PRO:CD	2.68	0.41
1:A:597:SER:CB	1:A:638:ASN:ND2	2.82	0.41
2:A:801:HEM:HMC2	2:A:801:HEM:CBC	2.45	0.41
1:B:331:THR:OG1	1:B:332:PRO:N	2.53	0.41
1:A:694:THR:O	1:A:697:ASP:HB2	2.19	0.41
1:B:639:TYR:C	1:B:641:GLY:N	2.79	0.41
1:B:697:ASP:OD1	1:B:697:ASP:N	2.51	0.41
1:B:322:ILE:HD13	1:B:322:ILE:HG21	1.84	0.41
1:B:395:ASP:O	1:B:399:ASP:CB	2.67	0.41
1:A:431:ARG:NH1	1:A:447:GLU:OE1	2.49	0.41
1:A:126:LYS:HG3	1:A:307:LEU:HD22	2.03	0.41
1:A:194:ARG:HH22	1:A:231:SER:HB2	1.86	0.41
1:A:365:LYS:O	1:A:366:ASN:CB	2.67	0.41
1:A:633:ARG:NH1	1:A:697:ASP:CG	2.70	0.41
1:A:610:PHE:O	1:A:613:ASP:HB3	2.20	0.41
1:A:672:ALA:O	1:A:673:ASP:HB3	2.20	0.41
1:B:275:ILE:CD1	2:B:801:HEM:HHC	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:PRO:HG3	1:B:709:LEU:CD2	2.49	0.41
1:A:325:GLY:O	1:A:355:SER:OG	2.28	0.41
1:A:339:MET:HB2	1:A:339:MET:HE2	1.68	0.41
1:A:353:THR:HG22	1:A:363:VAL:CG2	2.39	0.41
1:A:622:ALA:HB3	1:A:623:PRO:HD3	2.03	0.41
1:B:289:PRO:HD2	1:B:292:HIS:CD2	2.56	0.41
1:B:567:PRO:HB2	1:B:731:HIS:CE1	2.56	0.41
1:B:658:TYR:OH	1:B:697:ASP:HB3	2.21	0.41
1:B:667:THR:HG22	1:B:668:ALA:N	2.36	0.41
1:A:311:ASN:CG	1:A:322:ILE:HD12	2.46	0.41
1:A:365:LYS:O	1:A:366:ASN:HB3	2.20	0.41
1:A:367:ALA:O	1:A:382:LEU:HG	2.20	0.41
1:A:598:TYR:CD1	1:A:639:TYR:CE2	3.05	0.41
1:A:636:GLU:C	1:A:638:ASN:N	2.79	0.41
1:A:246:GLY:O	1:A:360:ASN:ND2	2.54	0.40
1:A:423:LEU:O	1:A:426:ARG:HG2	2.21	0.40
1:A:14:GLY:O	1:B:181:TYR:HD1	2.05	0.40
1:A:668:ALA:O	1:A:681:GLY:HA2	2.21	0.40
1:B:491:PHE:CG	1:B:492:ARG:N	2.90	0.40
1:B:634:VAL:HG12	1:B:653:LYS:O	2.21	0.40
1:A:386:LEU:C	1:A:388:THR:N	2.79	0.40
1:B:395:ASP:HB3	1:B:398:TYR:HB2	2.03	0.40
1:A:391:ALA:O	1:A:395:ASP:HB2	2.21	0.40
1:A:399:ASP:O	1:A:402:CYS:HB2	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:HIS:ND1	1:B:582:VAL:CG1[2_465]	2.06	0.14

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	707/768 (92%)	637 (90%)	52 (7%)	18 (2%)	4	17
1	B	707/768 (92%)	655 (93%)	38 (5%)	14 (2%)	6	22
All	All	1414/1536 (92%)	1292 (91%)	90 (6%)	32 (2%)	5	19

All (32) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	LYS
1	A	10	ASN
1	A	245	ASP
1	A	365	LYS
1	A	538	SER
1	B	8	LYS
1	B	10	ASN
1	B	534	LYS
1	B	536	ASN
1	A	185	GLU
1	A	192	GLU
1	A	291	HIS
1	A	366	ASN
1	A	637	ALA
1	A	640	ASP
1	B	560	GLN
1	A	367	ALA
1	A	387	THR
1	B	369	PRO
1	B	431	ARG
1	B	601	GLY
1	A	191	ASN
1	A	494	SER
1	A	581	ASP
1	B	244	PRO
1	B	296	GLU
1	B	366	ASN
1	B	535	PHE
1	B	517	ASP
1	A	396	PRO
1	A	244	PRO
1	B	372	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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	576/622 (93%)	538 (93%)	38 (7%)	15	43
1	B	576/622 (93%)	531 (92%)	45 (8%)	11	35
All	All	1152/1244 (93%)	1069 (93%)	83 (7%)	13	39

All (83) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	ARG
1	A	8	LYS
1	A	65	LYS
1	A	97	ARG
1	A	120	ASP
1	A	130	LEU
1	A	153	ASN
1	A	178	GLU
1	A	192	GLU
1	A	280	SER
1	A	336	LYS
1	A	339	MET
1	A	366	ASN
1	A	385	MET
1	A	388	THR
1	A	400	LYS
1	A	402	CYS
1	A	411	LYS
1	A	432	THR
1	A	468	LYS
1	A	505	ILE
1	A	512	GLU
1	A	529	GLU
1	A	532	GLN
1	A	538	SER
1	A	539	SER
1	A	540	SER

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Mol	Chain	Res	Type
1	A	582	VAL
1	A	586	THR
1	A	609	GLN
1	A	629	ILE
1	A	633	ARG
1	A	639	TYR
1	A	649	LYS
1	A	673	ASP
1	A	699	ILE
1	A	719	GLU
1	A	720	GLU
1	B	7	ARG
1	B	8	LYS
1	B	9	SER
1	B	64	THR
1	B	97	ARG
1	B	172	ASP
1	B	173	THR
1	B	227	SER
1	B	255	LYS
1	B	283	LYS
1	B	284	THR
1	B	293	VAL
1	B	303	GLU
1	B	347	LYS
1	B	349	ASP
1	B	368	GLU
1	B	384	THR
1	B	386	LEU
1	B	388	THR
1	B	406	LEU
1	B	428	MET
1	B	441	SER
1	B	447	GLU
1	B	468	LYS
1	B	471	LEU
1	B	496	LYS
1	B	512	GLU
1	B	534	LYS
1	B	545	SER
1	B	555	VAL
1	B	574	ASP

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Mol	Chain	Res	Type
1	B	582	VAL
1	B	600	LYS
1	B	602	THR
1	B	603	LYS
1	B	629	ILE
1	B	639	TYR
1	B	653	LYS
1	B	665	THR
1	B	674	ASN
1	B	678	VAL
1	B	680	ILE
1	B	687	HIS
1	B	697	ASP
1	B	719	GLU

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

Mol	Chain	Res	Type
1	A	19	HIS
1	A	191	ASN
1	A	226	GLN
1	A	233	HIS
1	A	304	HIS
1	A	378	ASN
1	A	579	HIS
1	B	33	GLN
1	B	221	HIS
1	B	226	GLN
1	B	291	HIS
1	B	292	HIS
1	B	304	HIS
1	B	532	GLN
1	B	591	HIS
1	B	609	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEM	A	801	1	50,50,50	1.53	6 (12%)	67,82,82	1.54	10 (14%)
2	HEM	B	801	1	50,50,50	1.52	6 (12%)	67,82,82	1.54	12 (17%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	801	1	-	2/14/54/54	-
2	HEM	B	801	1	-	2/14/54/54	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	FE-NB	4.34	2.08	1.94
2	B	801	HEM	FE-NC	4.19	2.09	1.95
2	B	801	HEM	FE-NB	4.04	2.07	1.94
2	A	801	HEM	FE-NC	3.92	2.08	1.95
2	A	801	HEM	C1B-NB	-3.74	1.33	1.40
2	B	801	HEM	C1B-NB	-3.68	1.33	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	HEM	C4D-ND	-3.44	1.34	1.40
2	A	801	HEM	C4D-ND	-3.15	1.34	1.40
2	A	801	HEM	C4B-NB	-3.13	1.32	1.38
2	B	801	HEM	C4B-NB	-2.51	1.33	1.38
2	A	801	HEM	O2A-CGA	-2.26	1.23	1.30
2	B	801	HEM	C3B-C4B	2.19	1.49	1.44

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	HEM	C1B-NB-C4B	5.33	111.52	105.21
2	B	801	HEM	C1B-NB-C4B	4.72	110.79	105.21
2	B	801	HEM	CHC-C4B-NB	4.60	129.37	124.42
2	A	801	HEM	CHC-C4B-NB	4.52	129.29	124.42
2	A	801	HEM	C3B-C4B-NB	-4.02	106.58	109.47
2	A	801	HEM	CHD-C1D-ND	3.76	128.47	124.42
2	B	801	HEM	CHD-C1D-ND	3.68	128.39	124.42
2	B	801	HEM	C3B-C4B-NB	-3.59	106.89	109.47
2	A	801	HEM	CHA-C4D-ND	2.87	127.92	124.37
2	A	801	HEM	CHB-C1B-NB	2.67	127.67	124.37
2	B	801	HEM	CHA-C4D-ND	2.67	127.67	124.37
2	B	801	HEM	CHD-C1D-C2D	-2.46	121.15	125.03
2	B	801	HEM	CHA-C4D-C3D	-2.43	120.74	125.23
2	B	801	HEM	CHB-C1B-NB	2.38	127.31	124.37
2	A	801	HEM	CHD-C1D-C2D	-2.35	121.33	125.03
2	A	801	HEM	CHA-C4D-C3D	-2.22	121.13	125.23
2	B	801	HEM	CAD-C3D-C4D	2.17	128.48	124.70
2	B	801	HEM	O2D-CGD-CBD	2.12	120.70	114.00
2	B	801	HEM	C4C-NC-C1C	2.09	109.22	105.82
2	B	801	HEM	C1A-CHA-C4D	-2.08	121.35	126.25
2	A	801	HEM	C4C-NC-C1C	2.08	109.21	105.82
2	A	801	HEM	O2D-CGD-O1D	-2.06	118.03	123.33

There are no chirality outliers.

All (4) torsion outliers are listed below:

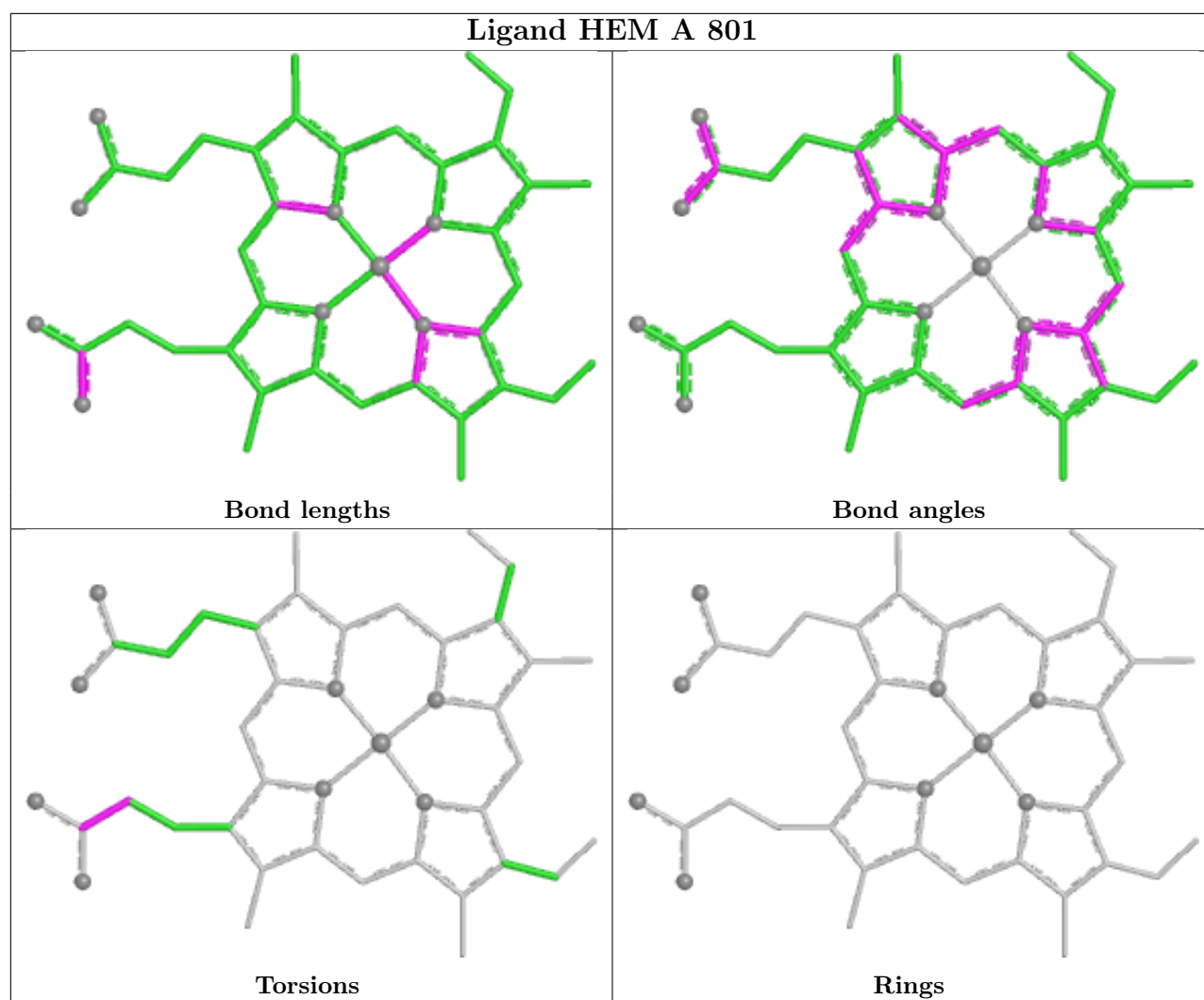
Mol	Chain	Res	Type	Atoms
2	A	801	HEM	CAA-CBA-CGA-O1A
2	A	801	HEM	CAA-CBA-CGA-O2A
2	B	801	HEM	CAA-CBA-CGA-O1A
2	B	801	HEM	CAA-CBA-CGA-O2A

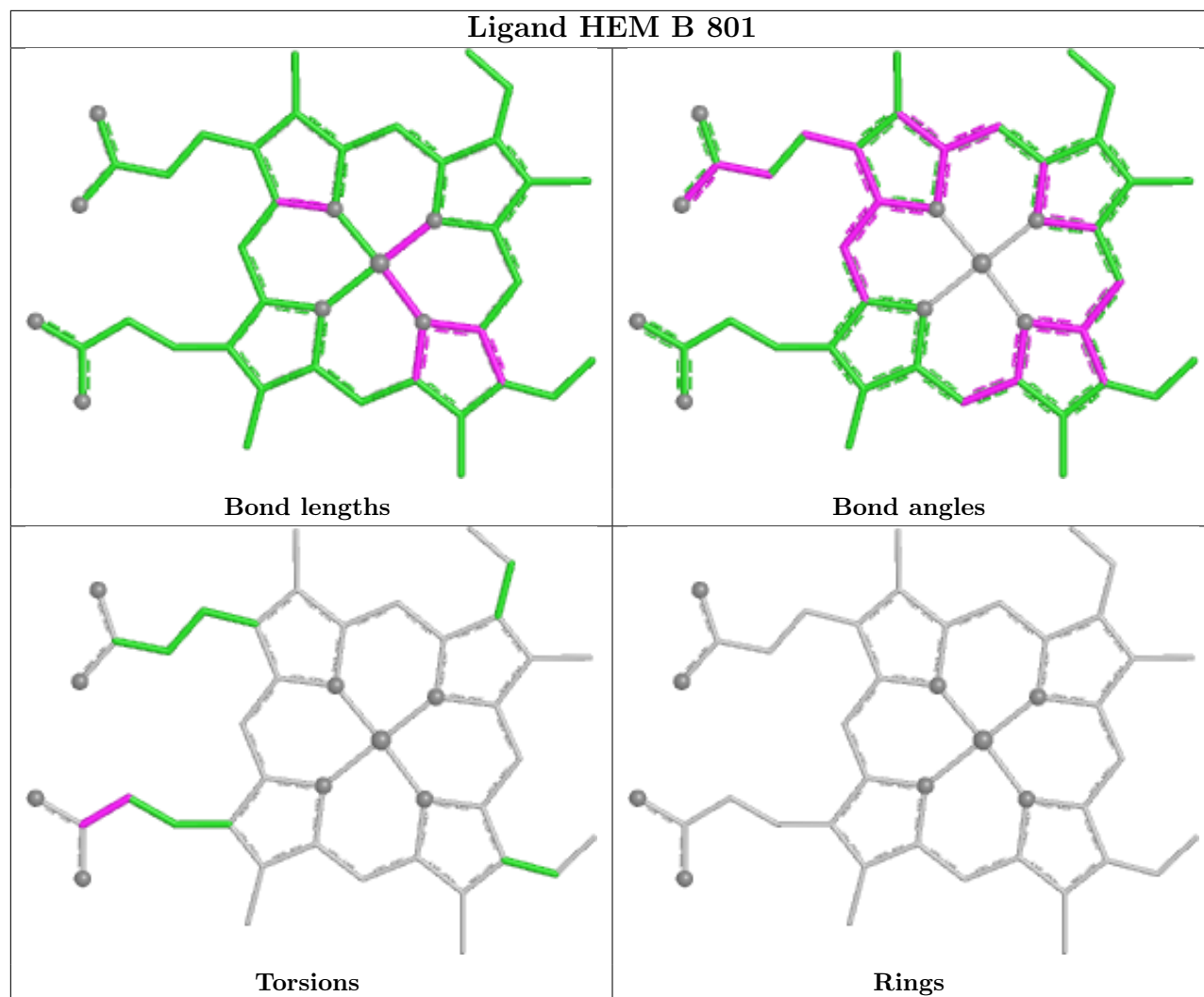
There are no ring outliers.

2 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	15	0
2	B	801	HEM	13	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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	711/768 (92%)	0.34	12 (1%) 69 61	26, 45, 75, 101	0
1	B	711/768 (92%)	0.22	9 (1%) 75 67	24, 42, 63, 87	0
All	All	1422/1536 (92%)	0.28	21 (1%) 72 64	24, 43, 70, 101	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	314	GLY	3.5
1	B	177	ASP	3.4
1	A	239	VAL	3.1
1	B	282	GLY	3.1
1	A	490	SER	2.8
1	B	371	ILE	2.7
1	A	363	VAL	2.7
1	A	375	TYR	2.5
1	A	407	ALA	2.5
1	B	686	THR	2.5
1	A	10	ASN	2.4
1	A	640	ASP	2.3
1	A	221	HIS	2.3
1	A	8	LYS	2.3
1	A	358	GLY	2.3
1	B	674	ASN	2.2
1	B	673	ASP	2.2
1	A	325	GLY	2.2
1	B	388	THR	2.1
1	B	11	VAL	2.0
1	B	741	LEU	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 [i](#)

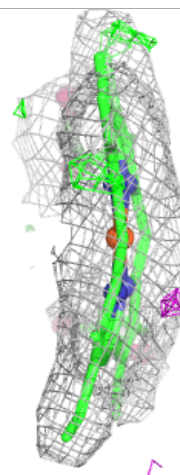
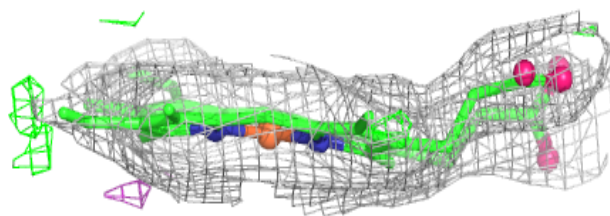
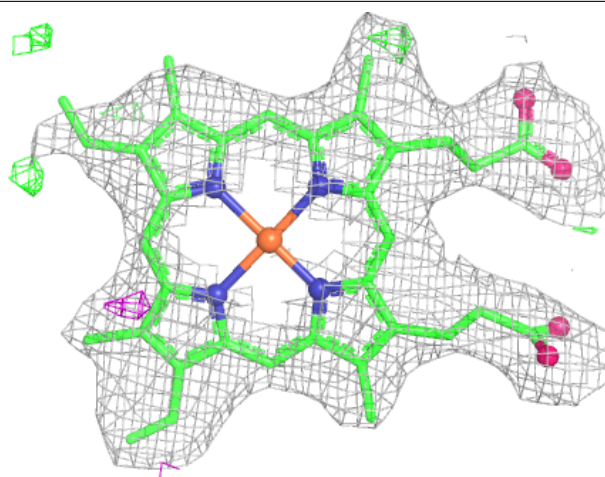
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	K	A	802	1/1	0.85	0.08	59,59,59,59	0
2	HEM	A	801	43/43	0.93	0.11	40,45,52,59	0
2	HEM	B	801	43/43	0.94	0.12	30,41,44,46	0
3	K	B	802	1/1	0.94	0.10	49,49,49,49	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.

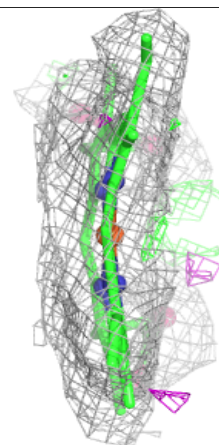
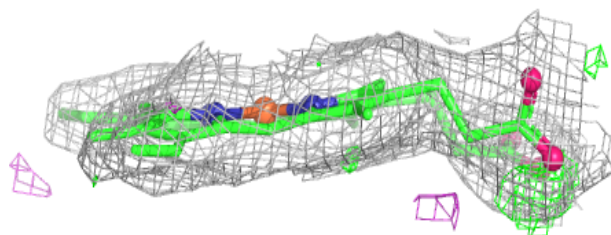
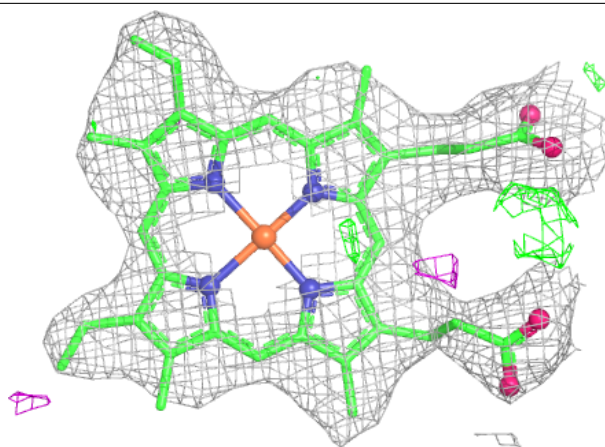
Electron density around HEM A 801:

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



Electron density around HEM B 801:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.