



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 07:09 PM UTC

PDB ID : 5C58 / pdb_00005c58
Title : A double mutant of serratia marcescens hemophore receptor HasR in complex with its hemophore HasA and heme
Authors : Becker, S.; Diederichs, K.; Welte, W.
Deposited on : 2015-06-19
Resolution : 2.79 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

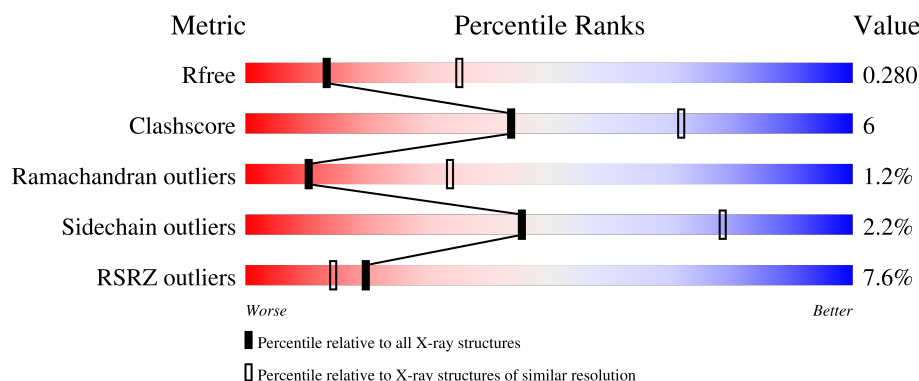
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.79 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	865	6% 63% 14% • 23%
2	B	206	4% 75% 9% 16%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6525 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 HasR protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	667	Total	C	N	O	S	0	0	0
			5226	3266	928	1019	13			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	297	ALA	ARG	engineered mutation	UNP Q79AD2
A	645	ALA	GLY	engineered mutation	UNP Q79AD2
A	800	ALA	ASN	engineered mutation	UNP Q79AD2

- Molecule 2 is a protein called Hemophore HasA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	173	Total	C	N	O	S	0	0	0
			1256	783	204	268	1			

There are 19 discrepancies between the modelled and reference sequences:

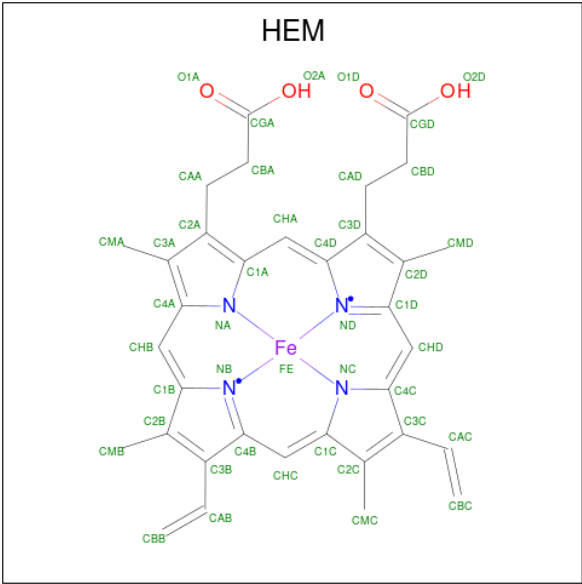
Chain	Residue	Modelled	Actual	Comment	Reference
B	-17	MET	-	initiating methionine	UNP Q54450
B	-16	ARG	-	expression tag	UNP Q54450
B	-15	GLY	-	expression tag	UNP Q54450
B	-14	SER	-	expression tag	UNP Q54450
B	-13	HIS	-	expression tag	UNP Q54450
B	-12	HIS	-	expression tag	UNP Q54450
B	-11	HIS	-	expression tag	UNP Q54450
B	-10	HIS	-	expression tag	UNP Q54450
B	-9	HIS	-	expression tag	UNP Q54450
B	-8	HIS	-	expression tag	UNP Q54450
B	-7	GLY	-	expression tag	UNP Q54450
B	-6	ILE	-	expression tag	UNP Q54450
B	-5	ARG	-	expression tag	UNP Q54450

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-4	MET	-	expression tag	UNP Q54450
B	-3	ARG	-	expression tag	UNP Q54450
B	-2	ALA	-	expression tag	UNP Q54450
B	-1	ARG	-	expression tag	UNP Q54450
B	0	TYR	-	expression tag	UNP Q54450
B	1	PRO	-	expression tag	UNP Q54450

- Molecule 3 is PROTOPORPHYRIN IX CONTAINING FE (CCD ID: HEM) (formula: C₃₄H₃₂FeN₄O₄).

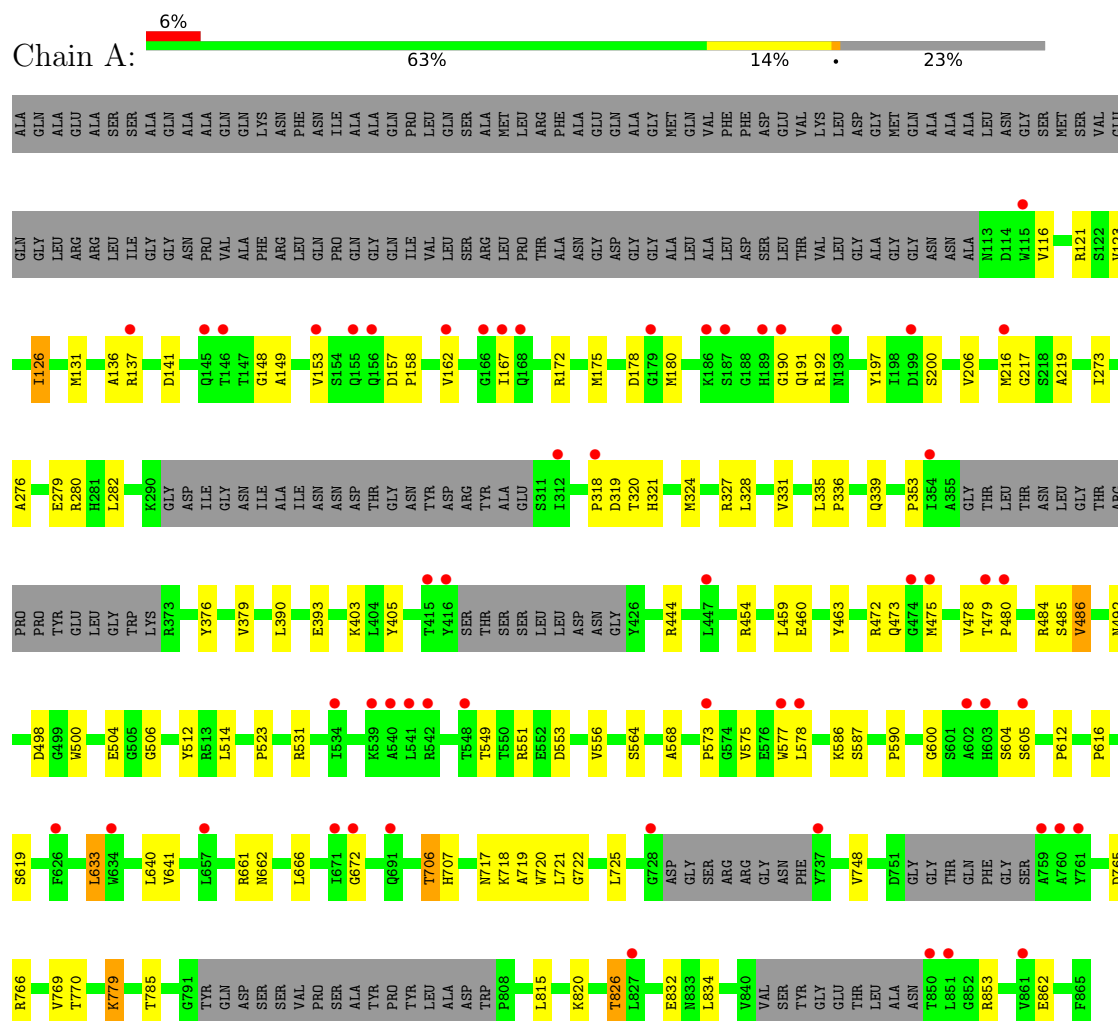


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

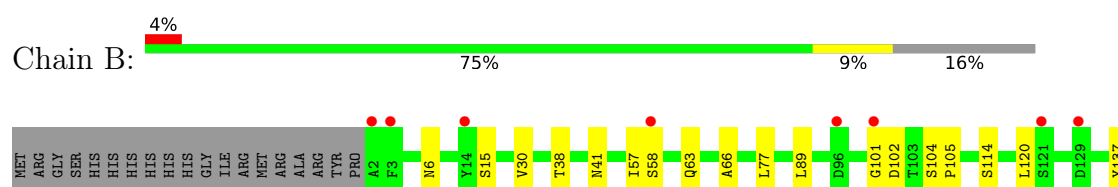
3 Residue-property plots

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: HasR protein



• Molecule 2: Hemophore HasA



T165	
A174	VAL
	GLY
	VAL
	GLN
	HIS
	ALA
	ASP
	SER
	PRO
	GLU
	LEU
	LEU
	ALA
	ALA

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	101.97Å 114.62Å 260.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.75 – 2.79 37.75 – 2.79	Depositor EDS
% Data completeness (in resolution range)	98.8 (37.75-2.79) 98.9 (37.75-2.79)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 2.81Å)	Xtriage
Refinement program	PHENIX (1.10pre-2083_1692: ???)	Depositor
R, R_{free}	0.247 , 0.296 (Not available) , 0.280	Depositor DCC
R_{free} test set	1884 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	78.8	Xtriage
Anisotropy	0.569	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6525	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.27% 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: 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	0.27	0/5340	0.67	0/7239
2	B	0.26	0/1284	0.62	0/1752
All	All	0.27	0/6624	0.66	0/8991

There are no bond length outliers.

There are no bond angle outliers.

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	5226	0	4992	65	0
2	B	1256	0	1137	10	0
3	B	43	0	30	4	0
All	All	6525	0	6159	77	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 6.

All (77) 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)
2:B:30:VAL:HG11	2:B:57:ILE:HD11	1.69	0.75
3:B:200:HEM:HHC	3:B:200:HEM:HBB2	1.69	0.74
1:A:180:MET:HE3	1:A:405:TYR:HB2	1.68	0.74
3:B:200:HEM:HBC2	3:B:200:HEM:HHD	1.72	0.72
1:A:178:ASP:O	1:A:403:LYS:NZ	2.23	0.72
1:A:531:ARG:HH11	1:A:725:LEU:HD11	1.58	0.68
2:B:30:VAL:HG12	2:B:41:ASN:HB2	1.79	0.65
1:A:149:ALA:O	1:A:766:ARG:NH2	2.30	0.63
1:A:587:SER:OG	1:A:619:SER:OG	2.22	0.58
1:A:633:LEU:HD22	1:A:640:LEU:HB2	1.85	0.58
2:B:104:SER:HB2	2:B:105:PRO:HD2	1.86	0.58
1:A:167:ILE:HG22	1:A:172:ARG:HB3	1.85	0.57
1:A:486:VAL:HA	1:A:512:TYR:HA	1.86	0.57
2:B:15:SER:HA	2:B:165:THR:HA	1.87	0.57
1:A:661:ARG:HD3	1:A:718:LYS:HA	1.88	0.56
1:A:137:ARG:HG2	1:A:282:LEU:HD13	1.88	0.56
1:A:280:ARG:HB2	1:A:324:MET:HG2	1.87	0.54
1:A:162:VAL:HG23	1:A:175:MET:HE3	1.88	0.54
1:A:720:TRP:CD1	1:A:721:LEU:HG	2.43	0.54
3:B:200:HEM:HBA2	3:B:200:HEM:HMA2	1.91	0.53
1:A:319:ASP:HB3	1:A:353:PRO:HB2	1.90	0.53
1:A:136:ALA:HB1	1:A:141:ASP:HB2	1.91	0.52
1:A:335:LEU:HB2	1:A:339:GLN:HB2	1.92	0.52
1:A:604:SER:O	1:A:604:SER:OG	2.25	0.52
1:A:273:ILE:HD13	1:A:331:VAL:HG22	1.91	0.52
1:A:717:ASN:O	1:A:719:ALA:N	2.37	0.51
1:A:590:PRO:HA	1:A:616:PRO:HB3	1.92	0.51
1:A:353:PRO:HA	1:A:376:TYR:HA	1.93	0.51
1:A:523:PRO:HB2	1:A:666:LEU:HB2	1.94	0.50
1:A:484:ARG:HB2	1:A:514:LEU:HD13	1.93	0.49
2:B:89:LEU:HD23	2:B:120:LEU:HD12	1.94	0.49
1:A:498:ASP:HB3	1:A:500:TRP:CD1	2.47	0.49
1:A:478:VAL:HG22	1:A:600:GLY:HA3	1.95	0.48
1:A:504:GLU:HB3	1:A:568:ALA:HB3	1.94	0.48
1:A:820:LYS:HG2	1:A:826:THR:HB	1.96	0.48
1:A:551:ARG:NH1	1:A:553:ASP:OD1	2.46	0.48
1:A:190:GLY:O	1:A:191:GLN:HG2	2.13	0.48
1:A:339:GLN:HG2	1:A:390:LEU:HD13	1.96	0.47
2:B:101:GLY:HA2	2:B:102:ASP:HA	1.59	0.47
1:A:126:ILE:HD11	1:A:131:MET:HG2	1.97	0.47
1:A:605:SER:OG	2:B:38:THR:HA	2.14	0.47
1:A:148:GLY:H	1:A:706:THR:HG21	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:VAL:HG22	1:A:577:TRP:H	1.80	0.46
1:A:556:VAL:HG22	1:A:612:PRO:HB3	1.97	0.46
1:A:717:ASN:C	1:A:719:ALA:H	2.23	0.46
1:A:121:ARG:HE	1:A:121:ARG:HB2	1.63	0.45
1:A:137:ARG:HB2	1:A:853:ARG:NH2	2.32	0.45
1:A:779:LYS:HE3	1:A:820:LYS:HG3	1.98	0.45
1:A:472:ARG:HG2	1:A:473:GLN:H	1.83	0.44
1:A:217:GLY:HA2	1:A:460:GLU:OE1	2.18	0.44
1:A:577:TRP:HD1	1:A:578:LEU:HB2	1.83	0.44
1:A:779:LYS:HA	1:A:779:LYS:HD2	1.61	0.44
1:A:832:GLU:OE1	1:A:853:ARG:NH2	2.51	0.44
1:A:121:ARG:HH21	1:A:123:VAL:HG11	1.84	0.43
1:A:463:TYR:CD2	1:A:485:SER:HB3	2.52	0.43
1:A:492:ASN:HB3	1:A:506:GLY:HA3	2.01	0.43
1:A:197:TYR:CE2	1:A:379:VAL:HG11	2.53	0.43
1:A:321:HIS:CE1	1:A:353:PRO:HG2	2.54	0.43
1:A:770:THR:HG22	1:A:785:THR:HG23	2.00	0.43
1:A:826:THR:HG23	1:A:862:GLU:HB3	2.00	0.43
1:A:720:TRP:C	1:A:722:GLY:H	2.27	0.42
2:B:58:SER:HA	2:B:66:ALA:HB2	2.02	0.42
2:B:6:ASN:HB2	2:B:114:SER:HB3	2.00	0.42
1:A:393:GLU:CD	1:A:393:GLU:H	2.28	0.42
2:B:137:TYR:HB2	3:B:200:HEM:CBC	2.50	0.41
1:A:444:ARG:HG2	1:A:454:ARG:HG3	2.02	0.41
1:A:707:HIS:ND1	1:A:765:ASP:OD1	2.53	0.41
1:A:475:MET:HA	1:A:478:VAL:HG23	2.02	0.41
1:A:137:ARG:HD3	1:A:853:ARG:NE	2.35	0.41
1:A:279:GLU:OE1	1:A:327:ARG:NH1	2.54	0.41
1:A:276:ALA:HB3	1:A:328:LEU:HB3	2.03	0.41
1:A:662:ASN:ND2	1:A:718:LYS:HE3	2.36	0.41
1:A:815:LEU:HD11	1:A:834:LEU:HD22	2.03	0.41
1:A:564:SER:HB3	1:A:586:LYS:O	2.21	0.40
1:A:126:ILE:HG23	1:A:206:VAL:HB	2.02	0.40
1:A:190:GLY:O	1:A:192:ARG:HG2	2.22	0.40
1:A:157:ASP:HA	1:A:158:PRO:HD2	1.97	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	651/865 (75%)	576 (88%)	67 (10%)	8 (1%)	10	34
2	B	171/206 (83%)	151 (88%)	18 (10%)	2 (1%)	10	34
All	All	822/1071 (77%)	727 (88%)	85 (10%)	10 (1%)	10	34

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	480	PRO
2	B	63	GLN
2	B	77	LEU
1	A	318	PRO
1	A	672	GLY
1	A	216	MET
1	A	219	ALA
1	A	573	PRO
1	A	633	LEU
1	A	336	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	546/693 (79%)	531 (97%)	15 (3%)	39	74
2	B	132/158 (84%)	132 (100%)	0	100	100
All	All	678/851 (80%)	663 (98%)	15 (2%)	45	78

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	116	VAL
1	A	126	ILE
1	A	153	VAL
1	A	200	SER
1	A	320	THR
1	A	459	LEU
1	A	479	THR
1	A	486	VAL
1	A	549	THR
1	A	641	VAL
1	A	706	THR
1	A	748	VAL
1	A	769	VAL
1	A	779	LYS
1	A	826	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	182	GLN
1	A	229	ASN
1	A	401	GLN
1	A	440	GLN
1	A	456	ASN
1	A	653	ASN
1	A	662	ASN
2	B	36	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	HEM	B	200	2	50,50,50	1.92	8 (16%)	67,82,82	1.48	9 (13%)

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	HEM	B	200	2	-	4/14/54/54	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	200	HEM	C3D-C2D	7.91	1.53	1.36
3	B	200	HEM	FE-NB	4.78	2.09	1.94
3	B	200	HEM	FE-ND	4.18	2.07	1.94
3	B	200	HEM	FE-NA	3.35	2.06	1.95
3	B	200	HEM	FE-NC	3.09	2.05	1.95
3	B	200	HEM	CAB-C3B	2.99	1.55	1.47
3	B	200	HEM	CAC-C3C	2.95	1.55	1.47
3	B	200	HEM	CMB-C2B	2.02	1.54	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	200	HEM	C4D-ND-C1D	5.44	111.65	105.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	200	HEM	C3B-C2B-C1B	2.94	108.61	106.41
3	B	200	HEM	C1B-NB-C4B	2.39	108.04	105.21
3	B	200	HEM	CMA-C3A-C4A	-2.39	121.78	125.42
3	B	200	HEM	CHC-C1C-NC	2.38	127.04	124.45
3	B	200	HEM	CBA-CAA-C2A	2.30	118.91	112.53
3	B	200	HEM	CAA-C2A-C3A	2.14	131.87	127.07
3	B	200	HEM	C3B-C4B-NB	-2.09	107.97	109.47
3	B	200	HEM	CMA-C3A-C2A	2.07	130.00	125.62

There are no chirality outliers.

All (4) torsion outliers are listed below:

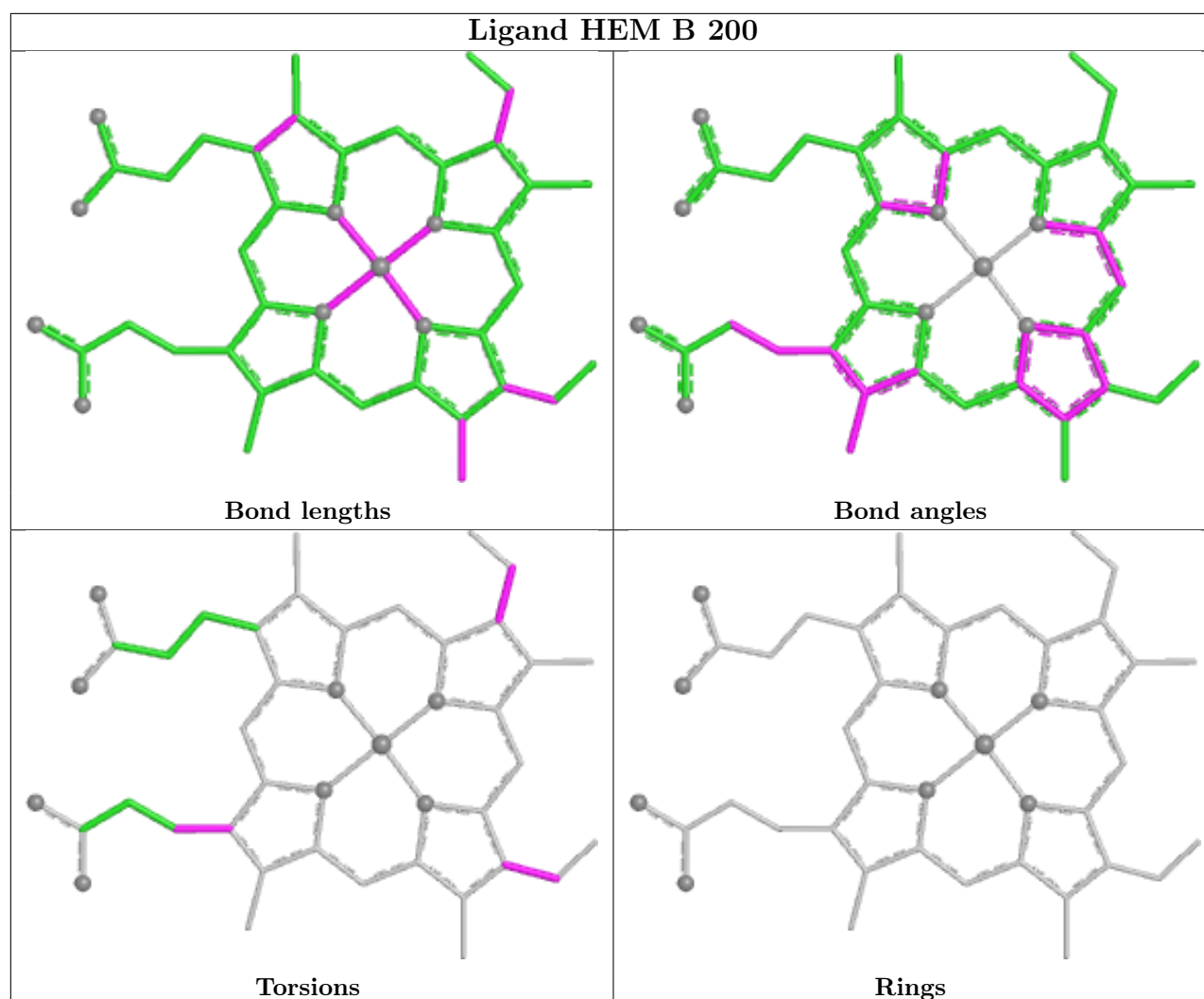
Mol	Chain	Res	Type	Atoms
3	B	200	HEM	C3A-C2A-CAA-CBA
3	B	200	HEM	C1A-C2A-CAA-CBA
3	B	200	HEM	C4B-C3B-CAB-CBB
3	B	200	HEM	C4C-C3C-CAC-CBC

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	200	HEM	4	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

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	667/865 (77%)	0.57	56 (8%)	17 12	66, 103, 169, 248	0
2	B	173/206 (83%)	0.55	8 (4%)	37 29	108, 142, 180, 230	0
All	All	840/1071 (78%)	0.57	64 (7%)	20 14	66, 112, 174, 248	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	759	ALA	4.8
1	A	760	ALA	4.6
1	A	728	GLY	4.0
1	A	115	TRP	3.9
1	A	737	TYR	3.8
1	A	187	SER	3.8
2	B	2	ALA	3.8
1	A	541	LEU	3.7
1	A	153	VAL	3.7
1	A	851	LEU	3.7
1	A	318	PRO	3.7
1	A	539	LYS	3.5
1	A	577	TRP	3.5
1	A	671	ILE	3.4
1	A	480	PRO	3.2
1	A	190	GLY	3.1
1	A	162	VAL	3.1
1	A	145	GLN	3.0
1	A	479	THR	3.0
1	A	155	GLN	2.9
1	A	850	THR	2.9
1	A	474	GLY	2.9
1	A	146	THR	2.9
1	A	199	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	354	ILE	2.7
1	A	578	LEU	2.7
1	A	603	HIS	2.7
1	A	861	VAL	2.7
1	A	827	LEU	2.6
1	A	168	GLN	2.6
2	B	58	SER	2.6
1	A	167	ILE	2.5
1	A	761	TYR	2.5
1	A	137	ARG	2.5
1	A	573	PRO	2.5
1	A	605	SER	2.4
1	A	475	MET	2.4
1	A	634	TRP	2.4
1	A	672	GLY	2.3
1	A	548	THR	2.3
2	B	101	GLY	2.3
1	A	166	GLY	2.3
1	A	540	ALA	2.2
1	A	216	MET	2.2
2	B	129	ASP	2.2
2	B	96	ASP	2.2
1	A	657	LEU	2.2
1	A	542	ARG	2.2
2	B	14	TYR	2.2
1	A	186	LYS	2.2
1	A	415	THR	2.2
1	A	416	TYR	2.2
1	A	691	GLN	2.1
2	B	121	SER	2.1
1	A	626	PHE	2.1
1	A	193	ASN	2.1
1	A	179	GLY	2.1
1	A	534	ILE	2.1
1	A	156	GLN	2.1
1	A	189	HIS	2.1
1	A	602	ALA	2.1
2	B	3	PHE	2.1
1	A	447	LEU	2.0
1	A	312	ILE	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](#)

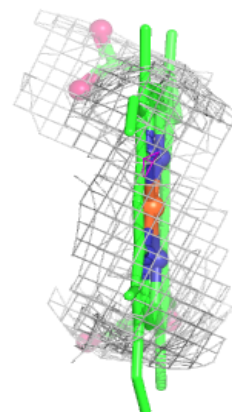
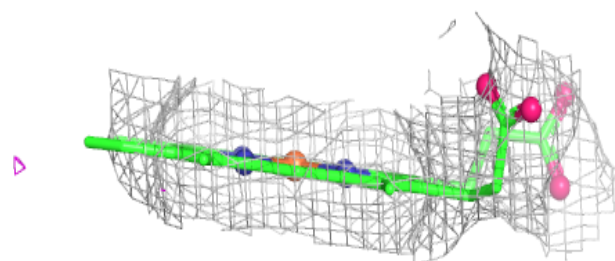
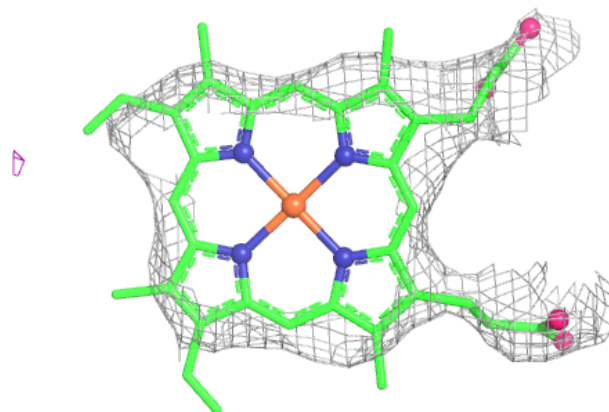
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	HEM	B	200	43/43	0.97	0.12	112,162,179,183	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 B 200:

$2mF_o-DF_c$ (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.