Full wwPDB X-ray Structure Validation Report ⓘ

May 19, 2024 – 08:04 AM EDT

PDB ID	:	3X16
Title	:	Crystal structure of the catalase-peroxidase KatG W78F mutant from Synechococcus elongatus PCC7942
Authors	:	Tada, T.; Wada, K.; Kamachi, S.
Deposited on	:	2014-10-30
Resolution	:	2.65 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:

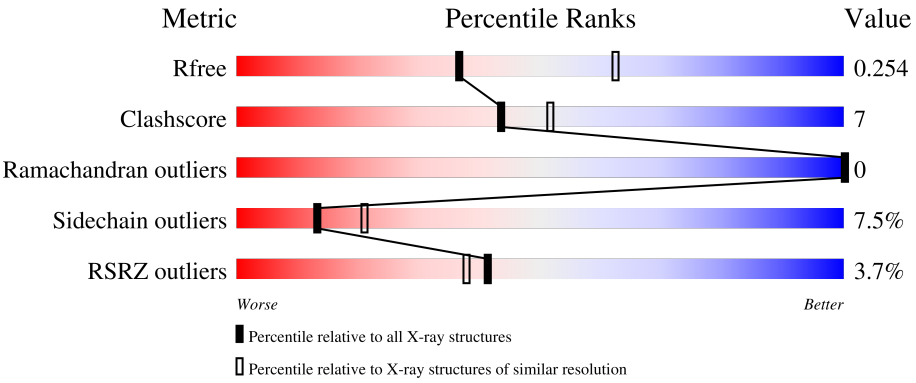
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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}	130704	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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 <=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	720	4% 80% 16%

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
2	HEB	A	801	X	-	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5780 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.

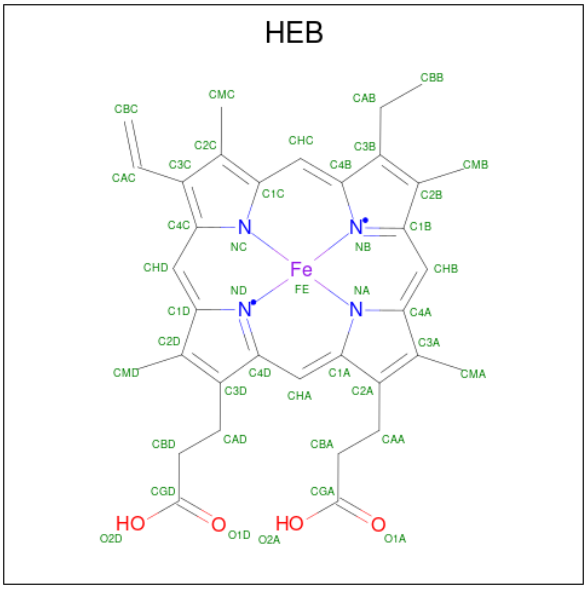
- Molecule 1 is a protein called Catalase-peroxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	710	5579	3521	979	1060	19	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	PHE	TRP	engineered mutation	UNP Q31MN3

- Molecule 2 is HEME B/C (three-letter code: HEB) (formula: $C_{34}H_{34}FeN_4O_4$).



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

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Na 3 3	0	0

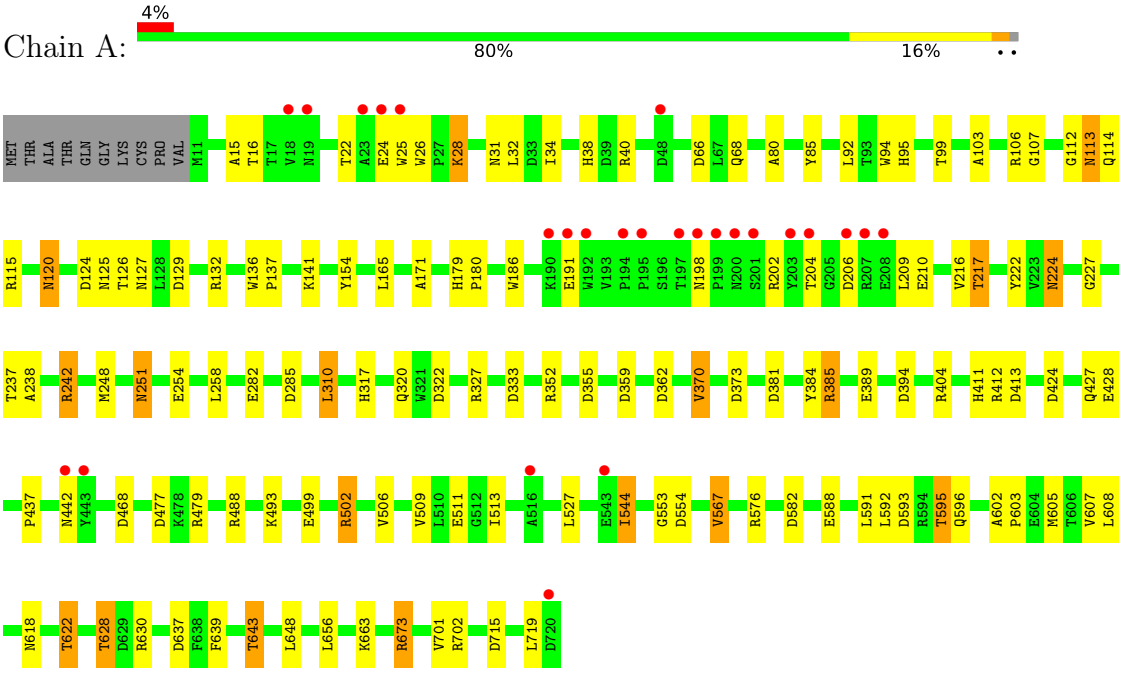
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	155	Total O 155 155	0	0

3 Residue-property plots (i)

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: Catalase-peroxidase



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	108.25Å 108.25Å 203.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.33 – 2.65 42.33 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.4 (42.33-2.65) 99.4 (42.33-2.65)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.39 (at 2.65Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.197 , 0.254 0.201 , 0.254	Depositor DCC
R_{free} test set	1784 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	45.0	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 31.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.53$, $< L^2 > = 0.37$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	5780	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: NA, HEB

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	0.81	1/5725 (0.0%)	0.96	17/7796 (0.2%)

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	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	ASP	CB-CG	6.02	1.64	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	322	ASP	CB-CG-OD1	6.71	124.33	118.30
1	A	242	ARG	NE-CZ-NH1	6.63	123.62	120.30
1	A	362	ASP	CB-CG-OD1	6.63	124.27	118.30
1	A	385	ARG	NE-CZ-NH1	6.41	123.50	120.30
1	A	355	ASP	CB-CG-OD2	-6.14	112.78	118.30
1	A	673	ARG	NE-CZ-NH1	6.11	123.36	120.30
1	A	327	ARG	NE-CZ-NH2	-6.07	117.26	120.30
1	A	424	ASP	CB-CG-OD1	-5.91	112.98	118.30
1	A	370	VAL	CB-CA-C	-5.75	100.47	111.40
1	A	362	ASP	CB-CG-OD2	-5.72	113.15	118.30
1	A	502	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	A	310	LEU	CB-CG-CD2	5.63	120.58	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	404	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	A	352	ARG	NE-CZ-NH2	-5.35	117.63	120.30
1	A	385	ARG	NE-CZ-NH2	-5.31	117.64	120.30
1	A	394	ASP	CB-CG-OD1	5.23	123.01	118.30
1	A	593	ASP	CB-CG-OD1	5.09	122.88	118.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	15	ALA	Peptide
1	A	210	GLU	Peptide

5.2 Too-close contacts (i)

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	5363	73	0
2	A	43	0	32	2	0
3	A	3	0	0	0	0
4	A	155	0	0	6	0
All	All	5780	0	5395	74	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 7.

All (74) 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:94:TRP:CH2	1:A:222:TYR:HE2	1.25	1.54
1:A:222:TYR:HE1	1:A:248:MET:SD	1.31	1.49
1:A:222:TYR:CE1	1:A:248:MET:SD	2.07	1.46
1:A:94:TRP:CH2	1:A:222:TYR:CE2	2.15	1.31
1:A:94:TRP:HH2	1:A:222:TYR:CE2	1.48	1.27
1:A:94:TRP:CZ2	1:A:222:TYR:HE2	1.84	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:GLN:HE21	1:A:132:ARG:HH11	1.27	0.80
1:A:222:TYR:CZ	1:A:248:MET:SD	2.75	0.79
1:A:94:TRP:CZ2	1:A:222:TYR:CE2	2.67	0.78
1:A:618:ASN:HB3	1:A:622:THR:HG22	1.69	0.74
1:A:648:LEU:C	1:A:648:LEU:HD12	2.13	0.69
1:A:38:HIS:H	1:A:179:HIS:HE1	1.43	0.66
1:A:385:ARG:NH2	1:A:389:GLU:OE1	2.29	0.65
1:A:595:THR:HG21	1:A:605:MET:SD	2.38	0.64
1:A:171:ALA:H	1:A:411:HIS:HE1	1.48	0.61
1:A:639:PHE:O	1:A:643:THR:HB	2.02	0.60
1:A:103:ALA:HA	1:A:567:VAL:HG22	1.84	0.60
1:A:320:GLN:HB2	4:A:953:HOH:O	2.02	0.59
1:A:114:GLN:HE21	1:A:132:ARG:NH1	1.98	0.59
1:A:106:ARG:HH21	1:A:596:GLN:HE21	1.51	0.59
1:A:618:ASN:CB	1:A:622:THR:HG22	2.33	0.58
1:A:251:ASN:HD22	1:A:251:ASN:C	2.09	0.56
1:A:488:ARG:O	1:A:493:LYS:HD3	2.06	0.56
1:A:99:THR:HG22	1:A:107:GLY:HA3	1.88	0.56
1:A:502:ARG:O	1:A:506:VAL:HG23	2.05	0.55
1:A:544:ILE:HG22	4:A:1020:HOH:O	2.05	0.55
1:A:428:GLU:HB2	4:A:949:HOH:O	2.07	0.55
1:A:237:THR:O	1:A:238:ALA:C	2.44	0.55
1:A:99:THR:HG22	1:A:107:GLY:CA	2.38	0.54
1:A:94:TRP:CD1	1:A:95:HIS:HD2	2.27	0.53
1:A:179:HIS:HD2	1:A:180:PRO:O	1.93	0.52
1:A:509:VAL:O	1:A:513:ILE:HD12	2.09	0.52
1:A:216:VAL:HG23	1:A:217:THR:HG22	1.93	0.51
1:A:38:HIS:H	1:A:179:HIS:CE1	2.26	0.50
1:A:488:ARG:NH2	1:A:554:ASP:HB3	2.27	0.49
1:A:66:ASP:OD2	1:A:141:LYS:NZ	2.44	0.49
1:A:591:LEU:O	1:A:595:THR:HG23	2.12	0.49
1:A:588:GLU:OE2	1:A:673:ARG:NH2	2.45	0.49
1:A:628:THR:HB	1:A:630:ARG:H	1.79	0.48
1:A:112:GLY:O	1:A:115:ARG:HG2	2.14	0.48
1:A:468:ASP:OD2	1:A:576:ARG:NH1	2.47	0.47
1:A:412:ARG:NH2	1:A:479:ARG:HD2	2.29	0.47
2:A:801:HEB:HBC1	2:A:801:HEB:HMC1	1.97	0.47
1:A:25:TRP:HB2	1:A:26:TRP:CE3	2.50	0.46
1:A:202:ARG:HD3	1:A:209:LEU:HD11	1.97	0.46
1:A:94:TRP:CH2	1:A:222:TYR:CZ	2.95	0.45
1:A:136:TRP:N	1:A:137:PRO:CD	2.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:ASN:ND2	1:A:254:GLU:H	2.14	0.45
1:A:127:ASN:HA	1:A:129:ASP:OD1	2.17	0.44
1:A:628:THR:HG22	1:A:637:ASP:OD2	2.17	0.44
1:A:224:ASN:HB3	1:A:227:GLY:O	2.18	0.44
1:A:602:ALA:HB3	1:A:603:PRO:HD3	2.00	0.43
1:A:126:THR:O	1:A:127:ASN:HB2	2.18	0.43
1:A:120:ASN:HD21	1:A:282:GLU:HG2	1.83	0.43
1:A:113:ASN:HD22	1:A:114:GLN:N	2.17	0.43
1:A:317:HIS:HD2	4:A:916:HOH:O	2.02	0.43
1:A:34:ILE:HD11	1:A:592:LEU:HG	2.01	0.43
1:A:381:ASP:HB3	1:A:384:TYR:HB2	2.01	0.42
1:A:94:TRP:CD1	1:A:95:HIS:CD2	3.07	0.42
1:A:80:ALA:HB2	1:A:85:TYR:CE1	2.55	0.42
1:A:618:ASN:ND2	4:A:1055:HOH:O	2.52	0.42
1:A:258:LEU:HB3	2:A:801:HEB:HMC1	2.01	0.41
1:A:317:HIS:CD2	4:A:916:HOH:O	2.73	0.41
1:A:251:ASN:HD21	1:A:254:GLU:H	1.69	0.41
1:A:499:GLU:OE1	1:A:576:ARG:NH2	2.54	0.41
1:A:80:ALA:HB2	1:A:85:TYR:CD1	2.56	0.41
1:A:95:HIS:ND1	1:A:125:ASN:ND2	2.68	0.41
1:A:28:LYS:H	1:A:28:LYS:HD3	1.86	0.40
1:A:413:ASP:HA	1:A:477:ASP:HB2	2.03	0.40
1:A:99:THR:HG23	1:A:186:TRP:CH2	2.57	0.40
1:A:701:VAL:O	1:A:702:ARG:C	2.58	0.40
1:A:715:ASP:C	1:A:715:ASP:OD1	2.59	0.40
1:A:437:PRO:O	1:A:553:GLY:HA3	2.21	0.40
1:A:591:LEU:O	1:A:595:THR:CG2	2.69	0.40

There are no symmetry-related clashes.

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	708/720 (98%)	670 (95%)	38 (5%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	573/581 (99%)	530 (92%)	43 (8%)	13 21

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	THR
1	A	22	THR
1	A	24	GLU
1	A	28	LYS
1	A	31	ASN
1	A	32	LEU
1	A	40	ARG
1	A	68	GLN
1	A	92	LEU
1	A	113	ASN
1	A	120	ASN
1	A	124	ASP
1	A	154	TYR
1	A	165	LEU
1	A	191	GLU
1	A	198	ASN
1	A	204	THR
1	A	206	ASP
1	A	217	THR
1	A	224	ASN
1	A	242	ARG
1	A	251	ASN
1	A	310	LEU

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Mol	Chain	Res	Type
1	A	333	ASP
1	A	359	ASP
1	A	370	VAL
1	A	373	ASP
1	A	427	GLN
1	A	442	ASN
1	A	511	GLU
1	A	527	LEU
1	A	544	ILE
1	A	567	VAL
1	A	582	ASP
1	A	595	THR
1	A	607	VAL
1	A	608	LEU
1	A	622	THR
1	A	628	THR
1	A	643	THR
1	A	656	LEU
1	A	663	LYS
1	A	719	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	31	ASN
1	A	37	GLN
1	A	68	GLN
1	A	113	ASN
1	A	114	GLN
1	A	120	ASN
1	A	125	ASN
1	A	179	HIS
1	A	224	ASN
1	A	251	ASN
1	A	317	HIS
1	A	411	HIS
1	A	440	ASN
1	A	446	GLN
1	A	535	GLN
1	A	572	HIS
1	A	596	GLN
1	A	655	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

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 3 are monoatomic - leaving 1 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	HEB	A	801	1	48,50,50	2.47	19 (39%)	55,82,82	3.08	30 (54%)

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	HEB	A	801	1	1/1/3/8	5/12/54/54	-

All (19) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEB	C1D-ND	-5.56	1.30	1.40
2	A	801	HEB	C4B-NB	-5.14	1.31	1.40
2	A	801	HEB	C2A-C3A	4.74	1.46	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEB	CHB-C4A	4.24	1.46	1.38
2	A	801	HEB	C1A-NA	-4.14	1.31	1.39
2	A	801	HEB	C3C-C2C	4.08	1.46	1.40
2	A	801	HEB	C3D-C2D	4.02	1.45	1.36
2	A	801	HEB	C3B-C2B	3.85	1.44	1.36
2	A	801	HEB	CHA-C1A	3.75	1.45	1.38
2	A	801	HEB	CHC-C4B	3.71	1.44	1.35
2	A	801	HEB	CHD-C1D	3.64	1.44	1.35
2	A	801	HEB	CHA-C4D	3.22	1.46	1.39
2	A	801	HEB	C4D-ND	-3.15	1.32	1.38
2	A	801	HEB	CHB-C1B	2.72	1.45	1.39
2	A	801	HEB	FE-NA	2.70	2.06	1.95
2	A	801	HEB	C4B-C3B	2.52	1.49	1.45
2	A	801	HEB	C4D-C3D	2.34	1.49	1.45
2	A	801	HEB	O1D-CGD	2.26	1.29	1.22
2	A	801	HEB	C4C-NC	-2.05	1.32	1.36

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	801	HEB	CAD-C3D-C4D	6.65	136.28	124.66
2	A	801	HEB	C3D-C4D-ND	6.23	116.39	110.36
2	A	801	HEB	C2B-C1B-NB	6.10	117.19	109.88
2	A	801	HEB	C2D-C1D-ND	5.87	116.80	109.84
2	A	801	HEB	C1B-C2B-C3B	-5.83	100.83	106.96
2	A	801	HEB	C3B-C4B-NB	5.17	115.92	110.17
2	A	801	HEB	CMC-C2C-C3C	5.14	134.29	124.68
2	A	801	HEB	CAB-C3B-C4B	4.69	130.90	124.81
2	A	801	HEB	C4A-C3A-C2A	-4.60	100.23	106.94
2	A	801	HEB	CHB-C1B-C2B	-4.47	118.00	124.98
2	A	801	HEB	C3C-C4C-NC	4.32	114.80	109.21
2	A	801	HEB	C4D-C3D-C2D	-4.19	100.79	106.90
2	A	801	HEB	CHA-C4D-ND	-4.12	119.94	124.42
2	A	801	HEB	C1D-C2D-C3D	-3.90	102.86	106.96
2	A	801	HEB	C3A-C4A-NA	3.30	115.78	109.69
2	A	801	HEB	CAA-CBA-CGA	-3.18	106.77	113.60
2	A	801	HEB	O1A-CGA-CBA	-3.14	112.99	123.08
2	A	801	HEB	CMB-C2B-C1B	3.07	129.72	125.04
2	A	801	HEB	C2A-C1A-NA	3.02	113.26	110.32
2	A	801	HEB	CBD-CAD-C3D	2.86	120.56	112.63
2	A	801	HEB	CHB-C4A-C3A	-2.74	119.74	125.48
2	A	801	HEB	CAD-C3D-C2D	-2.73	122.80	127.88

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	801	HEB	CMA-C3A-C2A	2.72	133.50	126.12
2	A	801	HEB	CHD-C1D-C2D	-2.62	119.48	126.72
2	A	801	HEB	C4B-NB-C1B	-2.49	102.50	105.07
2	A	801	HEB	O2A-CGA-CBA	2.40	121.74	114.03
2	A	801	HEB	C4B-C3B-C2B	-2.35	103.48	106.90
2	A	801	HEB	CAD-CBD-CGD	-2.28	108.70	113.60
2	A	801	HEB	CMD-C2D-C1D	2.26	128.48	125.04
2	A	801	HEB	CMC-C2C-C1C	-2.25	125.01	128.46

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	801	HEB	NA

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	HEB	C2D-C3D-CAD-CBD
2	A	801	HEB	C2B-C3B-CAB-CBB
2	A	801	HEB	CAA-CBA-CGA-O2A
2	A	801	HEB	CAA-CBA-CGA-O1A
2	A	801	HEB	C4D-C3D-CAD-CBD

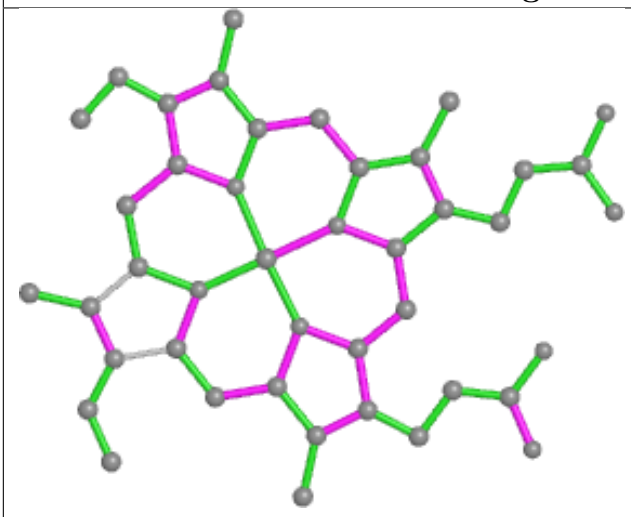
There are no ring outliers.

1 monomer is involved in 2 short contacts:

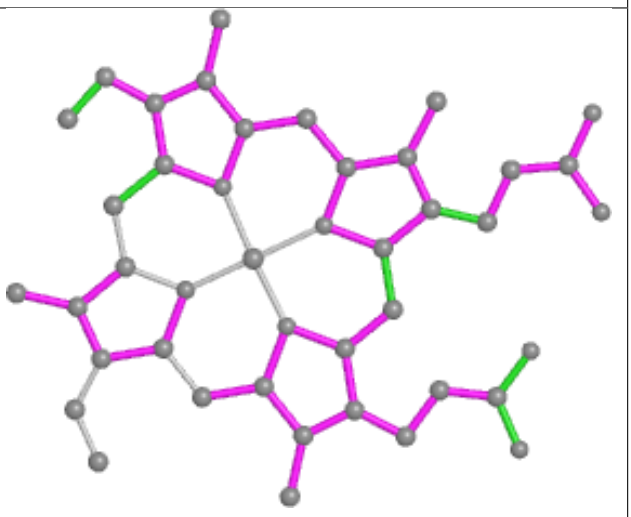
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEB	2	0

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 then 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.

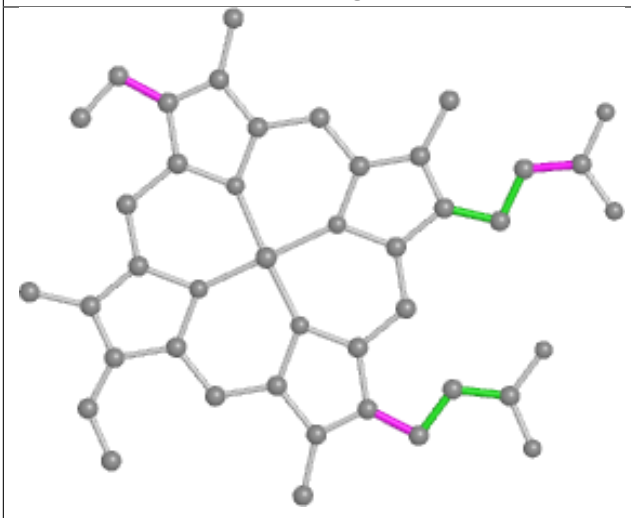
Ligand HEB A 801



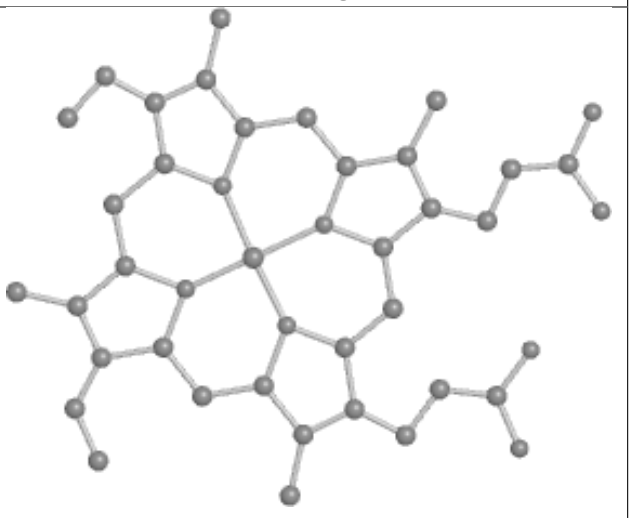
Bond lengths



Bond angles



Torsions



Rings

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, 95^{th} 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	710/720 (98%)	-0.07	26 (3%) 41 38	31, 46, 74, 119	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	199	PRO	6.4
1	A	200	ASN	5.9
1	A	206	ASP	5.8
1	A	204	THR	4.9
1	A	23	ALA	4.2
1	A	24	GLU	4.0
1	A	192	TRP	3.8
1	A	198	ASN	3.4
1	A	203	TYR	3.3
1	A	190	LYS	3.1
1	A	19	ASN	3.0
1	A	195	PRO	2.9
1	A	442	ASN	2.9
1	A	208	GLU	2.7
1	A	18	VAL	2.7
1	A	25	TRP	2.7
1	A	191	GLU	2.5
1	A	48	ASP	2.5
1	A	197	THR	2.4
1	A	207	ARG	2.4
1	A	543	GLU	2.3
1	A	201	SER	2.2
1	A	443	TYR	2.2
1	A	194	PRO	2.2
1	A	720	ASP	2.1
1	A	516	ALA	2.1

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 monosaccharides in this entry.

6.4 Ligands (i)

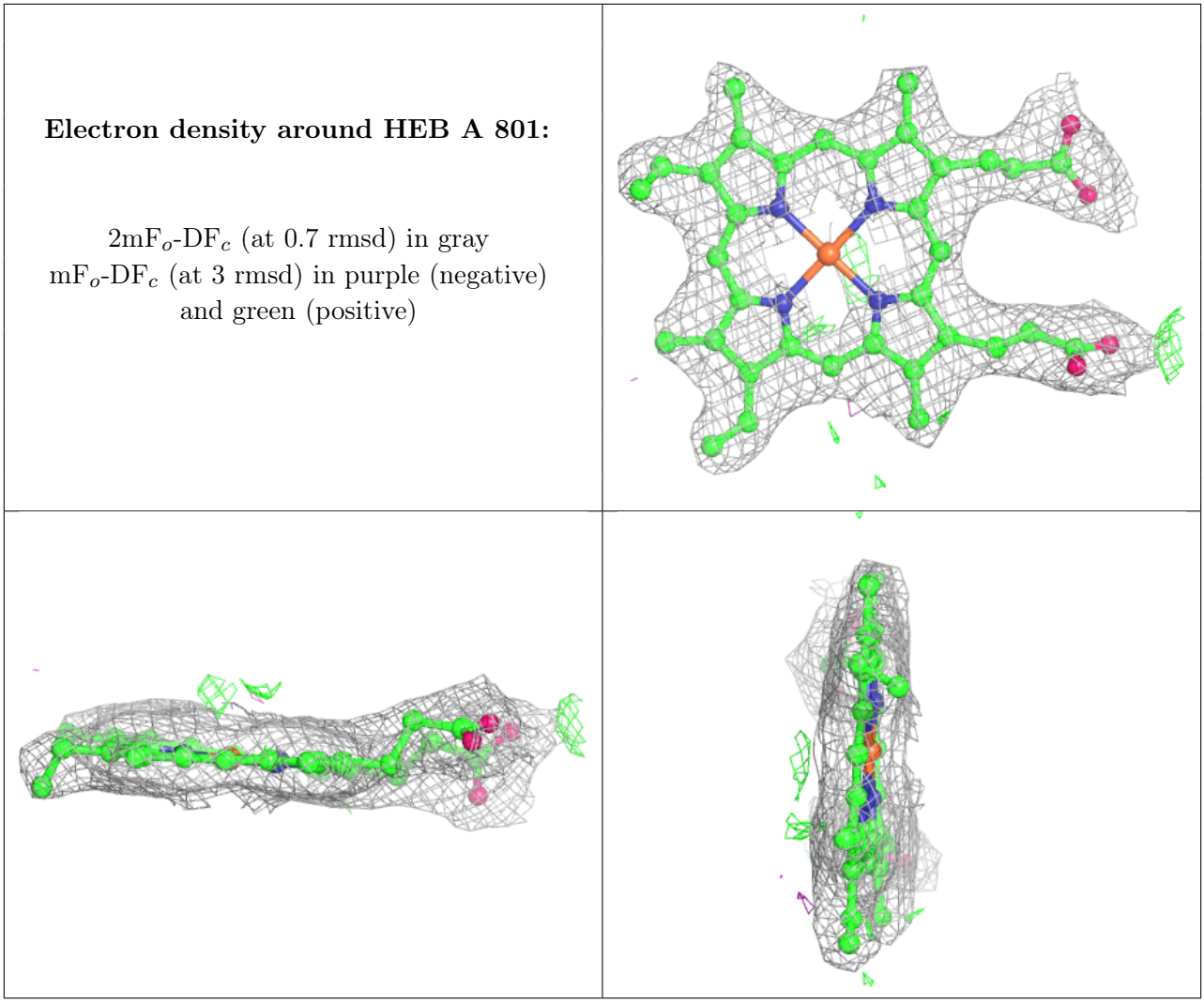
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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	NA	A	803	1/1	0.70	0.13	40,40,40,40	0
3	NA	A	802	1/1	0.96	0.05	38,38,38,38	0
3	NA	A	804	1/1	0.96	0.10	49,49,49,49	0
2	HEB	A	801	43/43	0.97	0.19	27,35,40,42	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 HEB 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)



6.5 Other polymers (i)

There are no such residues in this entry.