



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:18 PM GMT

PDB ID : 4L6G
Title : Crystal Structure of P450cin Y81F mutant, crystallized in 7 mM 1,8-cineole
Authors : Madrona, Y.; Poulos, T.L.
Deposited on : 2013-06-12
Resolution : 1.37 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

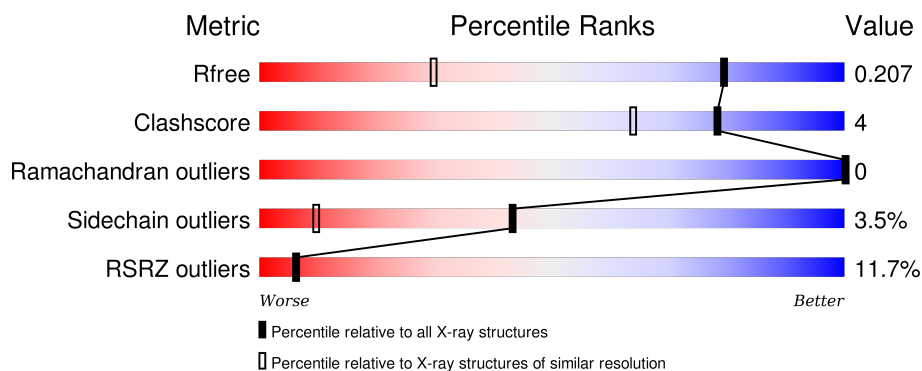
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.37 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}	91344	1918 (1.40-1.36)
Clashscore	102246	2042 (1.40-1.36)
Ramachandran outliers	100387	1993 (1.40-1.36)
Sidechain outliers	100360	1992 (1.40-1.36)
RSRZ outliers	91569	1917 (1.40-1.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	398	<div> <div>11%</div> <div>92%</div> <div>7%</div> </div>
1	B	398	<div> <div>12%</div> <div>89%</div> <div>10%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CNL	A	502	-	-	-	X
5	PGE	A	504	-	-	-	X
5	PGE	B	505	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7437 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.

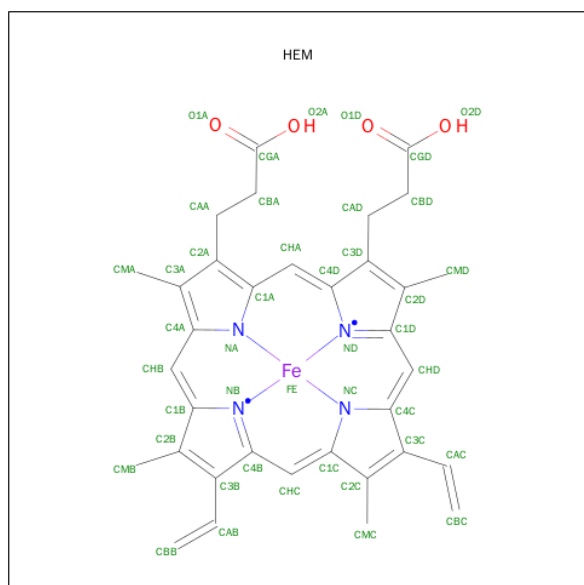
- Molecule 1 is a protein called P450cin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	397	Total	C	N	O	S	0	1	0
			3156	2012	552	581	11			
1	B	397	Total	C	N	O	S	0	1	0
			3154	2012	550	581	11			

There are 4 discrepancies between the modelled and reference sequences:

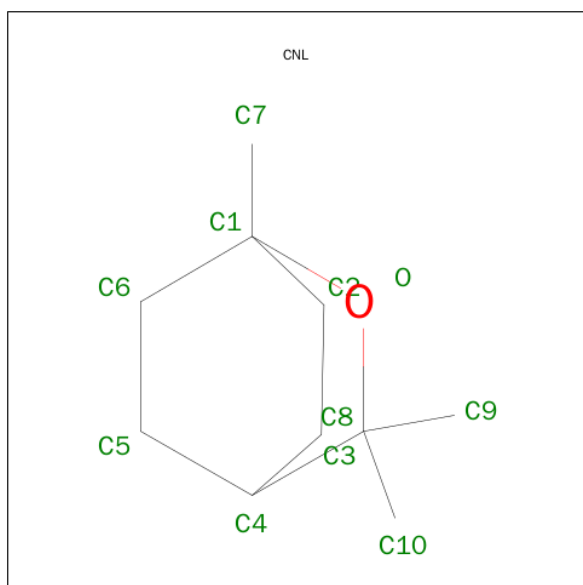
Chain	Residue	Modelled	Actual	Comment	Reference
A	7	MET	-	INITIATING METHIONINE	UNP Q8VQF6
A	81	PHE	TYR	ENGINEERED MUTATION	UNP Q8VQF6
B	7	MET	-	INITIATING METHIONINE	UNP Q8VQF6
B	81	PHE	TYR	ENGINEERED MUTATION	UNP Q8VQF6

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



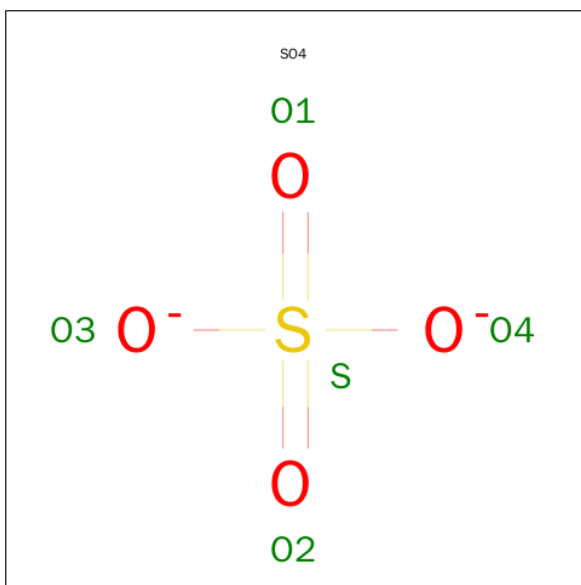
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		
2	B	1	Total	C	Fe	N	O	0	0
			43	34	1	4	4		

- Molecule 3 is 1,3,3-TRIMETHYL-2-OXABICYCLO[2.2.2]OCTANE (three-letter code: CNL) (formula: C₁₀H₁₈O).



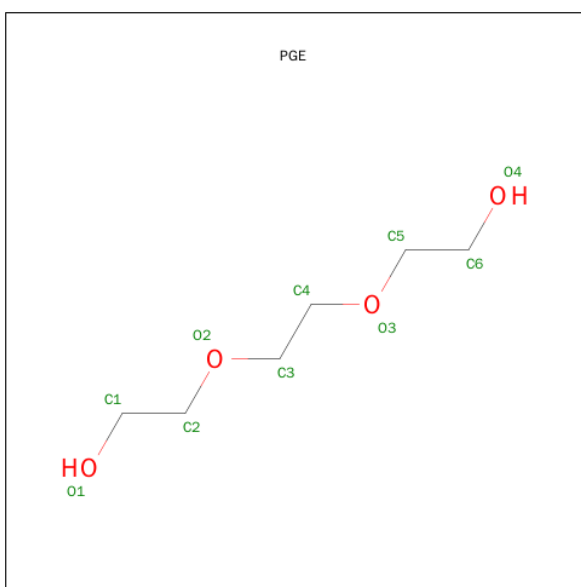
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	10	1		
3	B	1	Total	C	O	0	0
			11	10	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: C₆H₁₄O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			10	6	4		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			10	6	4		

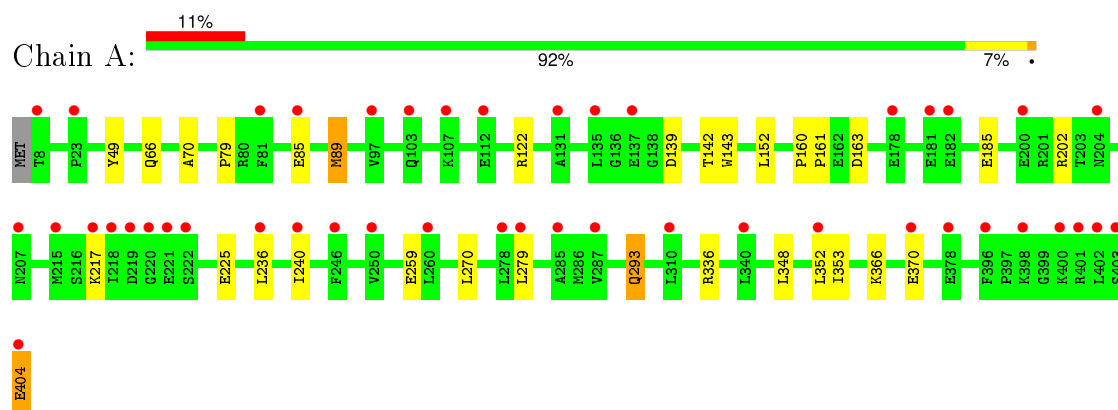
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	481	Total	O	0	6
			487	487		
6	B	489	Total	O	0	8
			497	497		

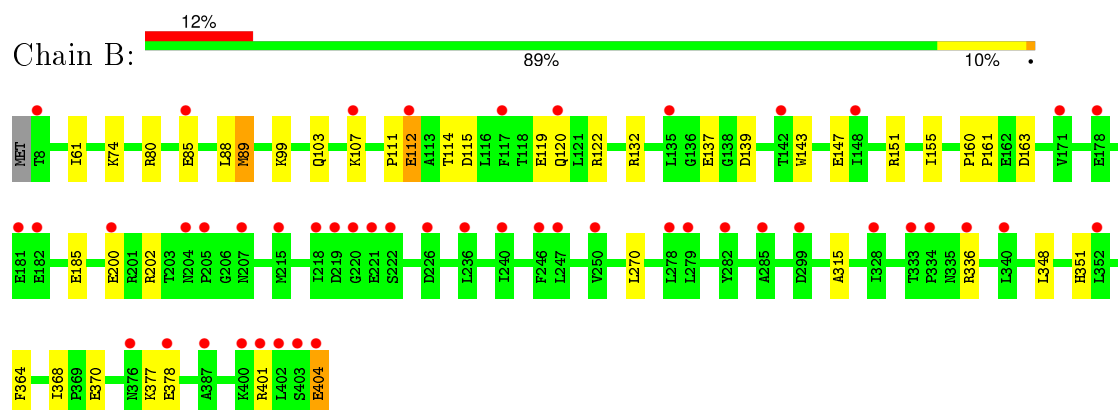
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: P450cin



• Molecule 1: P450cin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.81Å 103.77Å 127.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.75 – 1.37 34.75 – 1.37	Depositor EDS
% Data completeness (in resolution range)	96.8 (34.75-1.37) 96.8 (34.75-1.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 1.37Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.167 , 0.207 0.171 , 0.207	Depositor DCC
R_{free} test set	9321 reflections (5.30%)	DCC
Wilson B-factor (Å ²)	15.3	Xtriage
Anisotropy	0.035	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 61.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	5 of 185290 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7437	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.92 % 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 2.5485e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, CNL, PGE, SO4

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	0.39	0/3239	0.60	3/4402 (0.1%)
1	B	0.40	0/3237	0.58	0/4399
All	All	0.39	0/6476	0.59	3/8801 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	89	MET	CG-SD-CE	6.41	110.46	100.20
1	A	336	ARG	NE-CZ-NH1	6.38	123.49	120.30
1	A	336	ARG	NE-CZ-NH2	-5.90	117.35	120.30

There are no chirality outliers.

There are no planarity outliers.

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	3156	0	3112	16	0
1	B	3154	0	3112	27	0
2	A	43	0	30	0	0
2	B	43	0	30	0	0
3	A	11	0	18	0	0
3	B	11	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	0	0	0
4	B	10	0	0	1	0
5	A	10	0	14	1	0
5	B	10	0	14	2	0
6	A	487	0	0	7	2
6	B	497	0	0	12	2
All	All	7437	0	6348	46	2

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 4.

All (46) 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:377:LYS:NZ	6:B:951:HOH:O	2.19	0.75
5:B:505:PGE:H1	6:B:699:HOH:O	1.87	0.74
1:B:88:LEU:HA	6:B:770:HOH:O	1.91	0.69
1:B:122:ARG:NH2	4:B:504:SO4:O2	2.27	0.68
1:B:122:ARG:NH1	6:B:961:HOH:O	2.30	0.64
1:B:132:ARG:NH2	1:B:137:GLU:OE2	2.27	0.62
5:B:505:PGE:H5	6:B:699:HOH:O	2.00	0.61
1:B:99:LYS:NZ	1:B:103:GLN:OE1	2.34	0.60
1:A:152:LEU:HD21	1:A:352:LEU:HD11	1.85	0.59
1:A:225:GLU:OE2	6:A:829:HOH:O	2.17	0.58
1:A:70:ALA:HA	1:A:293:GLN:HG3	1.85	0.56
1:A:259:GLU:OE1	6:A:934:HOH:O	2.18	0.56
1:B:336:ARG:HA	6:B:960[A]:HOH:O	2.06	0.55
1:A:404:GLU:HG3	1:A:404:GLU:O	2.07	0.54
5:A:504:PGE:H4	6:A:754:HOH:O	2.09	0.52
1:B:200:GLU:HG2	6:B:700:HOH:O	2.11	0.51
1:A:66:GLN:HG3	6:A:1077:HOH:O	2.11	0.50
1:B:147:GLU:OE1	6:B:995:HOH:O	2.20	0.48
1:B:89:MET:HE2	1:B:89:MET:HA	1.96	0.48
1:B:114:THR:OG1	1:B:351:HIS:ND1	2.32	0.47
1:A:279:LEU:HD11	1:A:353:ILE:HD11	1.96	0.47
1:B:351:HIS:HB2	6:B:959:HOH:O	2.14	0.47
1:B:378:GLU:OE2	6:B:1072:HOH:O	2.20	0.47
1:A:240:ILE:HG22	6:A:939:HOH:O	2.13	0.46
1:A:139:ASP:O	1:A:143:TRP:HB3	2.15	0.46
1:B:200:GLU:OE2	6:B:890:HOH:O	2.21	0.45
1:B:115:ASP:OD1	1:B:351:HIS:HE1	2.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:364:PHE:CE1	1:B:368:ILE:HD12	2.52	0.45
1:B:80:ARG:NH2	6:B:1036:HOH:O	2.34	0.44
1:A:142:THR:HG21	6:A:910:HOH:O	2.17	0.44
1:B:119:GLU:OE2	1:B:122:ARG:NH1	2.51	0.44
1:A:236:LEU:O	1:A:240:ILE:HG12	2.17	0.43
1:A:122:ARG:HH11	1:A:122:ARG:HB2	1.84	0.43
1:B:111:PRO:HA	1:B:351:HIS:ND1	2.34	0.43
1:B:139:ASP:O	1:B:143:TRP:HB3	2.19	0.43
1:A:160:PRO:HA	1:A:161:PRO:HD3	1.85	0.42
1:A:49:TYR:CE2	1:A:79:PRO:HG3	2.55	0.42
1:B:74:LYS:HA	1:B:74:LYS:HD3	1.87	0.41
1:A:122:ARG:NH1	1:A:122:ARG:HB2	2.35	0.41
1:B:119:GLU:OE1	1:B:122:ARG:NH1	2.53	0.41
1:A:366:LYS:HE2	6:A:967:HOH:O	2.21	0.41
1:B:401:ARG:HD3	1:B:404:GLU:OXT	2.21	0.41
1:B:160:PRO:HA	1:B:161:PRO:HD3	1.87	0.41
1:B:112:GLU:HG3	1:B:112:GLU:H	1.31	0.40
1:B:61:ILE:HD12	1:B:315:ALA:HB2	2.03	0.40
1:B:151:ARG:O	1:B:155:ILE:HG12	2.22	0.40

All (2) 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)
6:A:870:HOH:O	6:B:800:HOH:O[1_455]	2.18	0.02
6:A:1073:HOH:O	6:B:957:HOH:O[1_455]	2.19	0.01

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	396/398 (100%)	389 (98%)	7 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	396/398 (100%)	387 (98%)	9 (2%)	0	100	100
All	All	792/796 (100%)	776 (98%)	16 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	334/334 (100%)	322 (96%)	12 (4%)	42	9
1	B	334/334 (100%)	322 (96%)	12 (4%)	42	9
All	All	668/668 (100%)	644 (96%)	24 (4%)	43	9

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	GLU
1	A	89	MET
1	A	163	ASP
1	A	185	GLU
1	A	202[A]	ARG
1	A	202[B]	ARG
1	A	217	LYS
1	A	270	LEU
1	A	293	GLN
1	A	348	LEU
1	A	370	GLU
1	A	404	GLU
1	B	85	GLU
1	B	89	MET
1	B	107	LYS
1	B	112	GLU
1	B	120	GLN
1	B	163	ASP

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Mol	Chain	Res	Type
1	B	185	GLU
1	B	202	ARG
1	B	270	LEU
1	B	348	LEU
1	B	370	GLU
1	B	404	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	HEM	A	501	1	30,50,50	2.21	8 (26%)	24,82,82	2.34	7 (29%)
3	CNL	A	502	-	12,12,12	2.21	4 (33%)	18,20,20	1.13	1 (5%)
4	SO4	A	503	-	4,4,4	0.15	0	6,6,6	0.14	0
5	PGE	A	504	-	9,9,9	0.68	0	8,8,8	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	HEM	B	501	1	30,50,50	2.29	10 (33%)	24,82,82	2.25	7 (29%)
3	CNL	B	502	-	12,12,12	2.07	3 (25%)	18,20,20	1.01	1 (5%)
4	SO4	B	503	-	4,4,4	0.20	0	6,6,6	0.19	0
4	SO4	B	504	-	4,4,4	0.23	0	6,6,6	0.12	0
5	PGE	B	505	-	9,9,9	0.61	0	8,8,8	0.83	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	HEM	A	501	1	-	0/10/54/54	0/0/8/8
3	CNL	A	502	-	-	0/0/24/24	0/0/2/2
4	SO4	A	503	-	-	0/0/0/0	0/0/0/0
5	PGE	A	504	-	-	0/7/7/7	0/0/0/0
2	HEM	B	501	1	-	0/10/54/54	0/0/8/8
3	CNL	B	502	-	-	0/0/24/24	0/0/2/2
4	SO4	B	503	-	-	0/0/0/0	0/0/0/0
4	SO4	B	504	-	-	0/0/0/0	0/0/0/0
5	PGE	B	505	-	-	0/7/7/7	0/0/0/0

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C3B-C4B	-7.13	1.45	1.51
2	A	501	HEM	C3B-C4B	-6.88	1.45	1.51
2	B	501	HEM	C3D-C4D	-5.96	1.43	1.51
2	A	501	HEM	C3D-C4D	-5.35	1.44	1.51
2	A	501	HEM	C2C-C1C	-3.73	1.45	1.52
2	B	501	HEM	C2C-C1C	-3.72	1.45	1.52
3	A	502	CNL	C5-C4	-3.43	1.43	1.53
3	B	502	CNL	C5-C4	-3.31	1.44	1.53
2	B	501	HEM	C2D-C1D	-2.43	1.43	1.51
2	A	501	HEM	C2D-C1D	-2.29	1.44	1.51
3	B	502	CNL	C2-C3	-2.25	1.48	1.53
3	A	502	CNL	C2-C3	-2.12	1.48	1.53
3	A	502	CNL	C7-C1	-2.06	1.48	1.52
2	B	501	HEM	C2B-C1B	-2.05	1.45	1.51
2	A	501	HEM	C4C-NC	2.10	1.38	1.36
2	B	501	HEM	C3C-CAC	2.15	1.55	1.51
2	B	501	HEM	CAA-C2A	2.18	1.55	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	501	HEM	C4C-NC	2.18	1.38	1.36
2	A	501	HEM	CAA-C2A	2.35	1.56	1.52
2	B	501	HEM	FE-NC	2.55	2.05	1.95
2	A	501	HEM	FE-NC	2.57	2.05	1.95
2	B	501	HEM	C1C-NC	2.93	1.39	1.36
2	A	501	HEM	C1C-NC	3.37	1.40	1.36
3	B	502	CNL	O-C8	4.85	1.56	1.46
3	A	502	CNL	O-C8	5.36	1.57	1.46

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	502	CNL	C10-C8-C9	-2.92	105.17	110.59
2	B	501	HEM	CMA-C3A-C4A	-2.88	123.59	128.36
3	B	502	CNL	C10-C8-C9	-2.59	105.79	110.59
2	A	501	HEM	CMA-C3A-C4A	-2.56	124.13	128.36
2	A	501	HEM	CBD-CAD-C3D	-2.22	107.10	113.55
2	B	501	HEM	CMD-C2D-C3D	2.44	125.16	114.35
2	A	501	HEM	CMD-C2D-C3D	2.64	126.01	114.35
2	B	501	HEM	C2D-C3D-C4D	2.90	106.41	101.50
2	B	501	HEM	CAD-C3D-C4D	4.30	127.64	112.47
2	B	501	HEM	CAD-C3D-C2D	4.43	125.94	113.22
2	A	501	HEM	CAD-C3D-C4D	4.44	128.14	112.47
2	B	501	HEM	CMC-C2C-C3C	4.73	128.34	116.53
2	B	501	HEM	CMB-C2B-C3B	4.77	128.44	116.53
2	A	501	HEM	CAD-C3D-C2D	4.93	127.38	113.22
2	A	501	HEM	CMB-C2B-C3B	4.93	128.85	116.53
2	A	501	HEM	CMC-C2C-C3C	5.26	129.65	116.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	504	PGE	1	0
4	B	504	SO4	1	0
5	B	505	PGE	2	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	397/398 (99%)	0.95	45 (11%) 7 7	10, 19, 35, 55	0
1	B	397/398 (99%)	0.93	48 (12%) 6 6	10, 19, 35, 56	0
All	All	794/796 (99%)	0.94	93 (11%) 6 6	10, 19, 35, 56	0

All (93) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	404	GLU	9.4
1	A	404	GLU	9.3
1	A	8	THR	8.3
1	B	8	THR	8.2
1	A	218	ILE	7.2
1	A	219	ASP	7.2
1	B	219	ASP	6.6
1	B	334	PRO	6.5
1	B	402	LEU	6.0
1	B	207	ASN	5.6
1	B	403	SER	5.6
1	A	403	SER	5.4
1	B	220	GLY	5.3
1	A	207	ASN	5.1
1	B	218	ILE	5.0
1	A	221	GLU	4.8
1	B	117	PHE	4.3
1	A	135	LEU	4.2
1	A	220	GLY	4.2
1	B	333	THR	4.1
1	B	221	GLU	3.9
1	A	402	LEU	3.8
1	A	112	GLU	3.7
1	A	204	ASN	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	279	LEU	3.7
1	A	181	GLU	3.6
1	B	250	VAL	3.6
1	A	240	ILE	3.5
1	B	400	LYS	3.5
1	A	400	LYS	3.5
1	B	246	PHE	3.4
1	B	181	GLU	3.4
1	A	401	ARG	3.4
1	B	204	ASN	3.3
1	A	340	LEU	3.2
1	A	222	SER	3.1
1	B	222	SER	3.1
1	B	135	LEU	3.0
1	B	279	LEU	3.0
1	A	215	MET	3.0
1	B	112	GLU	3.0
1	A	107	LYS	2.9
1	B	299	ASP	2.9
1	A	246	PHE	2.9
1	B	215	MET	2.9
1	A	396	PHE	2.9
1	B	378	GLU	2.9
1	B	200	GLU	2.8
1	A	103	GLN	2.7
1	A	137	GLU	2.7
1	B	240	ILE	2.7
1	B	376	ASN	2.6
1	A	398	LYS	2.6
1	B	205	PRO	2.6
1	A	236	LEU	2.6
1	B	282	TYR	2.6
1	A	278	LEU	2.5
1	A	250	VAL	2.5
1	B	247	LEU	2.5
1	B	171	VAL	2.5
1	B	352	LEU	2.5
1	A	182	GLU	2.5
1	B	107	LYS	2.5
1	B	85	GLU	2.4
1	B	142	THR	2.4
1	A	352	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	340	LEU	2.4
1	B	401	ARG	2.3
1	B	226	ASP	2.3
1	A	23	PRO	2.3
1	B	120	GLN	2.3
1	B	278	LEU	2.3
1	A	85	GLU	2.2
1	A	131	ALA	2.2
1	A	378	GLU	2.2
1	B	178	GLU	2.2
1	A	200	GLU	2.2
1	A	370	GLU	2.2
1	A	97	VAL	2.2
1	B	336	ARG	2.2
1	A	310	LEU	2.2
1	B	387	ALA	2.1
1	B	148	ILE	2.1
1	A	178	GLU	2.1
1	B	182	GLU	2.1
1	A	287	VAL	2.1
1	B	328	ILE	2.1
1	A	285	ALA	2.1
1	B	285	ALA	2.1
1	A	217	LYS	2.1
1	A	260	LEU	2.1
1	A	81	PHE	2.0
1	B	236	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.

The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	PGE	B	505	10/10	0.78	0.30	11.41	20,20,20,20	10
5	PGE	A	504	10/10	0.83	0.26	5.13	20,20,20,20	10
3	CNL	A	502	11/11	0.92	0.20	4.59	16,23,25,26	0
3	CNL	B	502	11/11	0.90	0.15	1.92	14,19,22,24	0
2	HEM	B	501	43/43	0.97	0.13	0.66	8,11,15,21	0
2	HEM	A	501	43/43	0.97	0.13	0.45	9,12,15,20	0
4	SO4	A	503	5/5	0.91	0.12	0.36	30,30,30,30	0
4	SO4	B	504	5/5	0.89	0.12	-0.18	30,30,30,30	5
4	SO4	B	503	5/5	0.77	0.20	-	30,30,30,30	5

6.5 Other polymers

There are no such residues in this entry.