



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 03:16 am GMT

PDB ID : 1XU5
Title : Soluble methane monooxygenase hydroxylase-phenol soaked
Authors : Sazinsky, M.H.; Lippard, S.J.
Deposited on : 2004-10-25
Resolution : 1.96 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

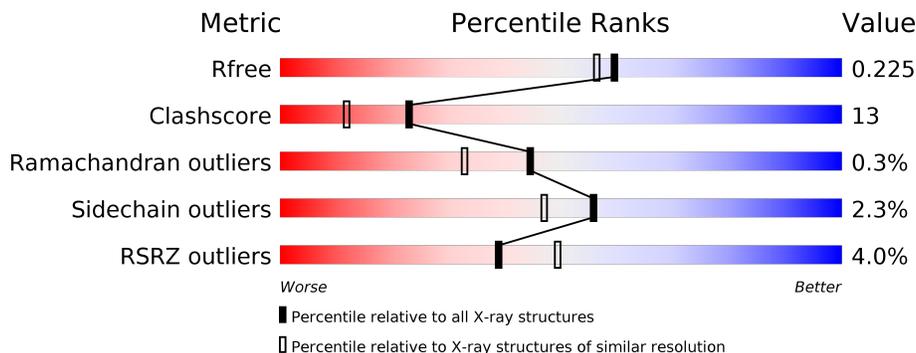
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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}	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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	527	<p>2% 71% 25% ..</p>
1	B	527	<p>2% 70% 25% ..</p>
2	C	389	<p>% 81% 18%</p>
2	D	389	<p>7% 69% 29% .</p>
3	E	170	<p>2% 79% 16% ..</p>
3	F	170	<p>16% 69% 26% ..</p>

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
6	IPH	B	2666	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 18452 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 Methane monooxygenase component A alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	510	Total	C	N	O	S	0	0	0
			4138	2649	709	762	18			
1	B	510	Total	C	N	O	S	0	0	0
			4137	2646	711	762	18			

- Molecule 2 is a protein called Methane monooxygenase component A beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	388	Total	C	N	O	S	0	0	0
			3163	2036	545	574	8			
2	D	388	Total	C	N	O	S	0	0	0
			3151	2028	543	572	8			

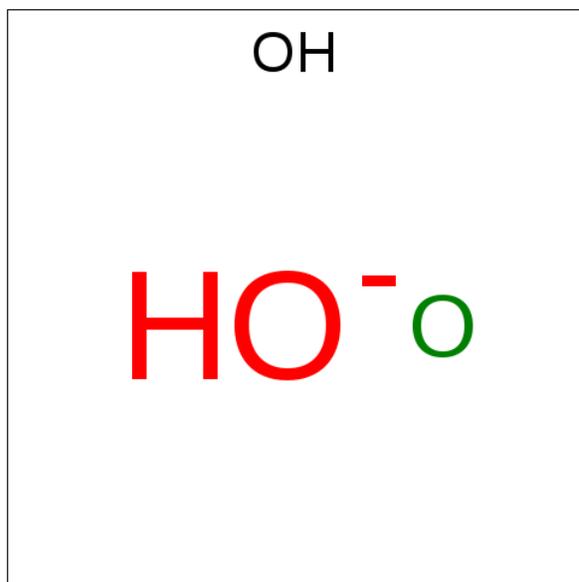
- Molecule 3 is a protein called Methane monooxygenase component A gamma chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	E	166	Total	C	N	O	S	0	0	0
			1364	864	245	250	5			
3	F	166	Total	C	N	O	S	0	0	0
			1358	860	243	250	5			

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

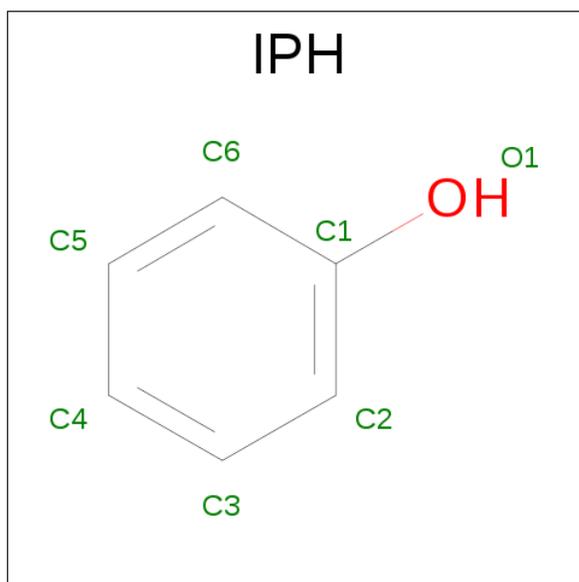
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf	
4	B	2	Total	Fe	0	0
			2	2		
4	A	2	Total	Fe	0	0
			2	2		

- Molecule 5 is HYDROXIDE ION (three-letter code: OH) (formula: HO).



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

- Molecule 6 is PHENOL (three-letter code: IPH) (formula: C₆H₆O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	1	Total C O 7 6 1	0	0
6	A	1	Total C O 7 6 1	0	0

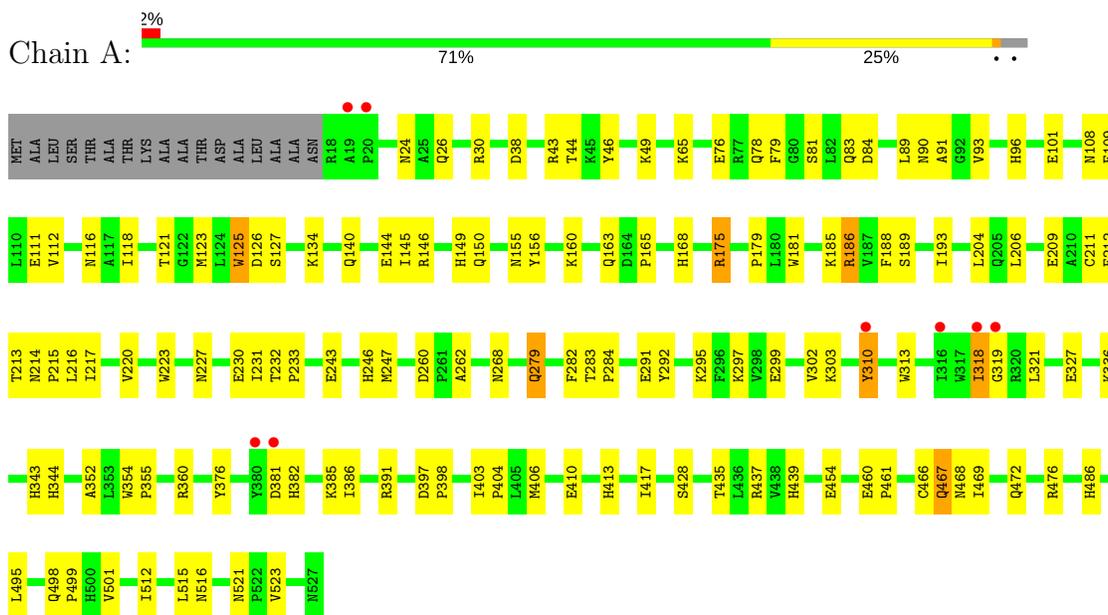
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	255	Total 255	O 255	0	0
7	B	246	Total 246	O 246	0	0
7	C	273	Total 273	O 273	0	0
7	D	159	Total 159	O 159	0	0
7	E	139	Total 139	O 139	0	0
7	F	49	Total 49	O 49	0	0

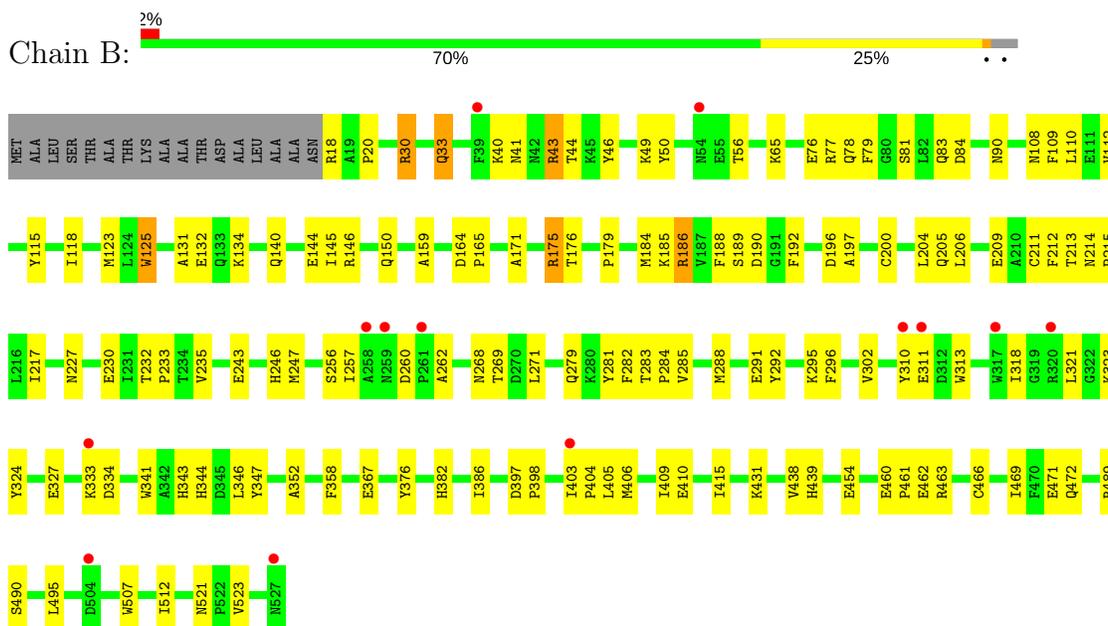
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

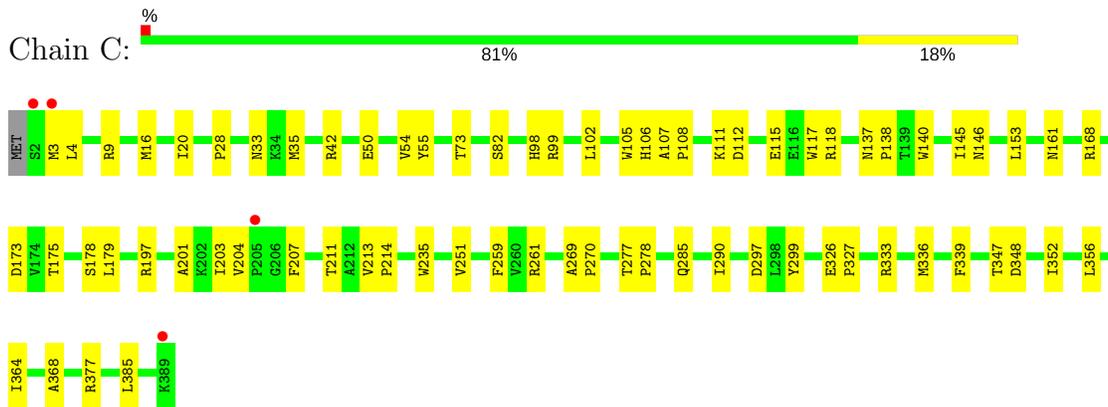
- Molecule 1: Methane monooxygenase component A alpha chain



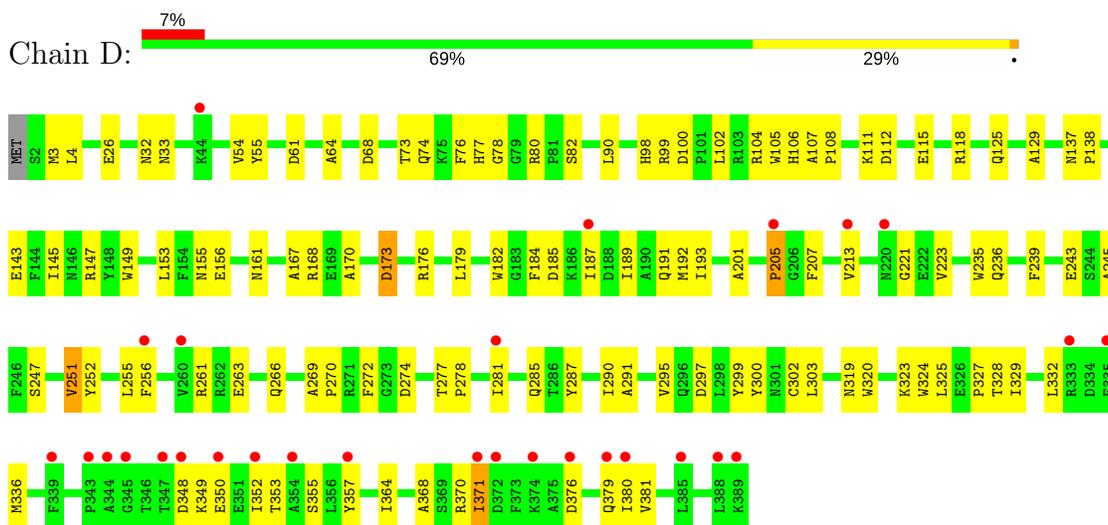
- Molecule 1: Methane monooxygenase component A alpha chain



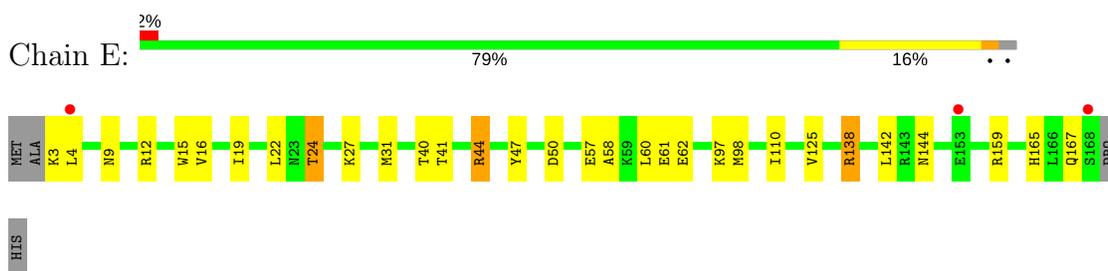
- Molecule 2: Methane monooxygenase component A beta chain



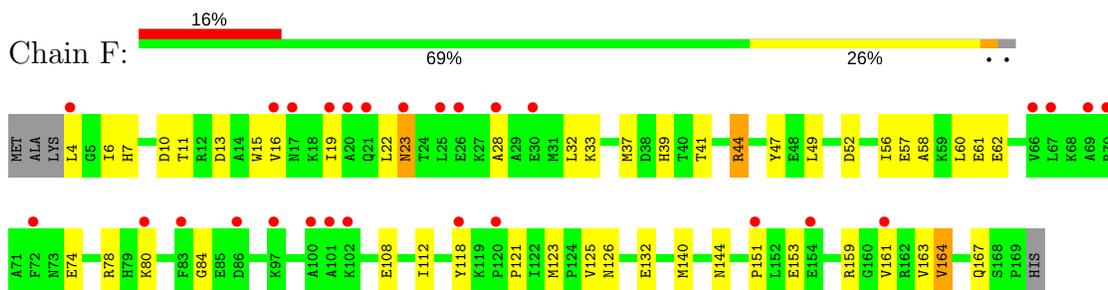
- Molecule 2: Methane monooxygenase component A beta chain



- Molecule 3: Methane monooxygenase component A gamma chain



- Molecule 3: Methane monooxygenase component A gamma chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	71.19Å 171.56Å 221.10Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.94 – 1.96 29.94 – 1.96	Depositor EDS
% Data completeness (in resolution range)	92.4 (29.94-1.96) 92.5 (29.94-1.96)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.66 (at 1.96Å)	Xtrriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.200 , 0.228 0.197 , 0.225	Depositor DCC
R_{free} test set	8959 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	20.3	Xtrriage
Anisotropy	0.045	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 54.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	18452	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.39% 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: IPH, FE, OH

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	0.33	0/4263	0.57	0/5797
1	B	0.33	0/4262	0.59	1/5796 (0.0%)
2	C	0.36	0/3259	0.58	0/4430
2	D	0.32	0/3247	0.53	0/4417
3	E	0.33	0/1392	0.58	0/1876
3	F	0.28	0/1387	0.52	0/1873
All	All	0.33	0/17810	0.57	1/24189 (0.0%)

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
2	C	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	175	ARG	C-N-CA	5.36	135.09	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	299	TYR	Sidechain

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	4138	0	3897	122	0
1	B	4137	0	3888	134	0
2	C	3163	0	2986	64	0
2	D	3151	0	2960	101	0
3	E	1364	0	1352	28	0
3	F	1358	0	1335	44	0
4	A	2	0	0	0	0
4	B	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
6	A	7	0	6	0	0
6	B	7	0	6	0	0
7	A	255	0	0	6	0
7	B	246	0	0	6	0
7	C	273	0	0	3	0
7	D	159	0	0	4	0
7	E	139	0	0	0	0
7	F	49	0	0	4	0
All	All	18452	0	16430	436	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 13.

The worst 5 of 436 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)
3:E:19:ILE:HD12	3:E:60:LEU:HD13	1.40	1.04
1:A:352:ALA:HA	1:A:404:PRO:HB2	1.46	0.95
1:A:78:GLN:HE22	1:A:150:GLN:HE21	1.05	0.93
1:A:118:ILE:HD13	1:A:145:ILE:HD13	1.49	0.93
1:B:78:GLN:HE22	1:B:150:GLN:HE21	1.04	0.93

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	508/527 (96%)	484 (95%)	24 (5%)	0	100	100
1	B	508/527 (96%)	484 (95%)	23 (4%)	1 (0%)	51	41
2	C	386/389 (99%)	375 (97%)	10 (3%)	1 (0%)	44	33
2	D	386/389 (99%)	366 (95%)	16 (4%)	4 (1%)	18	7
3	E	164/170 (96%)	161 (98%)	3 (2%)	0	100	100
3	F	164/170 (96%)	157 (96%)	6 (4%)	1 (1%)	28	15
All	All	2116/2172 (97%)	2027 (96%)	82 (4%)	7 (0%)	44	33

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	40	LYS
2	D	64	ALA
2	D	205	PRO
2	C	251	VAL
2	D	251	VAL

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	423/442 (96%)	410 (97%)	13 (3%)	45	32
1	B	422/442 (96%)	411 (97%)	11 (3%)	51	40
2	C	315/323 (98%)	311 (99%)	4 (1%)	73	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	D	312/323 (97%)	307 (98%)	5 (2%)	68	63
3	E	143/147 (97%)	140 (98%)	3 (2%)	59	50
3	F	142/147 (97%)	137 (96%)	5 (4%)	41	27
All	All	1757/1824 (96%)	1716 (98%)	41 (2%)	56	47

5 of 41 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	125	TRP
1	B	311	GLU
3	F	23	ASN
1	B	186	ARG
1	B	279	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 69 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	249	ASN
1	B	411	ASN
3	F	23	ASN
1	B	268	ASN
1	B	279	GLN

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](#)

Of 8 ligands modelled in this entry, 2 are modelled with single atom and 4 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
6	IPH	A	2667	-	7,7,7	2.21	3 (42%)	8,8,8	1.71	2 (25%)
6	IPH	B	2666	-	7,7,7	2.23	3 (42%)	8,8,8	1.74	2 (25%)

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
6	IPH	A	2667	-	-	0/0/0/0	0/1/1/1
6	IPH	B	2666	-	-	0/0/0/0	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	2667	IPH	C2-C1	2.33	1.43	1.38
6	B	2666	IPH	C2-C1	2.40	1.43	1.38
6	A	2667	IPH	C3-C2	3.04	1.44	1.38
6	B	2666	IPH	C3-C2	3.10	1.44	1.38
6	A	2667	IPH	C5-C6	3.38	1.45	1.38

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	2666	IPH	C3-C2-C1	-2.43	115.93	119.37
6	A	2667	IPH	C3-C2-C1	-2.42	115.95	119.37
6	A	2667	IPH	C6-C1-C2	3.21	125.52	119.74
6	B	2666	IPH	C6-C1-C2	3.28	125.64	119.74

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	510/527 (96%)	0.07	8 (1%) 72 80	12, 21, 37, 48	0
1	B	510/527 (96%)	0.09	13 (2%) 58 67	13, 23, 37, 49	0
2	C	388/389 (99%)	-0.22	4 (1%) 82 88	10, 16, 29, 44	0
2	D	388/389 (99%)	0.64	29 (7%) 15 23	17, 30, 49, 77	0
3	E	166/170 (97%)	-0.02	3 (1%) 69 78	13, 19, 31, 54	0
3	F	166/170 (97%)	1.09	28 (16%) 2 2	26, 39, 55, 64	0
All	All	2128/2172 (97%)	0.20	85 (3%) 39 49	10, 23, 44, 77	0

The worst 5 of 85 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	389	LYS	7.5
2	D	205	PRO	6.5
3	E	4	LEU	5.3
3	F	100	ALA	5.2
2	D	380	ILE	5.1

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 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
6	IPH	B	2666	7/7	0.92	0.18	2.61	26,27,29,32	0
6	IPH	A	2667	7/7	0.93	0.14	-0.20	29,30,31,32	0
5	OH	A	1177	1/1	0.99	0.05	-2.46	23,23,23,23	0
4	FE	B	1170	1/1	1.00	0.04	-3.36	19,19,19,19	0
5	OH	B	1173	1/1	0.99	0.04	-3.43	25,25,25,25	0
4	FE	A	1174	1/1	1.00	0.03	-3.85	19,19,19,19	0
4	FE	A	1175	1/1	0.99	0.03	-4.14	24,24,24,24	0
4	FE	B	1171	1/1	0.99	0.03	-4.80	26,26,26,26	0

6.5 Other polymers [i](#)

There are no such residues in this entry.