



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 02:47 AM GMT

PDB ID : 2INP  
Title : Structure of the Phenol Hydroxylase-Regulatory Protein Complex  
Authors : Sazinsky, M.S.; Dunten, P.W.; McCormick, M.S.; Lippard, S.J.  
Deposited on : 2006-10-08  
Resolution : 2.30 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](mailto: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.

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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

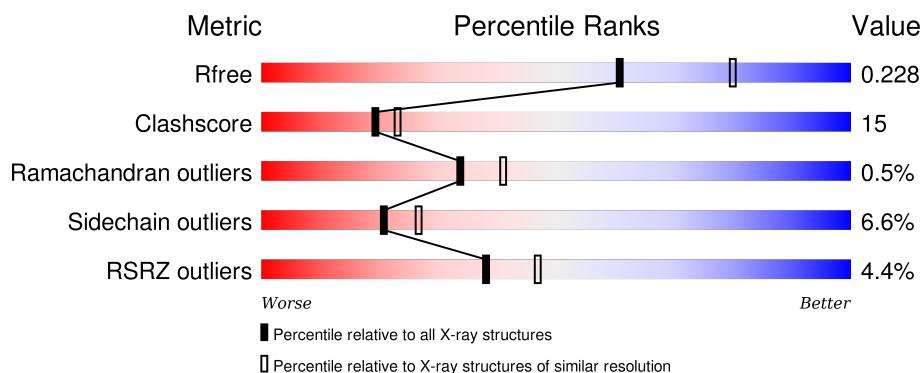
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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  $\geq 3$ , 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	494	<div> <div>0%</div> <div> <div></div> <div>75%</div> <div>21%</div> <div>•</div> </div> </div>
1	B	494	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>25%</div> <div>•</div> </div> </div>
2	C	328	<div> <div>2%</div> <div> <div></div> <div>71%</div> <div>22%</div> <div>• • •</div> </div> </div>
2	D	328	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>21%</div> <div>• •</div> </div> </div>
3	E	118	<div> <div>0%</div> <div> <div></div> <div>75%</div> <div>22%</div> <div>•</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	118	<div><div></div><div>4%</div><div>71%</div><div>27%</div><div></div></div>
4	L	89	<div><div></div><div>51%</div><div>38%</div><div>42%</div><div>12%</div><div>7%</div></div>

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 17022 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 Phenol hydroxylase component pHN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	494	Total	C	N	O	S	0	0	0
			4119	2649	692	754	24			
1	B	493	Total	C	N	O	S	0	4	0
			4153	2675	694	760	24			

- Molecule 2 is a protein called Phenol hydroxylase component pHL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	318	Total	C	N	O	S	0	0	0
			2589	1630	449	492	18			
2	D	328	Total	C	N	O	S	0	0	0
			2659	1673	461	507	18			

- Molecule 3 is a protein called Phenol hydroxylase component pHO.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	118	Total	C	N	O	S	0	0	0
			925	602	145	173	5			
3	F	118	Total	C	N	O	S	0	0	0
			925	602	145	173	5			

- Molecule 4 is a protein called Phenol hydroxylase component pHM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	83	Total	C	N	O	S	0	0	0
			624	389	105	125	5			

- Molecule 5 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Fe	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 2	Fe 2	0	0

- Molecule 6 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	1	Total 1	Zn 1	0	0
6	A	1	Total 1	Zn 1	0	0

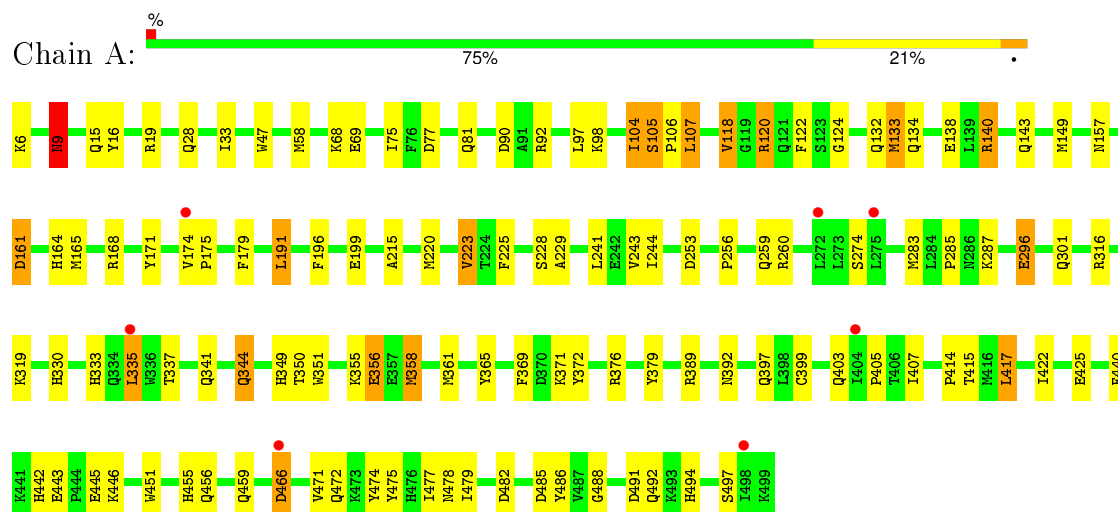
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	253	Total 253	O 253	0	0
7	B	245	Total 245	O 245	0	0
7	C	177	Total 177	O 177	0	0
7	D	219	Total 219	O 219	0	0
7	E	76	Total 76	O 76	0	0
7	F	49	Total 49	O 49	0	0
7	L	3	Total 3	O 3	0	0

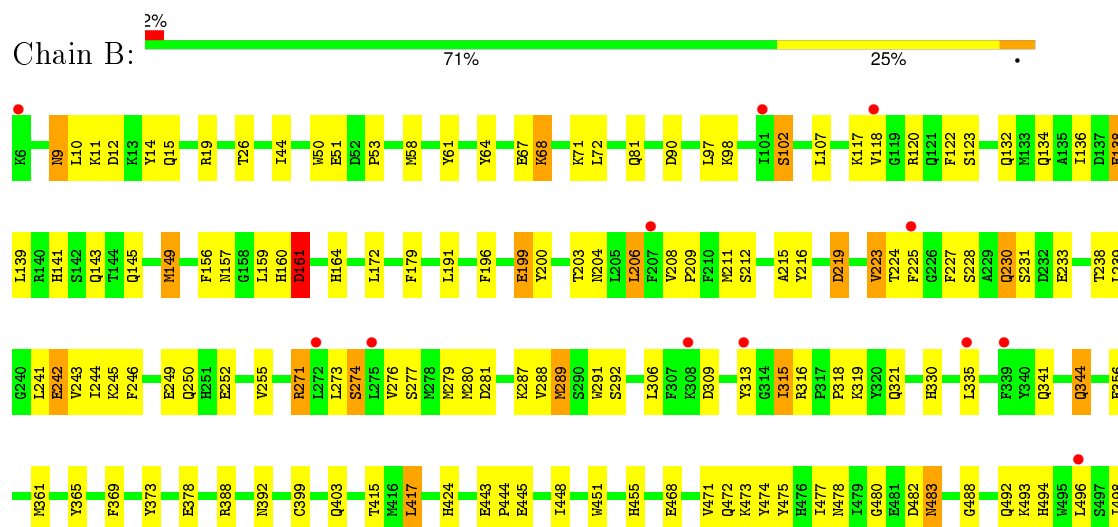
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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: Phenol hydroxylase component phN

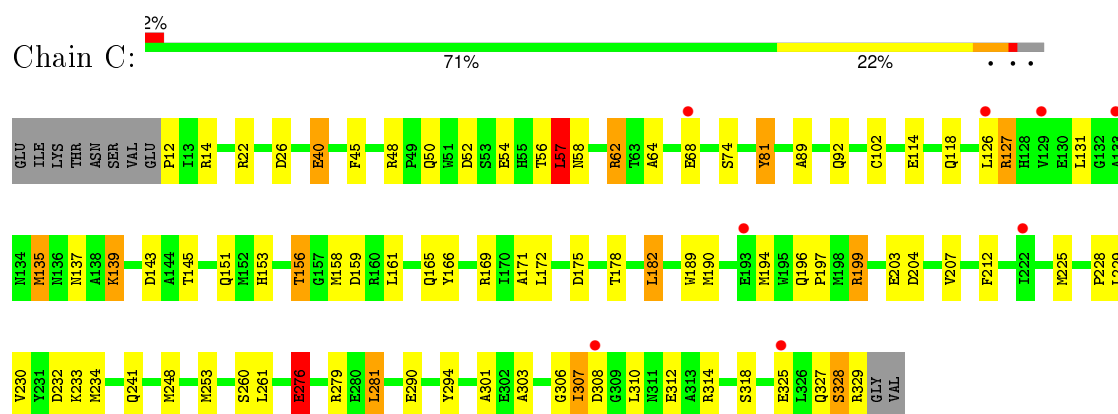


- Molecule 1: Phenol hydroxylase component phN

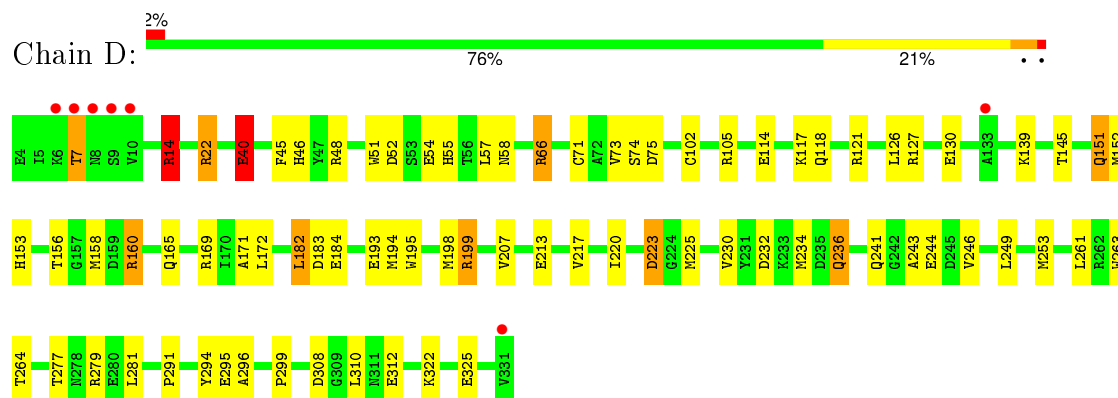


LYS

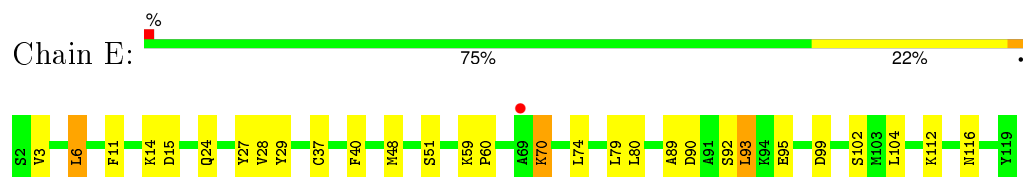
- Molecule 2: Phenol hydroxylase component phL



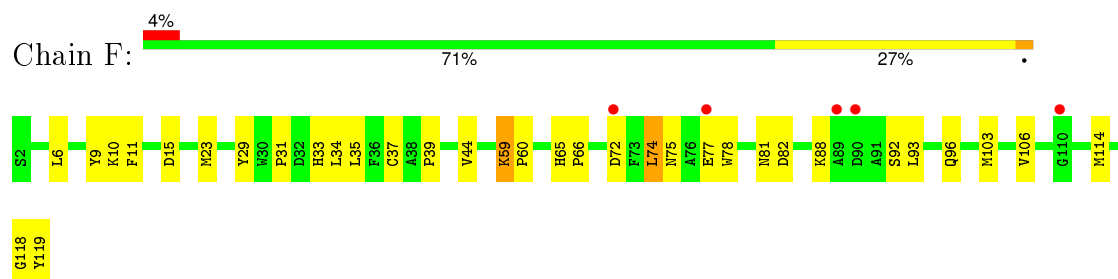
• Molecule 2: Phenol hydroxylase component pHL



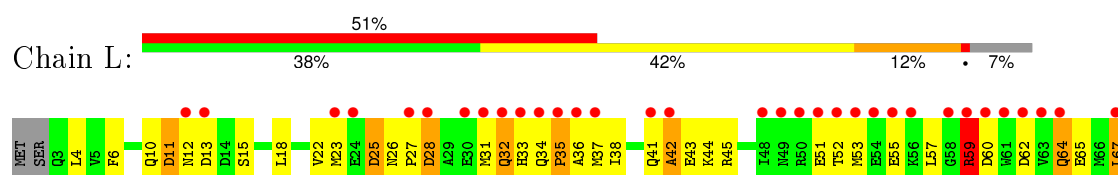
• Molecule 3: Phenol hydroxylase component pHO



• Molecule 3: Phenol hydroxylase component pHO



• Molecule 4: Phenol hydroxylase component pHM



I68	I69	V70	I71	S72	I73	A74	G75	I76	V77	I78	E79	I80	ASP	ASP	H83	F84	I85	L86	E87	W88	ASN



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	87.75Å 146.31Å 190.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.30 29.98 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-2.30) 99.8 (29.98-2.30)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.21 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.192 , 0.236 0.172 , 0.228	Depositor DCC
$R_{free}$ test set	5424 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	37.8	Xtriage
Anisotropy	0.508	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 55.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 108608 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	17022	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.09% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 ⓘ

### 5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, FE

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	1.17	11/4253 (0.3%)	1.03	13/5762 (0.2%)
1	B	1.23	7/4290 (0.2%)	0.98	10/5813 (0.2%)
2	C	1.21	7/2648 (0.3%)	1.16	18/3580 (0.5%)
2	D	1.16	3/2718 (0.1%)	1.15	21/3676 (0.6%)
3	E	1.18	0/953	1.03	3/1297 (0.2%)
3	F	1.03	0/953	1.02	1/1297 (0.1%)
4	L	0.61	0/632	0.83	2/857 (0.2%)
All	All	1.17	28/16447 (0.2%)	1.05	68/22282 (0.3%)

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	114	GLU	CG-CD	7.60	1.63	1.51
2	C	276	GLU	CB-CG	7.55	1.66	1.52
2	C	102	CYS	CB-SG	-6.66	1.71	1.82
2	D	325	GLU	CG-CD	6.52	1.61	1.51
1	B	138	GLU	CD-OE1	6.17	1.32	1.25

The worst 5 of 68 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	14	ARG	NE-CZ-NH2	-17.40	111.60	120.30
2	D	14	ARG	NE-CZ-NH1	12.60	126.60	120.30
2	D	22	ARG	NE-CZ-NH2	-12.36	114.12	120.30
2	C	127	ARG	NE-CZ-NH2	-11.28	114.66	120.30
2	C	127	ARG	NE-CZ-NH1	11.19	125.90	120.30

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	4119	0	3855	100	0
1	B	4153	0	3870	186	0
2	C	2589	0	2501	73	0
2	D	2659	0	2571	66	0
3	E	925	0	898	17	0
3	F	925	0	898	24	0
4	L	624	0	540	124	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
7	A	253	0	0	4	1
7	B	245	0	0	9	0
7	C	177	0	0	3	0
7	D	219	0	0	9	0
7	E	76	0	0	1	1
7	F	49	0	0	1	0
7	L	3	0	0	1	0
All	All	17022	0	15133	470	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 15.

The worst 5 of 470 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:64[B]:TYR:CE2	4:L:67:LEU:CD1	1.76	1.66
1:B:64[B]:TYR:CD2	4:L:67:LEU:CD1	1.91	1.49
1:B:64[B]:TYR:CZ	4:L:67:LEU:HD12	1.45	1.48
1:B:64[B]:TYR:CD2	4:L:67:LEU:HD12	1.47	1.45
1:B:227[A]:PHE:CD2	4:L:10:GLN:OE1	1.72	1.42

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)
7:A:686:HOH:O	7:E:140:HOH:O[3_645]	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	492/494 (100%)	472 (96%)	19 (4%)	1 (0%)	52	64
1	B	495/494 (100%)	475 (96%)	20 (4%)	0	100	100
2	C	316/328 (96%)	303 (96%)	13 (4%)	0	100	100
2	D	326/328 (99%)	314 (96%)	12 (4%)	0	100	100
3	E	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
3	F	116/118 (98%)	106 (91%)	8 (7%)	2 (2%)	11	10
4	L	77/89 (86%)	65 (84%)	5 (6%)	7 (9%)	1	0
All	All	1938/1969 (98%)	1847 (95%)	81 (4%)	10 (0%)	34	41

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
4	L	35	PRO
4	L	11	ASP
4	L	42	ALA
3	F	74	LEU

#### 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	433/434 (100%)	405 (94%)	28 (6%)	21	27
1	B	436/434 (100%)	411 (94%)	25 (6%)	25	34
2	C	272/281 (97%)	254 (93%)	18 (7%)	21	27
2	D	280/281 (100%)	266 (95%)	14 (5%)	30	41
3	E	98/98 (100%)	90 (92%)	8 (8%)	14	17
3	F	98/98 (100%)	91 (93%)	7 (7%)	18	23
4	L	60/81 (74%)	50 (83%)	10 (17%)	3	2
All	All	1677/1707 (98%)	1567 (93%)	110 (7%)	21	27

5 of 110 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	417	LEU
2	C	207	VAL
4	L	32	GLN
1	B	483	ASN
2	C	57	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 55 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	330	HIS
1	B	478	ASN
2	D	327	GLN
1	B	341	GLN
1	B	400	GLN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	494/494 (100%)	-0.28	7 (1%) 78 83	24, 36, 53, 67	0
1	B	493/494 (99%)	-0.15	12 (2%) 62 71	24, 37, 58, 69	0
2	C	318/328 (96%)	-0.10	8 (2%) 61 70	25, 39, 59, 78	0
2	D	328/328 (100%)	-0.24	7 (2%) 67 74	26, 37, 56, 82	0
3	E	118/118 (100%)	-0.27	1 (0%) 87 90	28, 37, 51, 58	0
3	F	118/118 (100%)	0.11	5 (4%) 40 49	39, 55, 70, 74	0
4	L	83/89 (93%)	2.38	45 (54%) 0 0	45, 57, 66, 83	81 (97%)
All	All	1952/1969 (99%)	-0.07	85 (4%) 38 47	24, 38, 61, 83	81 (4%)

The worst 5 of 85 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	L	27	PRO	7.7
2	D	331	VAL	7.1
4	L	53	MET	5.7
4	L	33	HIS	5.3
4	L	52	THR	4.7

### 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	FE	B	5	1/1	0.93	0.13	0.69	60,60,60,60	0
5	FE	B	4	1/1	0.99	0.10	-0.19	37,37,37,37	0
6	ZN	A	2	1/1	1.00	0.12	-0.92	36,36,36,36	0
6	ZN	B	500	1/1	0.99	0.10	-1.18	33,33,33,33	0
5	FE	A	1	1/1	1.00	0.08	-1.36	45,45,45,45	0
5	FE	A	3	1/1	0.99	0.06	-	41,41,41,41	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.