



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 04:07 am BST

PDB ID : 3ZC1
Title : Crystal structure of AfC3PO
Authors : Parizotto, E.A.; Lowe, E.D.; Parker, J.S.
Deposited on : 2012-11-14
Resolution : 3.27 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

<https://www.wwpdb.org/validation/2017/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:

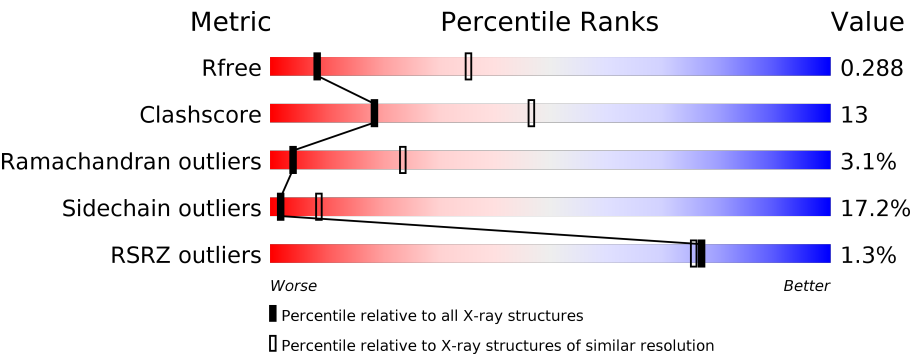
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 3.27 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	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)

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 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	199	<div><div>%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>64%24%7%• 5%</div></div>
1	B	199	<div><div>2%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>56%33%6%• 5%</div></div>
1	C	199	<div><div>%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>58%30%7%5%</div></div>
1	D	199	<div><div>2%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>54%33%8%6%</div></div>
1	E	199	<div><div>%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>55%31%10%5%</div></div>
1	F	199	<div><div>%</div><div><div></div><div></div><div></div><div></div><div></div></div><div>56%32%7%• 5%</div></div>

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Mol	Chain	Length	Quality of chain
1	G	199	<div><div>%</div><div><div></div><div>56%</div><div>33%</div><div>6%</div><div>5%</div></div></div>
1	H	199	<div><div>3%</div><div><div></div><div>59%</div><div>29%</div><div>6%</div><div>6%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11820 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 AFTRAX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	190	Total	C	N	O	S	0	0	0
			1487	950	250	279	8			
1	B	190	Total	C	N	O	S	0	0	0
			1495	950	255	282	8			
1	C	189	Total	C	N	O	S	0	0	0
			1478	939	249	283	7			
1	D	187	Total	C	N	O	S	0	0	0
			1479	943	249	280	7			
1	E	190	Total	C	N	O	S	0	0	0
			1494	955	255	276	8			
1	F	190	Total	C	N	O	S	0	0	0
			1486	948	251	279	8			
1	G	189	Total	C	N	O	S	0	0	0
			1451	920	244	279	8			
1	H	187	Total	C	N	O	S	0	0	0
			1437	911	245	273	8			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP O28024
A	-1	PRO	-	expression tag	UNP O28024
A	0	HIS	-	expression tag	UNP O28024
B	-2	GLY	-	expression tag	UNP O28024
B	-1	PRO	-	expression tag	UNP O28024
B	0	HIS	-	expression tag	UNP O28024
C	-2	GLY	-	expression tag	UNP O28024
C	-1	PRO	-	expression tag	UNP O28024
C	0	HIS	-	expression tag	UNP O28024
D	-2	GLY	-	expression tag	UNP O28024
D	-1	PRO	-	expression tag	UNP O28024
D	0	HIS	-	expression tag	UNP O28024
E	-2	GLY	-	expression tag	UNP O28024

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-1	PRO	-	expression tag	UNP O28024
E	0	HIS	-	expression tag	UNP O28024
F	-2	GLY	-	expression tag	UNP O28024
F	-1	PRO	-	expression tag	UNP O28024
F	0	HIS	-	expression tag	UNP O28024
G	-2	GLY	-	expression tag	UNP O28024
G	-1	PRO	-	expression tag	UNP O28024
G	0	HIS	-	expression tag	UNP O28024
H	-2	GLY	-	expression tag	UNP O28024
H	-1	PRO	-	expression tag	UNP O28024
H	0	HIS	-	expression tag	UNP O28024

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	1	Total Mg 1 1	0	0
2	B	1	Total Mg 1 1	0	0
2	D	1	Total Mg 1 1	0	0
2	C	1	Total Mg 1 1	0	0
2	F	1	Total Mg 1 1	0	0

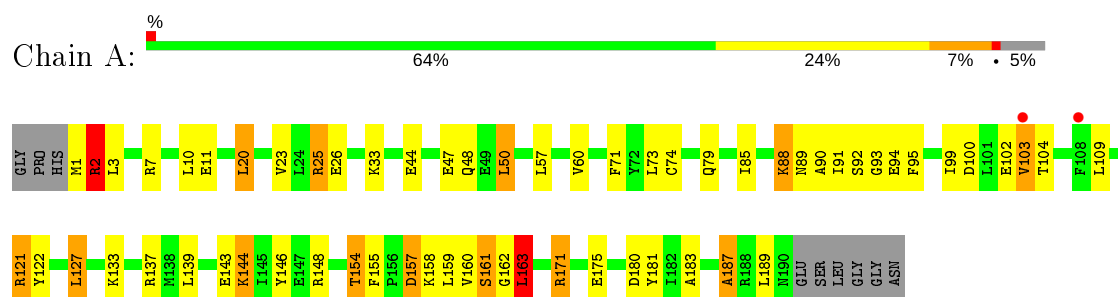
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	3	Total O 3 3	0	0
3	D	1	Total O 1 1	0	0
3	F	3	Total O 3 3	0	0
3	G	1	Total O 1 1	0	0

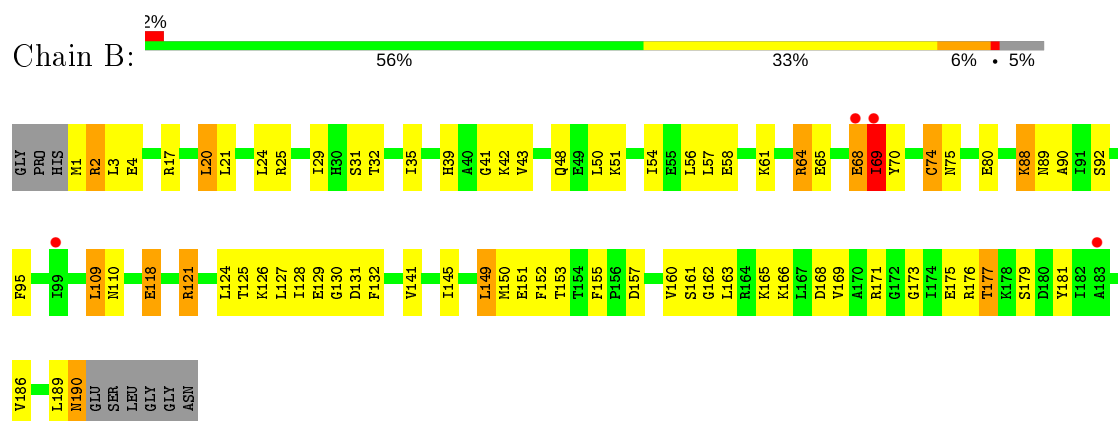
3 Residue-property plots [i](#)

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.

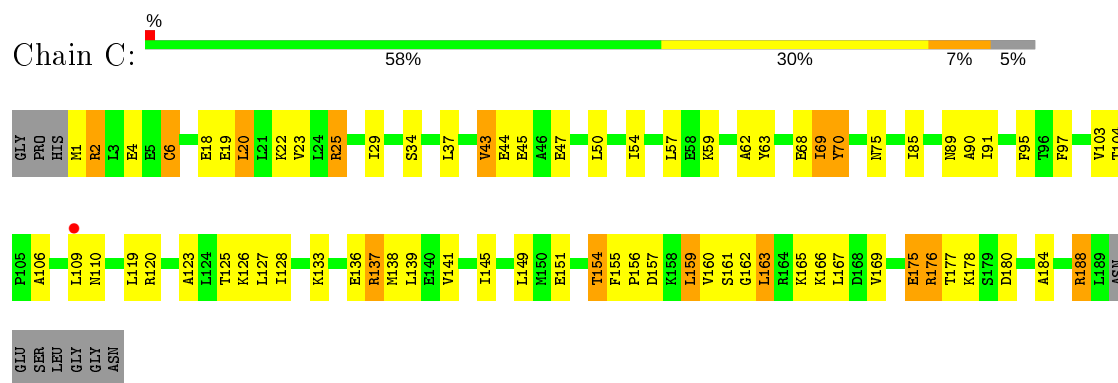
• Molecule 1: AFTRAX



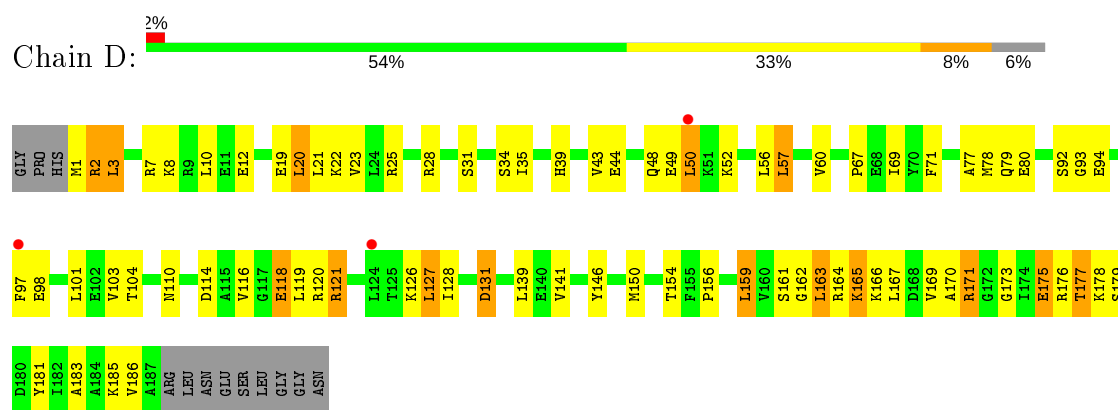
• Molecule 1: AFTRAX



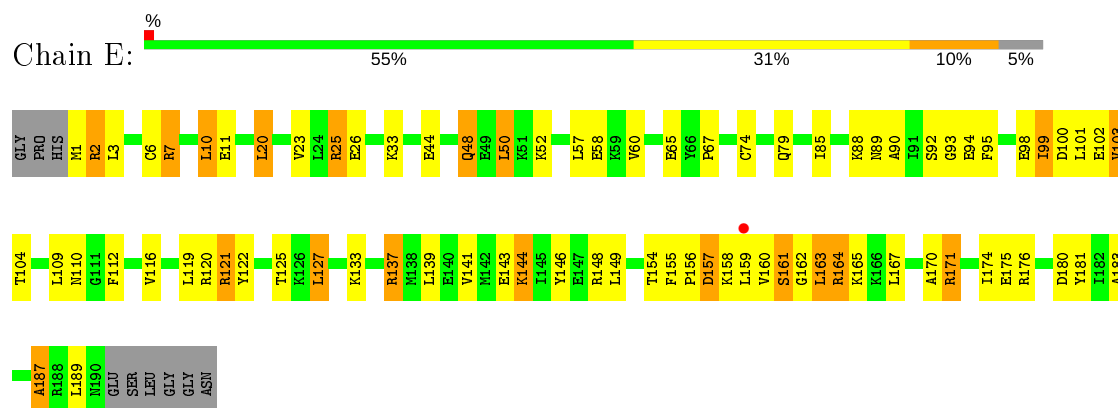
• Molecule 1: AFTRAX



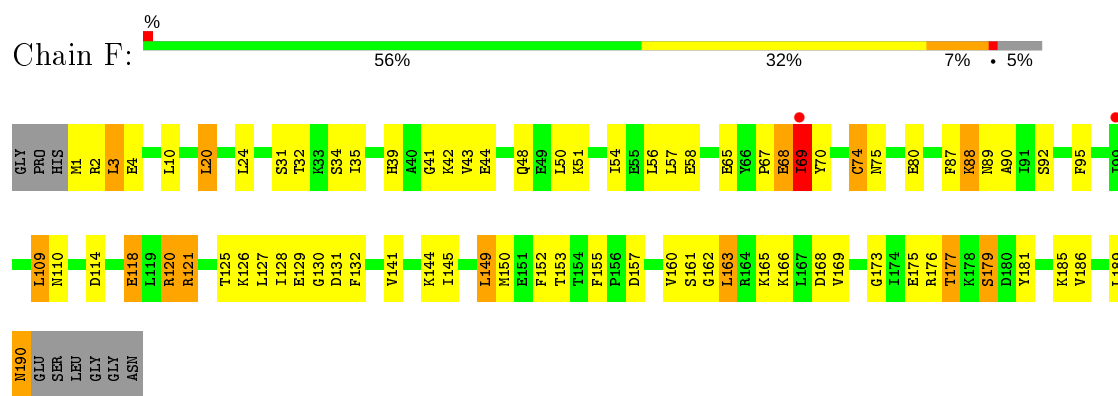
• Molecule 1: AFTRAX



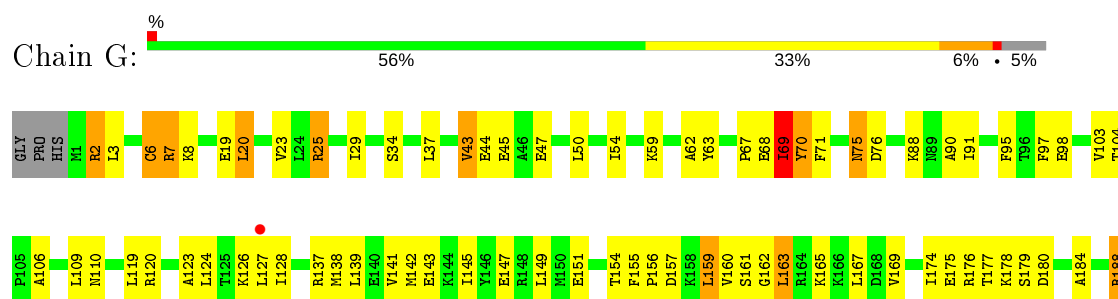
• Molecule 1: AFTRAX



• Molecule 1: AFTRAX



• Molecule 1: AFTRAX



L189
ASN
GLU
SER
LEU
GLY
GLY
ASN

● Molecule 1: AFTRAX



GLY	PRO	HIS	M1	R2	R7	L10	E14	E19	L20	L21	V23	L24	R25	H30	S31	S34	I35	H39	V43	E44	L50	K51	K52	L56	L57	K61	A62	Y63	I69	M78	Q79	E80	I85	S92	G93	E94	F97	E102	V103	T104
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F108	L109	N110	G111	F112	A113	D114	A115	V116	G117	E118	L119	R120	R121	K126	L127	I128	D131	S134	R137	M138	L139	E140	V141	Y146	F147	R148	L149	M150	E151	F152	T153	T154	S161	G162	L163	R164	K165	K166	D167	D168	V169	A170	R171	G172	G173	I174	E175	R176	T177	K178	S179	D180	Y181
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I182	A183	A184	K185	V186	A187	ARG	LEU	ASN	GLU	SER	LEU	GLY	GLY	ASN
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4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	183.31Å 183.31Å 111.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.56 – 3.27 70.75 – 3.27	Depositor EDS
% Data completeness (in resolution range)	99.9 (53.56-3.27) 98.1 (70.75-3.27)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 3.26Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.221 , 0.281 0.226 , 0.288	Depositor DCC
R_{free} test set	2000 reflections (6.70%)	wwPDB-VP
Wilson B-factor (Å ²)	102.8	Xtriage
Anisotropy	0.318	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 72.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11820	wwPDB-VP
Average B, all atoms (Å ²)	103.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 13.04% 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: MG

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	0.49	0/1506	0.63	0/2025
1	B	0.48	0/1515	0.65	0/2038
1	C	0.49	0/1497	0.66	0/2016
1	D	0.47	0/1499	0.62	1/2016 (0.0%)
1	E	0.50	1/1513 (0.1%)	0.63	0/2031
1	F	0.50	0/1505	0.65	0/2024
1	G	0.49	0/1470	0.66	0/1983
1	H	0.48	0/1456	0.63	1/1963 (0.1%)
All	All	0.49	1/11961 (0.0%)	0.64	2/16096 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	6	CYS	CB-SG	5.27	1.91	1.82

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	57	LEU	CA-CB-CG	5.68	128.36	115.30
1	H	57	LEU	CA-CB-CG	5.56	128.09	115.30

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	1487	0	1485	33	0
1	B	1495	0	1479	45	0
1	C	1478	0	1454	47	0
1	D	1479	0	1475	48	0
1	E	1494	0	1513	48	0
1	F	1486	0	1486	46	0
1	G	1451	0	1395	48	0
1	H	1437	0	1387	33	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
3	B	3	0	0	0	0
3	D	1	0	0	0	0
3	F	3	0	0	0	0
3	G	1	0	0	0	0
All	All	11820	0	11674	309	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 309 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:G:2:ARG:NH1	1:G:6:CYS:SG	2.50	0.85
1:C:2:ARG:NH1	1:C:6:CYS:SG	2.54	0.80
1:F:161:SER:OG	1:F:162:GLY:N	2.20	0.74
1:D:183:ALA:O	1:D:185:LYS:N	2.22	0.72
1:H:183:ALA:O	1:H:185:LYS:N	2.22	0.72

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	188/199 (94%)	164 (87%)	15 (8%)	9 (5%)	2	14
1	B	188/199 (94%)	159 (85%)	25 (13%)	4 (2%)	7	32
1	C	187/199 (94%)	160 (86%)	23 (12%)	4 (2%)	7	32
1	D	185/199 (93%)	152 (82%)	29 (16%)	4 (2%)	6	31
1	E	188/199 (94%)	164 (87%)	16 (8%)	8 (4%)	2	16
1	F	188/199 (94%)	164 (87%)	20 (11%)	4 (2%)	7	32
1	G	187/199 (94%)	159 (85%)	23 (12%)	5 (3%)	5	26
1	H	185/199 (93%)	147 (80%)	30 (16%)	8 (4%)	2	16
All	All	1496/1592 (94%)	1269 (85%)	181 (12%)	46 (3%)	4	24

5 of 46 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ARG
1	B	2	ARG
1	B	42	LYS
1	B	131	ASP
1	E	2	ARG

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	148/167 (89%)	123 (83%)	25 (17%)	2	9
1	B	149/167 (89%)	124 (83%)	25 (17%)	2	9
1	C	147/167 (88%)	127 (86%)	20 (14%)	3	16
1	D	149/167 (89%)	120 (80%)	29 (20%)	1	5
1	E	150/167 (90%)	125 (83%)	25 (17%)	2	9
1	F	149/167 (89%)	120 (80%)	29 (20%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	140/167 (84%)	119 (85%)	21 (15%)	3	12
1	H	138/167 (83%)	111 (80%)	27 (20%)	1	5
All	All	1170/1336 (88%)	969 (83%)	201 (17%)	2	9

5 of 201 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	141	VAL
1	E	99	ILE
1	H	56	LEU
1	D	164	ARG
1	E	20	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	79	GLN
1	H	79	GLN
1	E	39	HIS
1	B	79	GLN
1	F	110	ASN

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 5 ligands modelled in this entry, 5 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 [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	190/199 (95%)	-0.01	2 (1%) 80 80	70, 100, 132, 157	0
1	B	190/199 (95%)	-0.08	4 (2%) 63 61	61, 99, 141, 157	0
1	C	189/199 (94%)	-0.09	1 (0%) 91 90	68, 97, 134, 159	0
1	D	187/199 (93%)	-0.05	3 (1%) 72 69	75, 104, 137, 157	0
1	E	190/199 (95%)	-0.10	1 (0%) 91 90	69, 100, 131, 157	0
1	F	190/199 (95%)	-0.08	2 (1%) 80 80	57, 97, 138, 151	0
1	G	189/199 (94%)	-0.08	1 (0%) 91 90	70, 99, 139, 160	0
1	H	187/199 (93%)	0.09	5 (2%) 54 51	75, 102, 137, 157	0
All	All	1512/1592 (94%)	-0.05	19 (1%) 77 75	57, 100, 139, 160	0

The worst 5 of 19 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	97	PHE	4.5
1	B	69	ILE	4.4
1	H	152	PHE	3.5
1	H	85	ILE	3.4
1	H	112	PHE	3.2

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. 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(Å ²)	Q<0.9
2	MG	C	197	1/1	0.90	0.18	75,75,75,75	0
2	MG	F	197	1/1	0.91	0.12	95,95,95,95	0
2	MG	B	197	1/1	0.92	0.07	93,93,93,93	0
2	MG	D	197	1/1	0.94	0.07	90,90,90,90	0
2	MG	G	197	1/1	0.94	0.10	74,74,74,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.