



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 4, 2024 – 03:41 AM EST

PDB ID : 1OXH
Title : The crystal structure of beta-ketoacyl-[acyl carrier protein] synthase II from Streptococcus Pneumoniae, Triclinic form
Authors : Price, A.C.; Rock, C.O.; White, S.W.
Deposited on : 2003-04-02
Resolution : 2.09 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
Xtriage (Phenix) : 1.13
EDS : 2.36
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

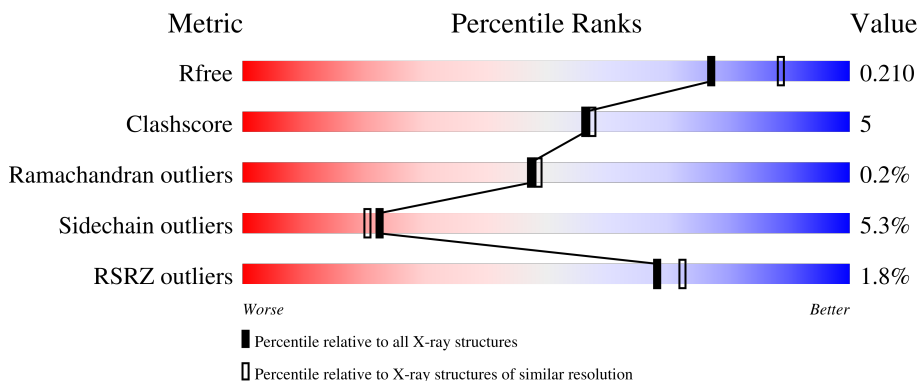
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.09 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	430	
1	B	430	
1	C	430	
1	D	430	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 12480 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 Beta ketoacyl-acyl carrier protein synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	408	3065	1934	523	596	12	0	0	0
1	B	408	3065	1934	523	596	12	0	0	0
1	C	408	3065	1934	523	596	12	0	0	0
1	D	408	3065	1934	523	596	12	0	0	0

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	GLY	-	cloning artifact	UNP Q9FBC2
A	-17	SER	-	cloning artifact	UNP Q9FBC2
A	-16	SER	-	cloning artifact	UNP Q9FBC2
A	-15	HIS	-	cloning artifact	UNP Q9FBC2
A	-14	HIS	-	cloning artifact	UNP Q9FBC2
A	-13	HIS	-	cloning artifact	UNP Q9FBC2
A	-12	HIS	-	cloning artifact	UNP Q9FBC2
A	-11	HIS	-	cloning artifact	UNP Q9FBC2
A	-10	HIS	-	cloning artifact	UNP Q9FBC2
A	-9	SER	-	cloning artifact	UNP Q9FBC2
A	-8	SER	-	cloning artifact	UNP Q9FBC2
A	-7	GLY	-	cloning artifact	UNP Q9FBC2
A	-6	LEU	-	cloning artifact	UNP Q9FBC2
A	-5	VAL	-	cloning artifact	UNP Q9FBC2
A	-4	PRO	-	cloning artifact	UNP Q9FBC2
A	-3	ARG	-	cloning artifact	UNP Q9FBC2
A	-2	GLY	-	cloning artifact	UNP Q9FBC2
A	-1	SER	-	cloning artifact	UNP Q9FBC2
A	0	HIS	-	cloning artifact	UNP Q9FBC2
B	-18	GLY	-	cloning artifact	UNP Q9FBC2
B	-17	SER	-	cloning artifact	UNP Q9FBC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	cloning artifact	UNP Q9FBC2
B	-15	HIS	-	cloning artifact	UNP Q9FBC2
B	-14	HIS	-	cloning artifact	UNP Q9FBC2
B	-13	HIS	-	cloning artifact	UNP Q9FBC2
B	-12	HIS	-	cloning artifact	UNP Q9FBC2
B	-11	HIS	-	cloning artifact	UNP Q9FBC2
B	-10	HIS	-	cloning artifact	UNP Q9FBC2
B	-9	SER	-	cloning artifact	UNP Q9FBC2
B	-8	SER	-	cloning artifact	UNP Q9FBC2
B	-7	GLY	-	cloning artifact	UNP Q9FBC2
B	-6	LEU	-	cloning artifact	UNP Q9FBC2
B	-5	VAL	-	cloning artifact	UNP Q9FBC2
B	-4	PRO	-	cloning artifact	UNP Q9FBC2
B	-3	ARG	-	cloning artifact	UNP Q9FBC2
B	-2	GLY	-	cloning artifact	UNP Q9FBC2
B	-1	SER	-	cloning artifact	UNP Q9FBC2
B	0	HIS	-	cloning artifact	UNP Q9FBC2
C	-18	GLY	-	cloning artifact	UNP Q9FBC2
C	-17	SER	-	cloning artifact	UNP Q9FBC2
C	-16	SER	-	cloning artifact	UNP Q9FBC2
C	-15	HIS	-	cloning artifact	UNP Q9FBC2
C	-14	HIS	-	cloning artifact	UNP Q9FBC2
C	-13	HIS	-	cloning artifact	UNP Q9FBC2
C	-12	HIS	-	cloning artifact	UNP Q9FBC2
C	-11	HIS	-	cloning artifact	UNP Q9FBC2
C	-10	HIS	-	cloning artifact	UNP Q9FBC2
C	-9	SER	-	cloning artifact	UNP Q9FBC2
C	-8	SER	-	cloning artifact	UNP Q9FBC2
C	-7	GLY	-	cloning artifact	UNP Q9FBC2
C	-6	LEU	-	cloning artifact	UNP Q9FBC2
C	-5	VAL	-	cloning artifact	UNP Q9FBC2
C	-4	PRO	-	cloning artifact	UNP Q9FBC2
C	-3	ARG	-	cloning artifact	UNP Q9FBC2
C	-2	GLY	-	cloning artifact	UNP Q9FBC2
C	-1	SER	-	cloning artifact	UNP Q9FBC2
C	0	HIS	-	cloning artifact	UNP Q9FBC2
D	-18	GLY	-	cloning artifact	UNP Q9FBC2
D	-17	SER	-	cloning artifact	UNP Q9FBC2
D	-16	SER	-	cloning artifact	UNP Q9FBC2
D	-15	HIS	-	cloning artifact	UNP Q9FBC2
D	-14	HIS	-	cloning artifact	UNP Q9FBC2
D	-13	HIS	-	cloning artifact	UNP Q9FBC2

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	HIS	-	cloning artifact	UNP Q9FBC2
D	-11	HIS	-	cloning artifact	UNP Q9FBC2
D	-10	HIS	-	cloning artifact	UNP Q9FBC2
D	-9	SER	-	cloning artifact	UNP Q9FBC2
D	-8	SER	-	cloning artifact	UNP Q9FBC2
D	-7	GLY	-	cloning artifact	UNP Q9FBC2
D	-6	LEU	-	cloning artifact	UNP Q9FBC2
D	-5	VAL	-	cloning artifact	UNP Q9FBC2
D	-4	PRO	-	cloning artifact	UNP Q9FBC2
D	-3	ARG	-	cloning artifact	UNP Q9FBC2
D	-2	GLY	-	cloning artifact	UNP Q9FBC2
D	-1	SER	-	cloning artifact	UNP Q9FBC2
D	0	HIS	-	cloning artifact	UNP Q9FBC2

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

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

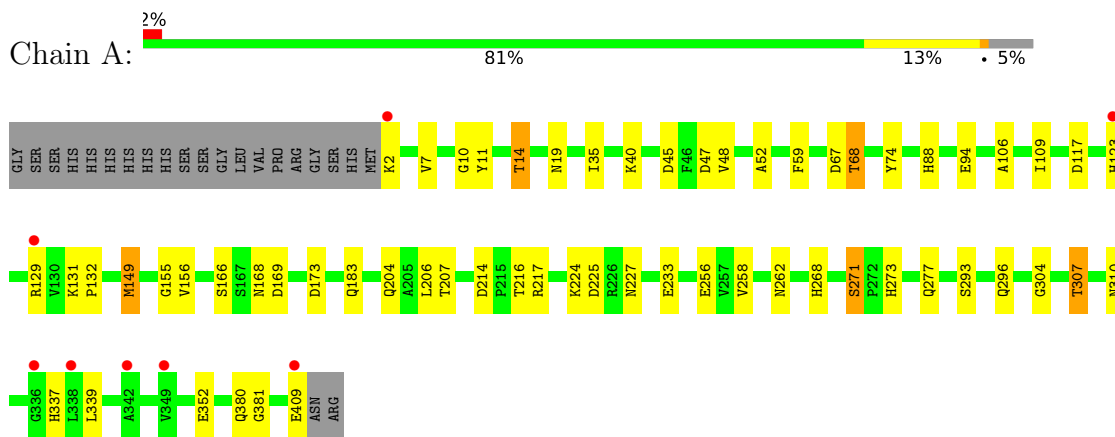
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	58	Total O 58 58	0	0
3	B	48	Total O 48 48	0	0
3	C	54	Total O 54 54	0	0
3	D	56	Total O 56 56	0	0

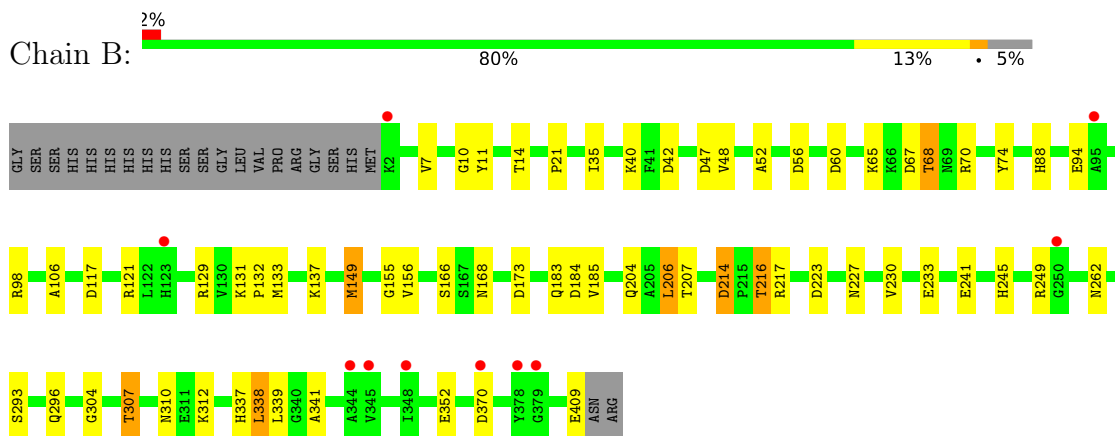
3 Residue-property plots [i](#)

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.

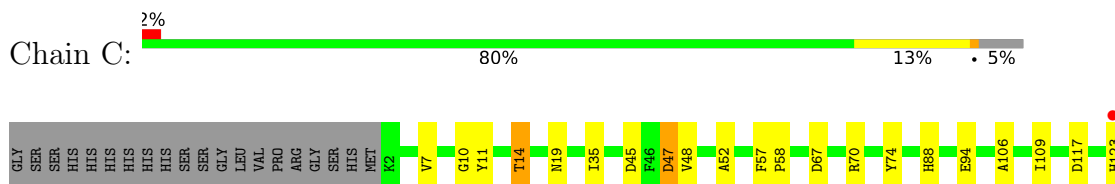
- Molecule 1: Beta ketoacyl-acyl carrier protein synthase

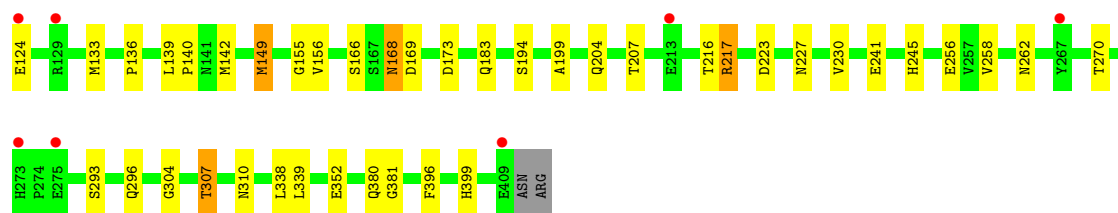


- Molecule 1: Beta ketoacyl-acyl carrier protein synthase

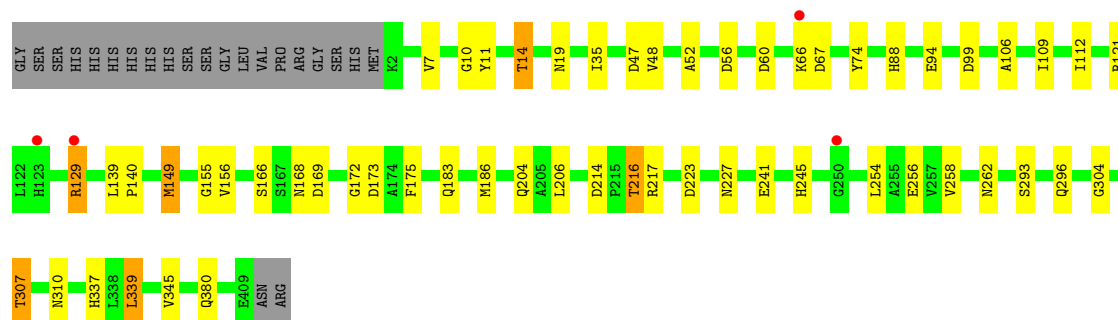
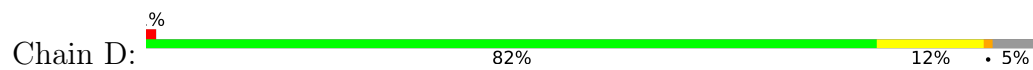


- Molecule 1: Beta ketoacyl-acyl carrier protein synthase





● Molecule 1: Beta ketoacyl-acyl carrier protein synthase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	61.52Å 71.65Å 96.10Å 89.83° 83.09° 69.15°	Depositor
Resolution (Å)	29.19 – 2.09 29.19 – 2.09	Depositor EDS
% Data completeness (in resolution range)	86.2 (29.19-2.09) 77.1 (29.19-2.09)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.82 (at 2.08Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.208 , 0.235 0.208 , 0.210	Depositor DCC
R_{free} test set	2368 reflections (3.03%)	wwPDB-VP
Wilson B-factor (Å ²)	31.0	Xtrriage
Anisotropy	0.861	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.9	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	0.95	EDS
Total number of atoms	12480	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.86	1/3128 (0.0%)	0.88	6/4239 (0.1%)
1	B	0.90	2/3128 (0.1%)	0.94	12/4239 (0.3%)
1	C	0.87	1/3128 (0.0%)	0.89	7/4239 (0.2%)
1	D	0.91	3/3128 (0.1%)	0.90	6/4239 (0.1%)
All	All	0.88	7/12512 (0.1%)	0.90	31/16956 (0.2%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	149	MET	SD-CE	7.11	2.17	1.77
1	C	149	MET	SD-CE	6.65	2.15	1.77
1	A	149	MET	SD-CE	6.46	2.14	1.77
1	D	149	MET	SD-CE	5.79	2.10	1.77
1	D	345	VAL	CB-CG1	-5.35	1.41	1.52
1	D	186	MET	CG-SD	-5.10	1.67	1.81
1	B	312	LYS	CD-CE	5.08	1.64	1.51

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	67	ASP	CB-CG-OD2	7.81	125.33	118.30
1	A	67	ASP	CB-CG-OD2	7.71	125.24	118.30
1	B	223	ASP	CB-CG-OD2	7.58	125.12	118.30
1	D	67	ASP	CB-CG-OD2	7.55	125.10	118.30
1	D	169	ASP	CB-CG-OD2	7.37	124.93	118.30
1	B	121	ARG	NE-CZ-NH2	-6.83	116.88	120.30
1	B	370	ASP	CB-CG-OD2	6.80	124.42	118.30
1	A	117	ASP	CB-CG-OD2	6.28	123.95	118.30
1	D	99	ASP	CB-CG-OD2	6.21	123.89	118.30
1	A	45	ASP	CB-CG-OD2	6.18	123.86	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	67	ASP	CB-CG-OD2	6.04	123.73	118.30
1	B	117	ASP	CB-CG-OD2	5.86	123.58	118.30
1	C	45	ASP	CB-CG-OD2	5.83	123.55	118.30
1	A	225	ASP	CB-CG-OD1	5.80	123.52	118.30
1	C	47	ASP	CB-CG-OD2	5.74	123.46	118.30
1	D	56	ASP	CB-CG-OD2	5.71	123.44	118.30
1	B	60	ASP	CB-CG-OD2	5.66	123.39	118.30
1	D	223	ASP	CB-CG-OD2	5.63	123.36	118.30
1	C	223	ASP	CB-CG-OD2	5.62	123.35	118.30
1	B	214	ASP	CB-CG-OD2	5.56	123.30	118.30
1	C	169	ASP	CB-CG-OD2	5.55	123.30	118.30
1	C	117	ASP	CB-CG-OD2	5.37	123.13	118.30
1	B	249	ARG	NE-CZ-NH1	5.33	122.96	120.30
1	B	42	ASP	CB-CG-OD2	5.32	123.09	118.30
1	A	169	ASP	CB-CG-OD2	5.32	123.08	118.30
1	B	56	ASP	CB-CG-OD2	5.27	123.05	118.30
1	A	214	ASP	CB-CG-OD2	5.26	123.03	118.30
1	D	60	ASP	CB-CG-OD2	5.06	122.85	118.30
1	C	217	ARG	NE-CZ-NH1	5.04	122.82	120.30
1	B	249	ARG	NE-CZ-NH2	-5.03	117.79	120.30
1	B	184	ASP	CB-CG-OD2	5.01	122.81	118.30

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	3065	0	2999	31	0
1	B	3065	0	2999	33	0
1	C	3065	0	2999	36	0
1	D	3065	0	2999	24	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	58	0	0	1	0
3	B	48	0	0	1	0
3	C	54	0	0	0	0
3	D	56	0	0	1	0
All	All	12480	0	11996	120	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 5.

All (120) 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:D:149:MET:SD	1:D:149:MET:CE	2.10	1.38
1:A:149:MET:SD	1:A:149:MET:CE	2.14	1.35
1:C:149:MET:CE	1:C:149:MET:SD	2.15	1.33
1:B:149:MET:CE	1:B:149:MET:SD	2.17	1.31
1:C:307:THR:HG22	1:C:310:ASN:H	1.46	0.80
1:D:307:THR:HG22	1:D:310:ASN:H	1.44	0.79
1:A:307:THR:HG22	1:A:310:ASN:H	1.48	0.79
1:B:307:THR:HG22	1:B:310:ASN:H	1.47	0.77
1:A:380:GLN:HE21	1:A:381:GLY:H	1.32	0.75
1:D:10:GLY:HA2	1:D:88:HIS:HD2	1.52	0.75
1:C:380:GLN:HE21	1:C:381:GLY:H	1.38	0.71
1:A:47:ASP:H	1:A:204:GLN:HE22	1.39	0.70
1:D:47:ASP:H	1:D:204:GLN:NE2	1.91	0.69
1:D:47:ASP:H	1:D:204:GLN:HE22	1.42	0.68
1:A:293:SER:H	1:A:296:GLN:HE21	1.44	0.66
1:A:47:ASP:H	1:A:204:GLN:NE2	1.94	0.65
1:D:11:TYR:CE2	1:D:254:LEU:HD23	2.33	0.63
1:A:59:PHE:CZ	1:A:68:THR:HG22	2.33	0.63
1:B:47:ASP:H	1:B:204:GLN:HE22	1.48	0.62
1:B:207:THR:O	1:B:207:THR:HG22	1.99	0.61
1:B:10:GLY:HA2	1:B:88:HIS:HD2	1.66	0.60
1:D:241:GLU:OE1	1:D:245:HIS:HD2	1.86	0.59
1:B:47:ASP:H	1:B:204:GLN:NE2	2.00	0.59
1:D:293:SER:H	1:D:296:GLN:HE21	1.51	0.59
1:C:10:GLY:HA2	1:C:88:HIS:HD2	1.68	0.58
1:D:121:ARG:HD3	1:D:129:ARG:O	2.04	0.58
1:C:293:SER:H	1:C:296:GLN:HE21	1.52	0.58
1:D:337:HIS:CD2	1:D:339:LEU:H	2.21	0.58
1:C:47:ASP:H	1:C:204:GLN:HE22	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:48:VAL:HG23	1:C:204:GLN:HE21	1.70	0.56
1:A:268:HIS:ND1	1:A:271:SER:HB2	2.20	0.56
1:A:155:GLY:HA3	1:A:183:GLN:HE22	1.70	0.56
1:B:337:HIS:CD2	1:B:339:LEU:H	2.24	0.55
1:C:35:ILE:HD13	1:C:52:ALA:HB2	1.88	0.55
1:A:380:GLN:HE21	1:A:381:GLY:N	2.04	0.54
1:C:47:ASP:H	1:C:204:GLN:NE2	2.05	0.54
1:C:11:TYR:OH	1:C:352:GLU:OE2	2.25	0.53
1:D:155:GLY:HA3	1:D:183:GLN:HE22	1.73	0.53
1:B:241:GLU:OE1	1:B:245:HIS:HD2	1.91	0.53
1:B:48:VAL:HG23	1:B:204:GLN:HE21	1.74	0.53
1:A:106:ALA:HB1	1:A:166:SER:HB3	1.90	0.53
1:B:65:LYS:O	1:B:68:THR:HG23	2.09	0.53
1:D:35:ILE:HD13	1:D:52:ALA:HB2	1.89	0.53
1:A:35:ILE:HD13	1:A:52:ALA:HB2	1.92	0.52
1:D:293:SER:H	1:D:296:GLN:NE2	2.08	0.52
1:A:48:VAL:HG23	1:A:204:GLN:HE21	1.75	0.52
1:B:11:TYR:HE1	1:B:21:PRO:HB3	1.74	0.52
1:C:155:GLY:HA3	1:C:183:GLN:HE22	1.74	0.52
1:C:262:ASN:ND2	1:D:156:VAL:HG13	2.25	0.51
1:A:207:THR:HG22	1:A:207:THR:O	2.10	0.51
1:B:185:VAL:CG2	1:B:245:HIS:CE1	2.94	0.51
1:C:136:PRO:O	1:C:142:MET:HG3	2.11	0.51
1:A:156:VAL:H	1:A:183:GLN:NE2	2.09	0.51
1:C:10:GLY:HA2	1:C:88:HIS:CD2	2.46	0.51
1:A:11:TYR:H	1:A:88:HIS:HD2	1.59	0.50
1:D:106:ALA:HB1	1:D:166:SER:HB3	1.92	0.50
1:B:35:ILE:HD13	1:B:52:ALA:HB2	1.92	0.50
3:A:931:HOH:O	1:B:262:ASN:HB2	2.10	0.50
1:B:11:TYR:OH	1:B:352:GLU:CD	2.50	0.50
1:B:10:GLY:HA2	1:B:88:HIS:CD2	2.47	0.50
1:C:262:ASN:HB2	3:D:906:HOH:O	2.11	0.50
1:B:106:ALA:HB1	1:B:166:SER:HB3	1.95	0.49
1:A:262:ASN:HB2	3:B:904:HOH:O	2.12	0.49
1:B:155:GLY:HA3	1:B:183:GLN:HE22	1.77	0.49
1:C:293:SER:H	1:C:296:GLN:NE2	2.11	0.49
1:A:293:SER:H	1:A:296:GLN:NE2	2.09	0.48
1:B:214:ASP:OD1	1:B:216:THR:HB	2.14	0.48
1:A:206:LEU:O	1:A:207:THR:HB	2.14	0.48
1:C:241:GLU:OE1	1:C:245:HIS:HD2	1.97	0.48
1:B:338:LEU:HB3	1:B:341:ALA:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:380:GLN:HE21	1:C:381:GLY:N	2.09	0.47
1:B:206:LEU:O	1:B:207:THR:HB	2.14	0.47
1:C:11:TYR:H	1:C:88:HIS:CD2	2.33	0.46
1:A:10:GLY:HA2	1:A:88:HIS:CD2	2.50	0.46
1:A:10:GLY:HA2	1:A:88:HIS:HD2	1.81	0.46
1:B:11:TYR:CE1	1:B:21:PRO:HB3	2.51	0.46
1:B:156:VAL:H	1:B:183:GLN:NE2	2.14	0.46
1:D:109:ILE:HG22	1:D:112:ILE:HB	1.98	0.46
1:A:131:LYS:HA	1:A:132:PRO:HD3	1.82	0.45
1:C:256:GLU:HG2	1:C:258:VAL:HG13	1.99	0.45
1:C:35:ILE:HD12	1:C:230:VAL:HG11	1.98	0.45
1:A:273:HIS:CD2	1:A:277:GLN:H	2.35	0.45
1:B:40:LYS:CE	1:B:233:GLU:OE2	2.65	0.45
1:C:194:SER:O	1:C:199:ALA:HB3	2.17	0.45
1:D:172:GLY:O	1:D:175:PHE:HB3	2.17	0.44
1:B:293:SER:H	1:B:296:GLN:HE21	1.65	0.44
1:C:380:GLN:NE2	1:C:381:GLY:H	2.12	0.44
1:B:131:LYS:HA	1:B:132:PRO:HD3	1.89	0.44
1:C:262:ASN:HD21	1:D:156:VAL:HG13	1.83	0.44
1:B:293:SER:H	1:B:296:GLN:NE2	2.16	0.43
1:C:139:LEU:HA	1:C:140:PRO:HD3	1.77	0.43
1:C:396:PHE:O	1:C:399:HIS:HD2	2.00	0.43
1:B:133:MET:O	1:B:137:LYS:HG3	2.19	0.43
1:C:106:ALA:HB1	1:C:166:SER:HB3	1.99	0.43
1:C:207:THR:O	1:C:207:THR:HG22	2.19	0.43
1:C:11:TYR:H	1:C:88:HIS:HD2	1.66	0.43
1:C:14:THR:HG22	1:C:19:ASN:OD1	2.19	0.43
1:A:262:ASN:ND2	1:B:156:VAL:HG13	2.34	0.42
1:D:14:THR:HG22	1:D:19:ASN:OD1	2.19	0.42
1:A:11:TYR:H	1:A:88:HIS:CD2	2.35	0.42
1:D:48:VAL:HG23	1:D:204:GLN:HE21	1.83	0.42
1:A:268:HIS:ND1	1:A:271:SER:CB	2.83	0.42
1:C:270:THR:HG23	1:C:396:PHE:CE1	2.55	0.42
1:A:256:GLU:HG2	1:A:258:VAL:HG13	2.00	0.42
1:A:14:THR:HG22	1:A:19:ASN:OD1	2.19	0.42
1:C:156:VAL:H	1:C:183:GLN:NE2	2.17	0.41
1:D:256:GLU:HG2	1:D:258:VAL:HG13	2.02	0.41
1:B:206:LEU:O	1:B:207:THR:CB	2.68	0.41
1:B:35:ILE:HD12	1:B:230:VAL:HG11	2.02	0.41
1:B:241:GLU:OE1	1:B:245:HIS:CD2	2.72	0.41
1:C:168:ASN:HD22	1:C:168:ASN:HA	1.71	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:40:LYS:CE	1:A:233:GLU:OE2	2.68	0.41
1:A:11:TYR:OH	1:A:352:GLU:OE2	2.38	0.41
1:A:268:HIS:CE1	1:A:271:SER:HB2	2.55	0.41
1:C:57:PHE:HA	1:C:58:PRO:HD3	1.96	0.41
1:C:133:MET:C	1:C:136:PRO:HD2	2.42	0.41
1:B:185:VAL:HG23	1:B:245:HIS:CE1	2.56	0.40
1:D:214:ASP:OD2	1:D:216:THR:HG22	2.22	0.40
1:C:156:VAL:HG13	1:D:262:ASN:ND2	2.36	0.40
1:D:139:LEU:HA	1:D:140:PRO:HD3	1.86	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	406/430 (94%)	390 (96%)	15 (4%)	1 (0%)	47	49
1	B	406/430 (94%)	389 (96%)	16 (4%)	1 (0%)	47	49
1	C	406/430 (94%)	388 (96%)	17 (4%)	1 (0%)	47	49
1	D	406/430 (94%)	388 (96%)	17 (4%)	1 (0%)	47	49
All	All	1624/1720 (94%)	1555 (96%)	65 (4%)	4 (0%)	47	49

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	304	GLY
1	A	304	GLY
1	B	304	GLY
1	C	304	GLY

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	320/339 (94%)	300 (94%)	20 (6%)	18	15
1	B	320/339 (94%)	303 (95%)	17 (5%)	22	20
1	C	320/339 (94%)	304 (95%)	16 (5%)	24	23
1	D	320/339 (94%)	305 (95%)	15 (5%)	26	25
All	All	1280/1356 (94%)	1212 (95%)	68 (5%)	22	20

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	7	VAL
1	A	14	THR
1	A	68	THR
1	A	74	TYR
1	A	94	GLU
1	A	109	ILE
1	A	123	HIS
1	A	129	ARG
1	A	168	ASN
1	A	173	ASP
1	A	216	THR
1	A	217	ARG
1	A	224	LYS
1	A	227	ASN
1	A	271	SER
1	A	307	THR
1	A	337	HIS
1	A	339	LEU
1	A	409	GLU
1	B	7	VAL
1	B	14	THR
1	B	68	THR
1	B	70	ARG

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Mol	Chain	Res	Type
1	B	74	TYR
1	B	94	GLU
1	B	98	ARG
1	B	129	ARG
1	B	168	ASN
1	B	173	ASP
1	B	206	LEU
1	B	216	THR
1	B	217	ARG
1	B	227	ASN
1	B	307	THR
1	B	338	LEU
1	B	409	GLU
1	C	7	VAL
1	C	14	THR
1	C	70	ARG
1	C	74	TYR
1	C	94	GLU
1	C	109	ILE
1	C	123	HIS
1	C	124	GLU
1	C	168	ASN
1	C	173	ASP
1	C	216	THR
1	C	217	ARG
1	C	227	ASN
1	C	307	THR
1	C	338	LEU
1	C	339	LEU
1	D	7	VAL
1	D	14	THR
1	D	66	LYS
1	D	74	TYR
1	D	94	GLU
1	D	129	ARG
1	D	168	ASN
1	D	173	ASP
1	D	206	LEU
1	D	216	THR
1	D	217	ARG
1	D	227	ASN
1	D	307	THR

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Mol	Chain	Res	Type
1	D	339	LEU
1	D	380	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	ASN
1	A	88	HIS
1	A	168	ASN
1	A	183	GLN
1	A	204	GLN
1	A	227	ASN
1	A	245	HIS
1	A	273	HIS
1	A	296	GLN
1	A	356	HIS
1	A	380	GLN
1	B	69	ASN
1	B	88	HIS
1	B	168	ASN
1	B	183	GLN
1	B	204	GLN
1	B	227	ASN
1	B	245	HIS
1	B	273	HIS
1	B	296	GLN
1	B	337	HIS
1	C	69	ASN
1	C	88	HIS
1	C	168	ASN
1	C	183	GLN
1	C	204	GLN
1	C	227	ASN
1	C	245	HIS
1	C	296	GLN
1	C	337	HIS
1	C	380	GLN
1	D	88	HIS
1	D	168	ASN
1	D	183	GLN
1	D	204	GLN
1	D	227	ASN

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Mol	Chain	Res	Type
1	D	245	HIS
1	D	268	HIS
1	D	273	HIS
1	D	296	GLN
1	D	337	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 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

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	408/430 (94%)	-0.04	8 (1%) 65 69	30, 40, 54, 69	0
1	B	408/430 (94%)	0.03	10 (2%) 57 62	32, 41, 57, 66	0
1	C	408/430 (94%)	-0.06	8 (1%) 65 69	32, 41, 57, 71	0
1	D	408/430 (94%)	-0.04	4 (0%) 82 85	32, 41, 56, 69	0
All	All	1632/1720 (94%)	-0.03	30 (1%) 68 72	30, 41, 57, 71	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	267	TYR	4.2
1	C	129	ARG	3.6
1	A	338	LEU	3.4
1	B	2	LYS	3.2
1	D	66	LYS	3.2
1	B	345	VAL	3.1
1	C	273	HIS	3.0
1	B	95	ALA	3.0
1	A	129	ARG	3.0
1	D	250	GLY	2.9
1	B	370	ASP	2.8
1	D	129	ARG	2.8
1	C	213	GLU	2.7
1	A	2	LYS	2.5
1	C	409	GLU	2.4
1	B	379	GLY	2.4
1	C	275	GLU	2.4
1	A	336	GLY	2.3
1	B	378	TYR	2.3
1	A	342	ALA	2.3
1	C	123	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	409	GLU	2.1
1	B	250	GLY	2.1
1	C	124	GLU	2.1
1	D	123	HIS	2.1
1	B	344	ALA	2.1
1	A	123	HIS	2.1
1	A	349	VAL	2.1
1	B	123	HIS	2.0
1	B	348	ILE	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 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, 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(\AA^2)	Q<0.9
2	MG	A	901	1/1	0.98	0.15	22,22,22,22	0
2	MG	B	902	1/1	0.98	0.18	29,29,29,29	0
2	MG	D	904	1/1	0.98	0.16	21,21,21,21	0
2	MG	C	903	1/1	0.99	0.14	25,25,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.