Full wwPDB X-ray Structure Validation Report (i)

Nov 7, 2023 – 04:47 AM EST

PDB ID	:	6C4C
Title	:	Crystal structure of 3-nitropropionate modified isocitrate lyase from Mycobacterium tuberculosis with glyoxylate and pyruvate
Authors	:	Kreitler, D.F.; Ray, S.; Murkin, A.S.; Gulick, A.M.
Deposited on	:	2018-01-11
Resolution	:	2.20 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 (i) 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 (i)) were used in the production of this report:

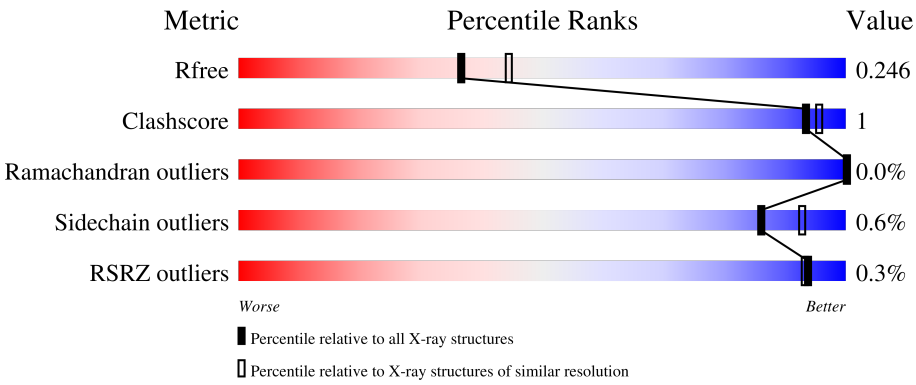
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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 <=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	442	92%
1	B	442	% 94%
1	C	442	% 92%
1	D	442	93%
1	E	442	93%

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Mol	Chain	Length	Quality of chain
1	F	442	93%
1	G	442	93%
1	H	442	93%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 53624 atoms, of which 25459 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 Isocitrate lyase 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	428	6489	2079	3180	574	646	10	0	0	0
1	B	427	6475	2074	3175	573	643	10	0	0	0
1	C	427	6468	2072	3169	575	643	9	0	0	0
1	D	428	6492	2080	3180	574	649	9	0	0	0
1	E	428	6553	2096	3210	586	652	9	0	9	0
1	F	428	6487	2079	3173	577	649	9	0	0	0
1	G	427	6468	2072	3169	575	643	9	0	0	0
1	H	428	6492	2081	3177	579	646	9	0	2	0

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP H8EVV4
A	-12	HIS	-	expression tag	UNP H8EVV4
A	-11	HIS	-	expression tag	UNP H8EVV4
A	-10	HIS	-	expression tag	UNP H8EVV4
A	-9	HIS	-	expression tag	UNP H8EVV4
A	-8	HIS	-	expression tag	UNP H8EVV4
A	-7	HIS	-	expression tag	UNP H8EVV4
A	-6	LEU	-	expression tag	UNP H8EVV4
A	-5	VAL	-	expression tag	UNP H8EVV4
A	-4	PRO	-	expression tag	UNP H8EVV4
A	-3	ARG	-	expression tag	UNP H8EVV4
A	-2	GLY	-	expression tag	UNP H8EVV4
A	-1	SER	-	expression tag	UNP H8EVV4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	0	HIS	-	expression tag	UNP H8EVV4
B	-13	MET	-	initiating methionine	UNP H8EVV4
B	-12	HIS	-	expression tag	UNP H8EVV4
B	-11	HIS	-	expression tag	UNP H8EVV4
B	-10	HIS	-	expression tag	UNP H8EVV4
B	-9	HIS	-	expression tag	UNP H8EVV4
B	-8	HIS	-	expression tag	UNP H8EVV4
B	-7	HIS	-	expression tag	UNP H8EVV4
B	-6	LEU	-	expression tag	UNP H8EVV4
B	-5	VAL	-	expression tag	UNP H8EVV4
B	-4	PRO	-	expression tag	UNP H8EVV4
B	-3	ARG	-	expression tag	UNP H8EVV4
B	-2	GLY	-	expression tag	UNP H8EVV4
B	-1	SER	-	expression tag	UNP H8EVV4
B	0	HIS	-	expression tag	UNP H8EVV4
C	-13	MET	-	initiating methionine	UNP H8EVV4
C	-12	HIS	-	expression tag	UNP H8EVV4
C	-11	HIS	-	expression tag	UNP H8EVV4
C	-10	HIS	-	expression tag	UNP H8EVV4
C	-9	HIS	-	expression tag	UNP H8EVV4
C	-8	HIS	-	expression tag	UNP H8EVV4
C	-7	HIS	-	expression tag	UNP H8EVV4
C	-6	LEU	-	expression tag	UNP H8EVV4
C	-5	VAL	-	expression tag	UNP H8EVV4
C	-4	PRO	-	expression tag	UNP H8EVV4
C	-3	ARG	-	expression tag	UNP H8EVV4
C	-2	GLY	-	expression tag	UNP H8EVV4
C	-1	SER	-	expression tag	UNP H8EVV4
C	0	HIS	-	expression tag	UNP H8EVV4
D	-13	MET	-	initiating methionine	UNP H8EVV4
D	-12	HIS	-	expression tag	UNP H8EVV4
D	-11	HIS	-	expression tag	UNP H8EVV4
D	-10	HIS	-	expression tag	UNP H8EVV4
D	-9	HIS	-	expression tag	UNP H8EVV4
D	-8	HIS	-	expression tag	UNP H8EVV4
D	-7	HIS	-	expression tag	UNP H8EVV4
D	-6	LEU	-	expression tag	UNP H8EVV4
D	-5	VAL	-	expression tag	UNP H8EVV4
D	-4	PRO	-	expression tag	UNP H8EVV4
D	-3	ARG	-	expression tag	UNP H8EVV4
D	-2	GLY	-	expression tag	UNP H8EVV4
D	-1	SER	-	expression tag	UNP H8EVV4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	0	HIS	-	expression tag	UNP H8EVV4
E	-13	MET	-	initiating methionine	UNP H8EVV4
E	-12	HIS	-	expression tag	UNP H8EVV4
E	-11	HIS	-	expression tag	UNP H8EVV4
E	-10	HIS	-	expression tag	UNP H8EVV4
E	-9	HIS	-	expression tag	UNP H8EVV4
E	-8	HIS	-	expression tag	UNP H8EVV4
E	-7	HIS	-	expression tag	UNP H8EVV4
E	-6	LEU	-	expression tag	UNP H8EVV4
E	-5	VAL	-	expression tag	UNP H8EVV4
E	-4	PRO	-	expression tag	UNP H8EVV4
E	-3	ARG	-	expression tag	UNP H8EVV4
E	-2	GLY	-	expression tag	UNP H8EVV4
E	-1	SER	-	expression tag	UNP H8EVV4
E	0	HIS	-	expression tag	UNP H8EVV4
F	-13	MET	-	initiating methionine	UNP H8EVV4
F	-12	HIS	-	expression tag	UNP H8EVV4
F	-11	HIS	-	expression tag	UNP H8EVV4
F	-10	HIS	-	expression tag	UNP H8EVV4
F	-9	HIS	-	expression tag	UNP H8EVV4
F	-8	HIS	-	expression tag	UNP H8EVV4
F	-7	HIS	-	expression tag	UNP H8EVV4
F	-6	LEU	-	expression tag	UNP H8EVV4
F	-5	VAL	-	expression tag	UNP H8EVV4
F	-4	PRO	-	expression tag	UNP H8EVV4
F	-3	ARG	-	expression tag	UNP H8EVV4
F	-2	GLY	-	expression tag	UNP H8EVV4
F	-1	SER	-	expression tag	UNP H8EVV4
F	0	HIS	-	expression tag	UNP H8EVV4
G	-13	MET	-	initiating methionine	UNP H8EVV4
G	-12	HIS	-	expression tag	UNP H8EVV4
G	-11	HIS	-	expression tag	UNP H8EVV4
G	-10	HIS	-	expression tag	UNP H8EVV4
G	-9	HIS	-	expression tag	UNP H8EVV4
G	-8	HIS	-	expression tag	UNP H8EVV4
G	-7	HIS	-	expression tag	UNP H8EVV4
G	-6	LEU	-	expression tag	UNP H8EVV4
G	-5	VAL	-	expression tag	UNP H8EVV4
G	-4	PRO	-	expression tag	UNP H8EVV4
G	-3	ARG	-	expression tag	UNP H8EVV4
G	-2	GLY	-	expression tag	UNP H8EVV4
G	-1	SER	-	expression tag	UNP H8EVV4

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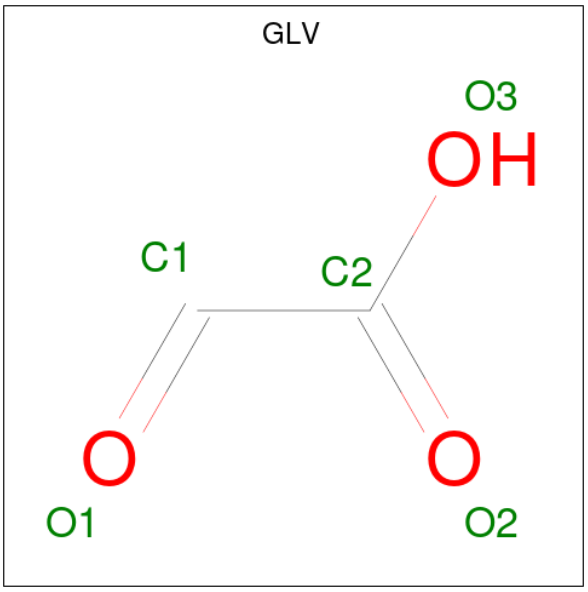
Chain	Residue	Modelled	Actual	Comment	Reference
G	0	HIS	-	expression tag	UNP H8EVV4
H	-13	MET	-	initiating methionine	UNP H8EVV4
H	-12	HIS	-	expression tag	UNP H8EVV4
H	-11	HIS	-	expression tag	UNP H8EVV4
H	-10	HIS	-	expression tag	UNP H8EVV4
H	-9	HIS	-	expression tag	UNP H8EVV4
H	-8	HIS	-	expression tag	UNP H8EVV4
H	-7	HIS	-	expression tag	UNP H8EVV4
H	-6	LEU	-	expression tag	UNP H8EVV4
H	-5	VAL	-	expression tag	UNP H8EVV4
H	-4	PRO	-	expression tag	UNP H8EVV4
H	-3	ARG	-	expression tag	UNP H8EVV4
H	-2	GLY	-	expression tag	UNP H8EVV4
H	-1	SER	-	expression tag	UNP H8EVV4
H	0	HIS	-	expression tag	UNP H8EVV4

- Molecule 2 is GLYOXYLIC ACID (three-letter code: GLV) (formula: $C_2H_2O_3$).

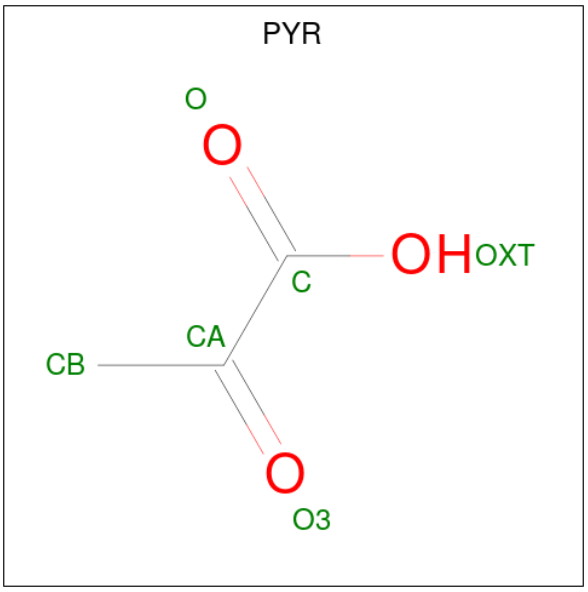


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
2	A	1	6	2	1	3	0	0
2	D	1	6	2	1	3	0	0
2	H	1	6	2	1	3	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	2	2	2	0	0
3	B	2	2	2	0	0
3	C	2	2	2	0	0
3	D	2	2	2	0	0
3	E	2	2	2	0	0
3	F	1	1	1	0	0
3	G	2	2	2	0	0
3	H	3	3	3	0	0

- Molecule 4 is PYRUVIC ACID (three-letter code: PYR) (formula: $C_3H_4O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	B	1	9	3	3	3	0	0
4	C	1	9	3	3	3	0	0
4	E	1	9	3	3	3	0	0
4	F	1	9	3	3	3	0	0

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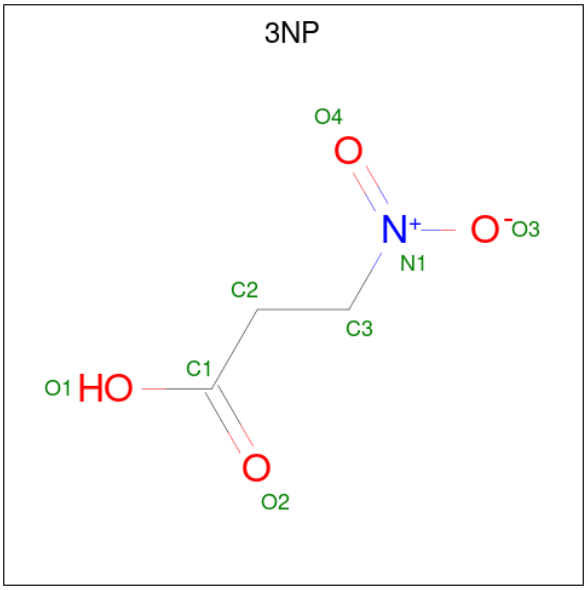
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	O		
4	G	1	9	3	3	3	0	0

- Molecule 5 is 3-NITROPROPANOIC ACID (three-letter code: 3NP) (formula: $C_3H_5NO_4$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
5	E	1	24	6	8	2	8	0	1

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	246	246	246	0	0
6	B	204	204	204	0	0
6	C	194	194	194	0	0
6	D	185	185	185	0	0
6	E	224	224	224	0	0
6	F	158	158	158	0	0
6	G	199	199	199	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	H	187	187	187	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: Isocitrate lyase 1

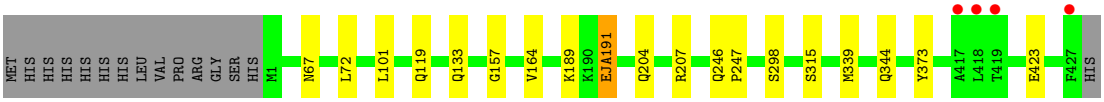
Chain A: 92%

• Molecule 1: Isocitrate lyase 1

Chain B: 94%

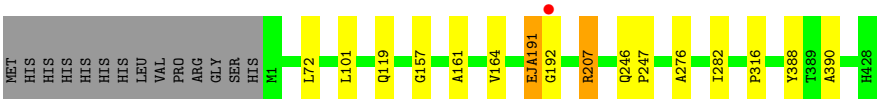
• Molecule 1: Isocitrate lyase 1

Chain C: 92%



• Molecule 1: Isocitrate lyase 1

Chain D: 93%

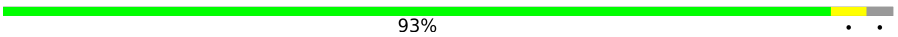


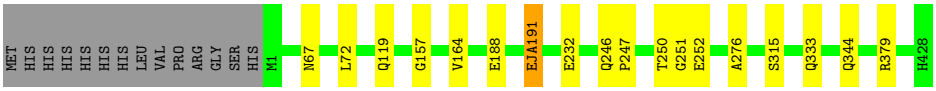
• Molecule 1: Isocitrate lyase 1

Chain E: 93%

• Molecule 1: Isocitrate lyase 1

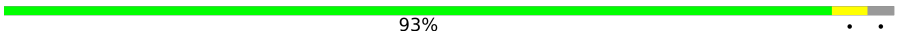
Chain F:





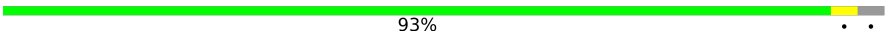
• Molecule 1: Isocitrate lyase 1

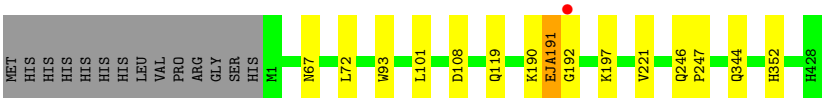
Chain G:



• Molecule 1: Isocitrate lyase 1

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	143.76Å 87.13Å 152.99Å 90.00° 116.55° 90.00°	Depositor
Resolution (Å)	47.39 – 2.20 77.93 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.4 (47.39-2.20) 84.6 (77.93-2.20)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	0.68 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.10.1_2155	Depositor
R, R_{free}	0.192 , 0.247 0.194 , 0.246	Depositor DCC
R_{free} test set	2001 reflections (1.18%)	wwPDB-VP
Wilson B-factor (Å^2)	25.7	Xtriage
Anisotropy	0.398	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 34.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	0.017 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	53624	wwPDB-VP
Average B, all atoms (Å^2)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.71% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: 3NP, MG, PYR, EJA, GLV

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	0.26	0/3366	0.44	0/4577
1	B	0.27	0/3357	0.43	0/4565
1	C	0.27	0/3356	0.43	0/4565
1	D	0.27	0/3369	0.44	0/4580
1	E	0.27	0/3433	0.43	0/4668
1	F	0.26	0/3372	0.43	0/4586
1	G	0.27	0/3356	0.43	0/4565
1	H	0.28	1/3381 (0.0%)	0.43	0/4598
All	All	0.27	1/26990 (0.0%)	0.43	0/36704

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	221	VAL	C-N	5.28	1.44	1.34

There are no bond angle outliers.

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	3309	3180	3175	12	0
1	B	3300	3175	3169	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3299	3169	3162	10	0
1	D	3312	3180	3174	8	0
1	E	3343	3210	3168	10	0
1	F	3314	3173	3166	12	0
1	G	3299	3169	3162	9	0
1	H	3315	3177	3160	7	0
2	A	5	1	1	0	0
2	D	5	1	1	0	0
2	H	5	1	1	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	2	0	0	0	0
3	D	2	0	0	0	0
3	E	2	0	0	0	0
3	F	1	0	0	0	0
3	G	2	0	0	0	0
3	H	3	0	0	0	0
4	B	6	3	0	0	0
4	C	6	3	0	0	0
4	E	6	3	0	0	0
4	F	6	3	0	0	0
4	G	6	3	0	0	0
5	E	16	8	8	5	0
6	A	246	0	0	1	0
6	B	204	0	0	2	0
6	C	194	0	0	2	0
6	D	185	0	0	0	0
6	E	224	0	0	3	0
6	F	158	0	0	4	0
6	G	199	0	0	1	0
6	H	187	0	0	0	0
All	All	28165	25459	25347	70	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 1.

All (70) 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)
5:E:504[A]:3NP:O4	6:E:601:HOH:O	2.04	0.75
1:B:17:TRP:O	6:B:601:HOH:O	2.08	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:290:ASP:OD2	6:G:601:HOH:O	2.09	0.71
1:E:25:ASP:O	6:E:602:HOH:O	2.14	0.66
1:E:379:ARG:NH2	5:E:504[A]:3NP:O3	2.35	0.57
1:B:401:TYR:OH	6:B:602:HOH:O	2.18	0.56
1:A:191:EJA:OT1	1:A:317:SER:OG	2.20	0.55
1:C:207:ARG:NH2	6:C:603:HOH:O	2.40	0.55
1:F:188:GLU:OE2	6:F:601:HOH:O	2.18	0.55
1:E:379:ARG:NH2	5:E:504[B]:3NP:O1	2.38	0.54
1:D:101:LEU:HD11	1:D:119:GLN:HG3	1.91	0.53
1:C:133:GLN:NE2	6:C:607:HOH:O	2.43	0.52
5:E:504[A]:3NP:O1	1:F:379:ARG:NH2	2.39	0.52
1:E:375:GLU:OE1	6:E:603:HOH:O	2.19	0.51
1:F:232:GLU:OE1	6:F:602:HOH:O	2.19	0.50
1:C:298:SER:OG	1:C:339:MET:O	2.28	0.49
5:E:504[B]:3NP:O4	1:F:379:ARG:NH2	2.42	0.48
1:F:119:GLN:NE2	6:F:613:HOH:O	2.45	0.48
1:F:191:EJA:CZ	1:F:315:SER:HG	2.27	0.48
1:C:191:EJA:CZ	1:C:315:SER:HG	2.27	0.47
1:A:188:GLU:O	6:A:601:HOH:O	2.20	0.47
1:C:246:GLN:N	1:C:247:PRO:HD2	2.29	0.47
1:D:276:ALA:HA	1:D:282:ILE:HD11	1.97	0.46
1:E:67:ASN:HA	1:E:344:GLN:O	2.15	0.46
1:A:240:ASP:HB3	1:A:249:ILE:HD13	1.98	0.46
1:F:250:THR:O	1:F:252:GLU:N	2.41	0.46
1:B:11:GLU:N	1:B:11:GLU:OE1	2.49	0.46
1:B:90:LEU:HB3	1:B:152:ALA:HA	1.97	0.46
1:D:246:GLN:N	1:D:247:PRO:HD2	2.31	0.46
1:B:67:ASN:HA	1:B:344:GLN:O	2.15	0.45
1:C:157:GLY:HA3	1:C:164:VAL:HG22	1.98	0.45
1:A:226:ILE:HG12	1:A:281:LEU:HB2	1.97	0.45
1:H:67:ASN:HA	1:H:344:GLN:O	2.16	0.45
1:H:101:LEU:HD11	1:H:119:GLN:HG3	1.97	0.45
1:D:161:ALA:HB2	1:D:207:ARG:HD3	1.98	0.45
1:G:246:GLN:N	1:G:247:PRO:CD	2.80	0.45
1:H:246:GLN:N	1:H:247:PRO:CD	2.80	0.45
1:A:67:ASN:HA	1:A:344:GLN:O	2.18	0.44
1:G:101:LEU:HD11	1:G:119:GLN:HG3	1.98	0.44
1:E:276:ALA:HA	1:E:282:ILE:HD11	2.00	0.44
1:E:93:TRP:CD1	1:E:108:ASP:HB2	2.52	0.44
1:H:191:EJA:OZ	1:H:192:GLY:N	2.40	0.44
1:A:93:TRP:CD1	1:A:108:ASP:HB2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:ARG:NH2	1:A:220:ASP:O	2.50	0.43
1:D:191:EJA:OZ	1:D:192:GLY:N	2.41	0.43
1:E:9:SER:OG	1:E:12:GLN:HG3	2.19	0.43
1:E:101:LEU:HD11	1:E:119:GLN:HG3	2.01	0.43
1:A:367:GLN:HG3	1:G:252:GLU:OE2	2.19	0.42
1:G:276:ALA:HA	1:G:282:ILE:HD11	2.01	0.42
1:A:190:LYS:NZ	1:B:415:THR:O	2.39	0.42
1:H:93:TRP:CD1	1:H:108:ASP:HB2	2.54	0.42
1:F:246:GLN:N	1:F:247:PRO:CD	2.82	0.42
1:A:190:LYS:NZ	1:A:196:GLY:O	2.53	0.42
1:G:67:ASN:HA	1:G:344:GLN:O	2.19	0.42
1:G:380:GLU:OE2	1:H:352:HIS:ND1	2.45	0.42
1:C:204:GLN:HG3	1:C:207:ARG:HH11	1.85	0.42
1:A:101:LEU:HD21	1:A:119:GLN:HG3	2.02	0.42
1:A:191:EJA:OZ	1:A:192:GLY:N	2.39	0.41
1:C:67:ASN:HA	1:C:344:GLN:O	2.20	0.41
1:C:101:LEU:HD11	1:C:119:GLN:HG3	2.01	0.41
1:C:373:TYR:OH	1:D:316:PRO:HB3	2.20	0.41
1:G:190:LYS:HB2	1:G:197:LYS:HG2	2.02	0.41
1:F:276:ALA:O	6:F:603:HOH:O	2.22	0.41
1:H:190:LYS:HB2	1:H:197:LYS:HG2	2.03	0.41
1:D:157:GLY:HA3	1:D:164:VAL:HG22	2.02	0.40
1:F:157:GLY:HA3	1:F:164:VAL:HG22	2.02	0.40
1:F:67:ASN:HA	1:F:344:GLN:O	2.22	0.40
1:G:93:TRP:CD1	1:G:108:ASP:HB2	2.56	0.40
1:D:388:TYR:CZ	1:D:390:ALA:HB3	2.57	0.40
1:E:370:MET:HG2	1:F:333:GLN:HG3	2.04	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	425/442 (96%)	418 (98%)	7 (2%)	0	100	100
1	B	424/442 (96%)	415 (98%)	9 (2%)	0	100	100
1	C	424/442 (96%)	417 (98%)	7 (2%)	0	100	100
1	D	425/442 (96%)	415 (98%)	10 (2%)	0	100	100
1	E	434/442 (98%)	425 (98%)	9 (2%)	0	100	100
1	F	425/442 (96%)	418 (98%)	6 (1%)	1 (0%)	47	55
1	G	424/442 (96%)	418 (99%)	6 (1%)	0	100	100
1	H	427/442 (97%)	419 (98%)	8 (2%)	0	100	100
All	All	3408/3536 (96%)	3345 (98%)	62 (2%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	251	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	334/351 (95%)	332 (99%)	2 (1%)	86	93
1	B	333/351 (95%)	329 (99%)	4 (1%)	71	83
1	C	332/351 (95%)	329 (99%)	3 (1%)	78	88
1	D	334/351 (95%)	332 (99%)	2 (1%)	86	93
1	E	340/351 (97%)	339 (100%)	1 (0%)	92	97
1	F	334/351 (95%)	333 (100%)	1 (0%)	92	97
1	G	332/351 (95%)	330 (99%)	2 (1%)	86	93
1	H	334/351 (95%)	333 (100%)	1 (0%)	92	97
All	All	2673/2808 (95%)	2657 (99%)	16 (1%)	86	93

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	LEU
1	A	101	LEU
1	B	64	GLU
1	B	72	LEU
1	B	90	LEU
1	B	391	THR
1	C	72	LEU
1	C	189	LYS
1	C	423	GLU
1	D	72	LEU
1	D	207	ARG
1	E	72	LEU
1	F	72	LEU
1	G	72	LEU
1	G	283	TRP
1	H	72	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	F	75	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)

8 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	EJA	C	191	1	8,12,13	1.77	2 (25%)	5,14,16	2.32	2 (40%)
1	EJA	D	191	1	8,12,13	1.83	2 (25%)	5,14,16	2.14	1 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
1	EJA	G	191	1	8,12,13	1.81	3 (37%)	5,14,16	2.06	1 (20%)
1	EJA	H	191	1	8,12,13	1.82	2 (25%)	5,14,16	2.22	2 (40%)
1	EJA	F	191	1	8,12,13	1.72	3 (37%)	5,14,16	2.38	2 (40%)
1	EJA	A	191	1	8,12,13	1.80	3 (37%)	5,14,16	2.29	2 (40%)
1	EJA	E	191	1	8,12,13	1.89	2 (25%)	5,14,16	1.93	1 (20%)
1	EJA	B	191	1	8,12,13	1.76	1 (12%)	5,14,16	2.36	1 (20%)

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
1	EJA	C	191	1	-	3/6/13/15	-
1	EJA	D	191	1	-	2/6/13/15	-
1	EJA	G	191	1	-	3/6/13/15	-
1	EJA	H	191	1	-	3/6/13/15	-
1	EJA	F	191	1	-	4/6/13/15	-
1	EJA	A	191	1	-	3/6/13/15	-
1	EJA	E	191	1	-	3/6/13/15	-
1	EJA	B	191	1	-	4/6/13/15	-

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	191	EJA	CE-CZ	3.84	1.57	1.51
1	E	191	EJA	CE-CZ	3.63	1.56	1.51
1	H	191	EJA	CE-CZ	3.48	1.56	1.51
1	D	191	EJA	CB-SG	3.25	1.88	1.81
1	C	191	EJA	CB-SG	3.14	1.88	1.81
1	A	191	EJA	CB-SG	3.13	1.88	1.81
1	F	191	EJA	CB-SG	3.12	1.88	1.81
1	G	191	EJA	CB-SG	3.12	1.88	1.81
1	A	191	EJA	CE-CZ	3.06	1.55	1.51
1	D	191	EJA	CE-CZ	3.02	1.55	1.51
1	G	191	EJA	CE-CZ	2.90	1.55	1.51
1	E	191	EJA	CB-SG	2.77	1.87	1.81
1	C	191	EJA	CE-CZ	2.77	1.55	1.51
1	H	191	EJA	CB-SG	2.76	1.87	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	191	EJA	CE-CZ	2.72	1.55	1.51
1	A	191	EJA	OT1-CZ	2.07	1.29	1.22
1	F	191	EJA	OT1-CZ	2.04	1.28	1.22
1	G	191	EJA	OT1-CZ	2.01	1.28	1.22

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	191	EJA	OZ-NE-CD	4.62	118.72	110.85
1	F	191	EJA	OZ-NE-CD	4.46	118.44	110.85
1	C	191	EJA	OZ-NE-CD	4.24	118.06	110.85
1	A	191	EJA	OZ-NE-CD	4.23	118.05	110.85
1	D	191	EJA	OZ-NE-CD	4.13	117.88	110.85
1	H	191	EJA	OZ-NE-CD	4.00	117.66	110.85
1	G	191	EJA	OZ-NE-CD	3.91	117.50	110.85
1	E	191	EJA	OZ-NE-CD	3.64	117.04	110.85
1	C	191	EJA	OT2-CZ-CE	2.11	121.26	114.54
1	H	191	EJA	OT2-CZ-CE	2.05	121.10	114.54
1	F	191	EJA	OT2-CZ-CE	2.02	121.00	114.54
1	A	191	EJA	OT2-CZ-CE	2.01	120.97	114.54

There are no chirality outliers.

All (25) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	191	EJA	CE-CD-SG-CB
1	A	191	EJA	CD-CE-CZ-OT1
1	A	191	EJA	CD-CE-CZ-OT2
1	B	191	EJA	CE-CD-SG-CB
1	C	191	EJA	CE-CD-SG-CB
1	C	191	EJA	CD-CE-CZ-OT1
1	C	191	EJA	CD-CE-CZ-OT2
1	D	191	EJA	CE-CD-SG-CB
1	E	191	EJA	CE-CD-SG-CB
1	F	191	EJA	CE-CD-SG-CB
1	F	191	EJA	CD-CE-CZ-OT1
1	F	191	EJA	CD-CE-CZ-OT2
1	G	191	EJA	CE-CD-SG-CB
1	H	191	EJA	CE-CD-SG-CB
1	H	191	EJA	CD-CE-CZ-OT1
1	H	191	EJA	CD-CE-CZ-OT2
1	B	191	EJA	CD-CE-CZ-OT1

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Mol	Chain	Res	Type	Atoms
1	B	191	EJA	CD-CE-CZ-OT2
1	E	191	EJA	CD-CE-CZ-OT1
1	G	191	EJA	CD-CE-CZ-OT1
1	G	191	EJA	CD-CE-CZ-OT2
1	B	191	EJA	N-CA-CB-SG
1	D	191	EJA	N-CA-CB-SG
1	E	191	EJA	N-CA-CB-SG
1	F	191	EJA	N-CA-CB-SG

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	191	EJA	1	0
1	D	191	EJA	1	0
1	H	191	EJA	1	0
1	F	191	EJA	1	0
1	A	191	EJA	2	0

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 26 ligands modelled in this entry, 16 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
4	PYR	C	501	3	5,5,5	2.88	3 (60%)	3,6,6	1.81	1 (33%)
4	PYR	G	501	3	5,5,5	2.89	3 (60%)	3,6,6	1.81	2 (66%)
2	GLV	D	501	3	4,4,4	2.30	1 (25%)	3,4,4	1.73	1 (33%)
5	3NP	E	504[B]	-	5,7,7	2.16	1 (20%)	4,8,8	1.22	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	PYR	E	501	3	5,5,5	2.93	3 (60%)	3,6,6	1.63	1 (33%)
2	GLV	A	501	3	4,4,4	2.35	1 (25%)	3,4,4	1.69	1 (33%)
4	PYR	F	501	3	5,5,5	2.88	3 (60%)	3,6,6	1.76	2 (66%)
4	PYR	B	501	3	5,5,5	2.98	3 (60%)	3,6,6	1.52	0
5	3NP	E	504[A]	-	5,7,7	2.05	1 (20%)	4,8,8	1.21	0
2	GLV	H	502	3	4,4,4	2.32	1 (25%)	3,4,4	1.71	1 (33%)

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
4	PYR	C	501	3	-	1/4/4/4	-
4	PYR	G	501	3	-	0/4/4/4	-
2	GLV	D	501	3	-	0/0/2/2	-
5	3NP	E	504[B]	-	-	2/4/5/5	-
4	PYR	E	501	3	-	0/4/4/4	-
2	GLV	A	501	3	-	0/0/2/2	-
4	PYR	F	501	3	-	0/4/4/4	-
4	PYR	B	501	3	-	0/4/4/4	-
5	3NP	E	504[A]	-	-	2/4/5/5	-
2	GLV	H	502	3	-	0/0/2/2	-

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	501	PYR	CA-C	-4.43	1.38	1.54
4	B	501	PYR	CA-C	-4.42	1.38	1.54
5	E	504[B]	3NP	C2-C1	4.41	1.60	1.50
4	C	501	PYR	CA-C	-4.27	1.39	1.54
4	F	501	PYR	CA-C	-4.16	1.39	1.54
5	E	504[A]	3NP	C2-C1	4.15	1.60	1.50
2	A	501	GLV	C1-C2	4.05	1.53	1.44
4	G	501	PYR	CA-C	-4.01	1.39	1.54
2	H	502	GLV	C1-C2	4.00	1.53	1.44
2	D	501	GLV	C1-C2	3.96	1.53	1.44
4	C	501	PYR	O3-CA	3.69	1.31	1.23
4	F	501	PYR	O3-CA	3.67	1.31	1.23
4	B	501	PYR	O3-CA	3.65	1.31	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	G	501	PYR	O3-CA	3.57	1.31	1.23
4	G	501	PYR	O-C	3.56	1.32	1.22
4	E	501	PYR	O3-CA	3.53	1.31	1.23
4	B	501	PYR	O-C	3.40	1.31	1.22
4	E	501	PYR	O-C	3.27	1.31	1.22
4	F	501	PYR	O-C	3.27	1.31	1.22
4	C	501	PYR	O-C	3.09	1.30	1.22

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	C	501	PYR	OXT-C-CA	2.42	120.58	113.97
4	G	501	PYR	OXT-C-CA	2.36	120.43	113.97
2	D	501	GLV	O3-C2-C1	2.32	120.65	113.52
2	H	502	GLV	O3-C2-C1	2.28	120.54	113.52
4	F	501	PYR	OXT-C-CA	2.25	120.12	113.97
2	A	501	GLV	O3-C2-C1	2.24	120.42	113.52
4	E	501	PYR	OXT-C-CA	2.14	119.83	113.97
4	G	501	PYR	OXT-C-O	-2.05	118.92	123.61
4	F	501	PYR	OXT-C-O	-2.01	119.00	123.61

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	504[B]	3NP	O1-C1-C2-C3
5	E	504[B]	3NP	O2-C1-C2-C3
5	E	504[A]	3NP	O1-C1-C2-C3
5	E	504[A]	3NP	O2-C1-C2-C3
4	C	501	PYR	OXT-C-CA-O3

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	504[B]	3NP	2	0
5	E	504[A]	3NP	3	0

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	427/442 (96%)	-0.37	0	100	100	23, 36, 53, 75	0
1	B	426/442 (96%)	-0.28	3 (0%)	87	86	27, 43, 65, 127	0
1	C	426/442 (96%)	-0.33	4 (0%)	84	83	26, 40, 68, 95	0
1	D	427/442 (96%)	-0.32	1 (0%)	95	94	27, 42, 67, 97	0
1	E	427/442 (96%)	-0.41	0	100	100	27, 38, 56, 87	0
1	F	427/442 (96%)	-0.33	0	100	100	25, 44, 69, 101	0
1	G	426/442 (96%)	-0.31	0	100	100	24, 43, 63, 101	0
1	H	427/442 (96%)	-0.30	1 (0%)	95	94	29, 43, 64, 88	0
All	All	3413/3536 (96%)	-0.33	9 (0%)	94	93	23, 41, 64, 127	0

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	192	GLY	7.3
1	B	1	MET	3.9
1	C	418	LEU	3.5
1	C	427	PHE	3.1
1	C	419	THR	2.7
1	C	417	ALA	2.5
1	B	427	PHE	2.4
1	H	192	GLY	2.4
1	B	418	LEU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains (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
1	EJA	D	191	13/14	0.85	0.18	60,65,79,79	0
1	EJA	C	191	13/14	0.92	0.13	37,42,50,50	0
1	EJA	A	191	13/14	0.92	0.16	52,53,64,64	0
1	EJA	B	191	13/14	0.94	0.14	32,35,42,44	0
1	EJA	F	191	13/14	0.94	0.13	38,42,50,50	0
1	EJA	H	191	13/14	0.95	0.13	46,48,58,58	0
1	EJA	G	191	13/14	0.96	0.11	36,38,46,46	0
1	EJA	E	191	13/14	0.96	0.10	33,36,43,43	0

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(Å^2)	Q<0.9
3	MG	D	503	1/1	0.81	0.08	43,43,43,43	0
5	3NP	E	504[A]	8/8	0.81	0.17	59,61,74,74	12
5	3NP	E	504[B]	8/8	0.81	0.17	59,61,74,74	12
3	MG	E	503	1/1	0.88	0.07	51,51,51,51	0
3	MG	B	503	1/1	0.93	0.04	46,46,46,46	0
3	MG	C	503	1/1	0.93	0.06	37,37,37,37	0
2	GLV	H	502	5/5	0.93	0.10	37,38,39,46	0
4	PYR	G	501	6/6	0.95	0.13	32,33,39,39	0
3	MG	H	503	1/1	0.95	0.03	22,22,22,22	0
4	PYR	C	501	6/6	0.95	0.17	34,39,49,49	0
3	MG	F	502	1/1	0.96	0.04	23,23,23,23	0
3	MG	A	502	1/1	0.96	0.11	31,31,31,31	0
4	PYR	B	501	6/6	0.96	0.12	26,28,33,33	0
3	MG	D	502	1/1	0.96	0.08	33,33,33,33	0
4	PYR	E	501	6/6	0.96	0.11	31,32,39,39	0
4	PYR	F	501	6/6	0.96	0.09	34,35,43,43	0
2	GLV	D	501	5/5	0.96	0.10	35,36,37,44	0
3	MG	E	502	1/1	0.96	0.03	26,26,26,26	0
3	MG	C	502	1/1	0.96	0.06	27,27,27,27	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	MG	H	501	1/1	0.97	0.05	37,37,37,37	0
2	GLV	A	501	5/5	0.97	0.08	28,29,30,34	0
3	MG	H	504	1/1	0.97	0.15	57,57,57,57	0
3	MG	B	502	1/1	0.97	0.06	30,30,30,30	0
3	MG	G	502	1/1	0.97	0.04	19,19,19,19	0
3	MG	A	503	1/1	0.98	0.04	31,31,31,31	0
3	MG	G	503	1/1	0.98	0.06	34,34,34,34	0

6.5 Other polymers (i)

There are no such residues in this entry.