



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:44 pm BST

PDB ID : 4M26
Title : Crystal structure of non-heme iron oxygenase OrfP in complex with Fe, succinate, and (3S)-hydroxy-L-Arg
Authors : Chang, C.Y.; Liu, Y.C.; Lyu, S.Y.; Wu, C.C.; Li, T.L.
Deposited on : 2013-08-05
Resolution : 2.02 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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11
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

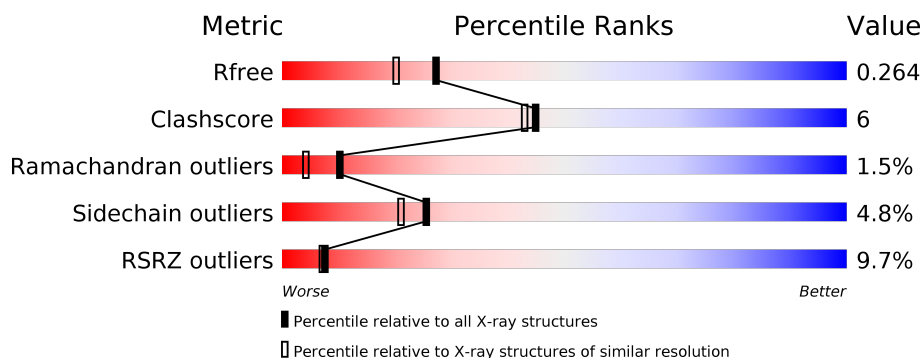
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 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	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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	364	<div> <div>5%</div> <div> <div></div> <div>79%</div> <div>13%</div> <div>•</div> <div>8%</div> </div> </div>
1	B	364	<div> <div>10%</div> <div> <div></div> <div>73%</div> <div>10%</div> <div>•</div> <div>14%</div> </div> </div>
1	C	364	<div> <div>9%</div> <div> <div></div> <div>79%</div> <div>10%</div> <div>•</div> <div>9%</div> </div> </div>
1	D	364	<div> <div>12%</div> <div> <div></div> <div>74%</div> <div>16%</div> <div>•</div> <div>8%</div> </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11335 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 L-arginine beta-hydroxylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	1	0
			2701	1699	491	504	7			
1	B	314	Total	C	N	O	S	0	1	0
			2521	1590	454	470	7			
1	C	332	Total	C	N	O	S	0	0	0
			2660	1676	483	494	7			
1	D	336	Total	C	N	O	S	0	0	0
			2690	1693	487	503	7			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	EXPRESSION TAG	UNP G9MBV2
A	-18	GLY	-	EXPRESSION TAG	UNP G9MBV2
A	-17	SER	-	EXPRESSION TAG	UNP G9MBV2
A	-16	SER	-	EXPRESSION TAG	UNP G9MBV2
A	-15	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-14	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-13	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-12	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-11	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-10	HIS	-	EXPRESSION TAG	UNP G9MBV2
A	-9	SER	-	EXPRESSION TAG	UNP G9MBV2
A	-8	SER	-	EXPRESSION TAG	UNP G9MBV2
A	-7	GLY	-	EXPRESSION TAG	UNP G9MBV2
A	-6	LEU	-	EXPRESSION TAG	UNP G9MBV2
A	-5	VAL	-	EXPRESSION TAG	UNP G9MBV2
A	-4	PRO	-	EXPRESSION TAG	UNP G9MBV2
A	-3	ARG	-	EXPRESSION TAG	UNP G9MBV2
A	-2	GLY	-	EXPRESSION TAG	UNP G9MBV2
A	-1	SER	-	EXPRESSION TAG	UNP G9MBV2
A	0	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-19	MET	-	EXPRESSION TAG	UNP G9MBV2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP G9MBV2
B	-17	SER	-	EXPRESSION TAG	UNP G9MBV2
B	-16	SER	-	EXPRESSION TAG	UNP G9MBV2
B	-15	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-14	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-13	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-12	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-11	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-10	HIS	-	EXPRESSION TAG	UNP G9MBV2
B	-9	SER	-	EXPRESSION TAG	UNP G9MBV2
B	-8	SER	-	EXPRESSION TAG	UNP G9MBV2
B	-7	GLY	-	EXPRESSION TAG	UNP G9MBV2
B	-6	LEU	-	EXPRESSION TAG	UNP G9MBV2
B	-5	VAL	-	EXPRESSION TAG	UNP G9MBV2
B	-4	PRO	-	EXPRESSION TAG	UNP G9MBV2
B	-3	ARG	-	EXPRESSION TAG	UNP G9MBV2
B	-2	GLY	-	EXPRESSION TAG	UNP G9MBV2
B	-1	SER	-	EXPRESSION TAG	UNP G9MBV2
B	0	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-19	MET	-	EXPRESSION TAG	UNP G9MBV2
C	-18	GLY	-	EXPRESSION TAG	UNP G9MBV2
C	-17	SER	-	EXPRESSION TAG	UNP G9MBV2
C	-16	SER	-	EXPRESSION TAG	UNP G9MBV2
C	-15	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-14	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-13	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-12	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-11	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-10	HIS	-	EXPRESSION TAG	UNP G9MBV2
C	-9	SER	-	EXPRESSION TAG	UNP G9MBV2
C	-8	SER	-	EXPRESSION TAG	UNP G9MBV2
C	-7	GLY	-	EXPRESSION TAG	UNP G9MBV2
C	-6	LEU	-	EXPRESSION TAG	UNP G9MBV2
C	-5	VAL	-	EXPRESSION TAG	UNP G9MBV2
C	-4	PRO	-	EXPRESSION TAG	UNP G9MBV2
C	-3	ARG	-	EXPRESSION TAG	UNP G9MBV2
C	-2	GLY	-	EXPRESSION TAG	UNP G9MBV2
C	-1	SER	-	EXPRESSION TAG	UNP G9MBV2
C	0	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-19	MET	-	EXPRESSION TAG	UNP G9MBV2
D	-18	GLY	-	EXPRESSION TAG	UNP G9MBV2
D	-17	SER	-	EXPRESSION TAG	UNP G9MBV2

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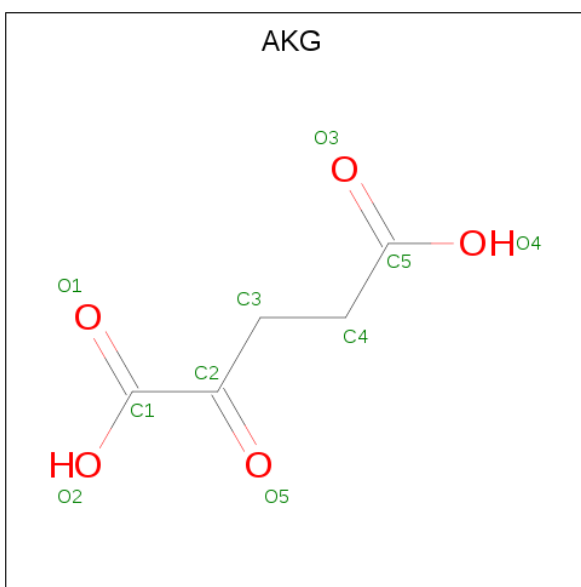
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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP G9MBV2
D	-15	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-14	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-13	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-12	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-11	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-10	HIS	-	EXPRESSION TAG	UNP G9MBV2
D	-9	SER	-	EXPRESSION TAG	UNP G9MBV2
D	-8	SER	-	EXPRESSION TAG	UNP G9MBV2
D	-7	GLY	-	EXPRESSION TAG	UNP G9MBV2
D	-6	LEU	-	EXPRESSION TAG	UNP G9MBV2
D	-5	VAL	-	EXPRESSION TAG	UNP G9MBV2
D	-4	PRO	-	EXPRESSION TAG	UNP G9MBV2
D	-3	ARG	-	EXPRESSION TAG	UNP G9MBV2
D	-2	GLY	-	EXPRESSION TAG	UNP G9MBV2
D	-1	SER	-	EXPRESSION TAG	UNP G9MBV2
D	0	HIS	-	EXPRESSION TAG	UNP G9MBV2

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

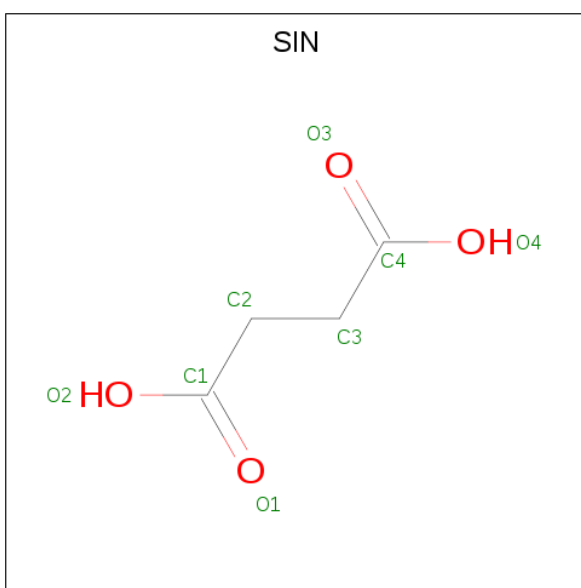
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Fe 1 1	0	0
2	A	2	Total Fe 2 2	0	0
2	D	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0

- Molecule 3 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: C₅H₆O₅).



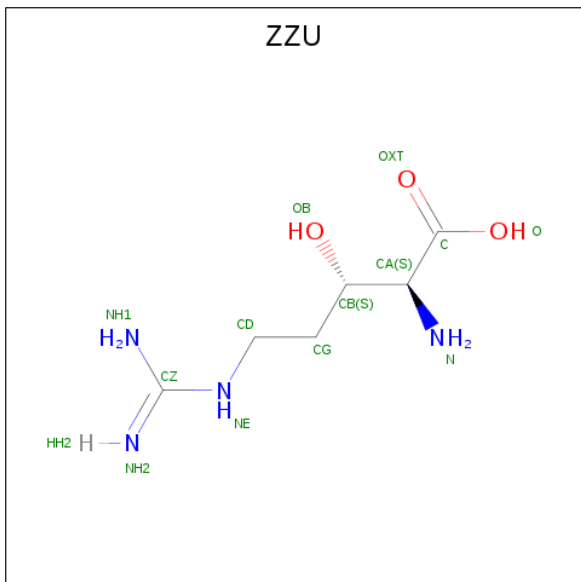
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			10	5	5		
3	B	1	Total	C	O	0	0
			10	5	5		

- Molecule 4 is SUCCINIC ACID (three-letter code: SIN) (formula: C₄H₆O₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			8	4	4		
4	D	1	Total	C	O	0	0
			8	4	4		

- Molecule 5 is (2S,3S)-3-HYDROXYARGININE (three-letter code: ZGU) (formula: $C_6H_{14}N_4O_3$).

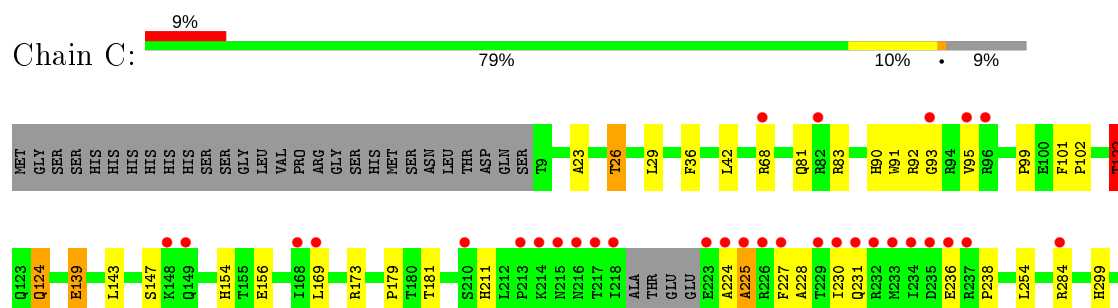
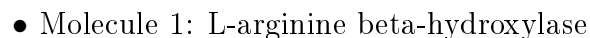
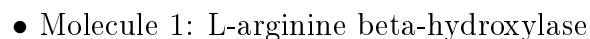


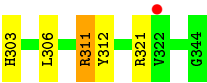
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	C	1	Total	C	N	O	0	0
			13	6	4	3		
5	D	1	Total	C	N	O	0	0
			13	6	4	3		

- Molecule 6 is water.

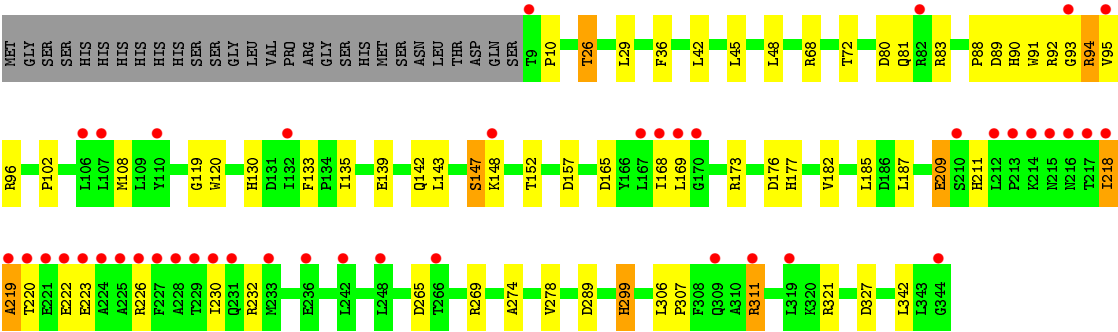
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	213	Total	O	0	0
			213	213		
6	B	144	Total	O	0	0
			144	144		
6	C	204	Total	O	0	0
			204	204		
6	D	135	Total	O	0	0
			135	135		

- Molecule 1: L-arginine beta-hydroxylase





● Molecule 1: L-arginine beta-hydroxylase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	68.11Å 116.70Å 96.15Å 90.00° 91.47° 90.00°	Depositor
Resolution (Å)	30.00 – 2.02 25.90 – 2.02	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-2.02) 99.7 (25.90-2.02)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.80 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.208 , 0.265 0.208 , 0.264	Depositor DCC
R_{free} test set	4888 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.098	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.026 for h,-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11335	wwPDB-VP
Average B, all atoms (Å ²)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.70% 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: ZZU, AKG, FE, SIN

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	0.58	2/2771 (0.1%)	0.68	0/3768
1	B	0.57	1/2587 (0.0%)	0.70	0/3518
1	C	0.58	0/2729	0.69	0/3710
1	D	0.56	2/2760 (0.1%)	0.67	0/3754
All	All	0.57	5/10847 (0.0%)	0.68	0/14750

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	120	TRP	CD2-CE2	5.34	1.47	1.41
1	D	120	TRP	CD2-CE2	5.32	1.47	1.41
1	D	91	TRP	CD2-CE2	5.31	1.47	1.41
1	A	153	TRP	CD2-CE2	5.15	1.47	1.41
1	B	91	TRP	CD2-CE2	5.05	1.47	1.41

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	2701	0	2618	31	0
1	B	2521	0	2439	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2660	0	2581	32	0
1	D	2690	0	2606	37	0
2	A	2	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
3	A	10	0	4	0	0
3	B	10	0	4	0	0
4	C	8	0	4	0	0
4	D	8	0	4	0	0
5	C	13	0	11	2	0
5	D	13	0	11	0	0
6	A	213	0	0	6	0
6	B	144	0	0	1	0
6	C	204	0	0	2	0
6	D	135	0	0	2	0
All	All	11335	0	10282	136	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 6.

All (136) 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:82:ARG:HH11	1:B:82:ARG:CG	1.61	1.10
1:B:82:ARG:HH11	1:B:82:ARG:HG3	1.22	1.05
1:C:26:THR:HG23	1:C:102:PRO:HB3	1.44	1.00
1:D:26:THR:HG23	1:D:102:PRO:HB3	1.49	0.94
1:C:90:HIS:CD2	1:C:92:ARG:HB2	2.06	0.90
1:A:26:THR:HG23	1:A:102:PRO:HB3	1.58	0.84
1:B:321:ARG:HG2	1:B:321:ARG:HH11	1.42	0.84
1:A:26:THR:HG21	6:A:574:HOH:O	1.77	0.83
1:B:82:ARG:HH11	1:B:82:ARG:HG2	1.48	0.79
1:C:26:THR:HG21	6:C:510:HOH:O	1.83	0.79
1:C:211:HIS:HB3	1:C:230:ILE:HD13	1.64	0.77
1:B:82:ARG:NH1	1:B:82:ARG:HG3	1.93	0.77
1:D:142:GLN:HE22	1:D:152:THR:H	1.33	0.76
1:B:82:ARG:NH1	1:B:82:ARG:CG	2.34	0.74
1:B:237:ARG:N	1:B:238:PRO:HD3	2.02	0.74
1:D:211:HIS:HB3	1:D:230:ILE:HD13	1.69	0.73
1:A:209:GLU:HA	1:A:212:LEU:HD13	1.71	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:169:LEU:CD2	1:D:321:ARG:HG3	2.18	0.73
1:C:36:PHE:CD1	1:C:36:PHE:O	2.44	0.70
1:B:233:MET:HG3	1:B:234:ILE:H	1.57	0.70
1:D:169:LEU:HD23	1:D:321:ARG:HG3	1.73	0.70
1:D:157:ASP:OD1	1:D:211:HIS:HE1	1.76	0.69
1:C:236:GLU:HG3	1:C:238:PRO:HD3	1.76	0.67
1:D:177:HIS:HD2	1:D:289:ASP:OD1	1.78	0.67
1:C:91:TRP:CE3	1:C:92:ARG:HA	2.30	0.66
1:D:26:THR:HG23	1:D:102:PRO:CB	2.23	0.66
1:C:95:VAL:HB	6:C:668:HOH:O	1.96	0.65
1:B:149:GLN:HG2	1:B:305:ARG:O	1.96	0.64
1:A:176:ASP:OD2	1:A:311:ARG:NH2	2.31	0.64
1:A:90:HIS:HD2	1:A:92[B]:ARG:H	1.44	0.62
1:B:321:ARG:NH1	1:B:321:ARG:HG2	2.08	0.62
1:B:144:GLY:O	1:B:145:MET:HB2	1.98	0.61
1:C:90:HIS:HD2	1:C:92:ARG:HB2	1.63	0.61
1:C:169:LEU:CD2	1:C:321:ARG:HG3	2.30	0.61
1:B:135:ILE:HG22	1:B:138:HIS:H	1.65	0.61
1:A:90:HIS:HD2	1:A:92[A]:ARG:H	1.46	0.60
1:A:90:HIS:CD2	1:A:92[A]:ARG:HG3	2.36	0.60
1:D:327:ASP:OD1	6:D:536:HOH:O	2.17	0.60
1:C:90:HIS:HD2	1:C:92:ARG:H	1.50	0.60
1:A:90:HIS:CD2	1:A:92[B]:ARG:H	2.20	0.59
1:A:36:PHE:CE1	1:A:108:MET:HG3	2.36	0.59
1:A:252:MET:HE1	1:A:279:VAL:HG21	1.83	0.59
1:C:169:LEU:HD23	1:C:321:ARG:HG3	1.84	0.59
1:C:122:THR:HG22	1:C:227:PHE:CE2	2.37	0.59
1:A:90:HIS:CD2	1:A:92[A]:ARG:H	2.21	0.58
1:C:139:GLU:HG2	1:C:312:TYR:OH	2.04	0.58
1:B:237:ARG:HD2	1:B:237:ARG:N	2.20	0.56
1:A:177:HIS:HD2	1:A:289:ASP:OD1	1.89	0.56
1:B:146:GLY:O	1:B:305:ARG:NH2	2.39	0.55
1:B:241:PRO:O	1:B:253:ARG:NH1	2.38	0.54
1:A:187:LEU:HD22	1:A:250:PRO:HD3	1.90	0.53
1:D:169:LEU:HD21	1:D:321:ARG:HG3	1.90	0.53
1:B:26:THR:HG21	1:B:106:LEU:HB2	1.91	0.53
1:B:149:GLN:O	1:B:150:LEU:HB2	2.08	0.53
1:C:225:ALA:HB1	1:C:228:ALA:HB2	1.91	0.53
1:B:151:LEU:HD12	1:B:181:THR:HG21	1.91	0.53
1:B:321:ARG:CG	1:B:321:ARG:HH11	2.19	0.53
1:A:214:LYS:HE3	1:A:218:ILE:HD11	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:179:PRO:HG2	1:C:306:LEU:HD12	1.91	0.52
1:A:96:ARG:HD3	6:A:629:HOH:O	2.09	0.52
1:D:209:GLU:C	1:D:211:HIS:H	2.13	0.52
1:D:130:HIS:HD2	1:D:321:ARG:HH12	1.58	0.51
1:D:139:GLU:HG2	1:D:148:LYS:HB2	1.93	0.51
1:D:81:GLN:NE2	1:D:173:ARG:HH11	2.08	0.51
1:A:192:ALA:HA	1:A:195:ILE:HD12	1.92	0.50
1:C:90:HIS:CD2	1:C:92:ARG:H	2.30	0.50
1:A:223:GLU:HG2	1:A:226:ARG:NH2	2.25	0.50
1:A:219:ALA:O	1:A:223:GLU:HB2	2.12	0.50
1:D:10:PRO:O	1:D:72:THR:HG22	2.12	0.50
1:D:90:HIS:HD2	1:D:92:ARG:H	1.60	0.49
1:D:265:ASP:O	1:D:269:ARG:HG3	2.13	0.49
1:B:9:THR:N	6:B:546:HOH:O	2.46	0.48
1:B:237:ARG:H	1:B:238:PRO:HD3	1.78	0.48
1:A:23:ALA:O	1:A:26:THR:HG22	2.13	0.48
1:D:218:ILE:HG22	1:D:219:ALA:H	1.78	0.48
1:D:176:ASP:OD1	1:D:311:ARG:NH2	2.47	0.48
1:B:193:GLU:O	1:B:197:VAL:HG12	2.14	0.47
1:C:311:ARG:HB2	1:C:311:ARG:HH11	1.79	0.47
1:D:222:GLU:CD	1:D:223:GLU:H	2.17	0.47
1:D:165:ASP:OD1	1:D:299:HIS:CE1	2.68	0.47
1:D:142:GLN:NE2	1:D:152:THR:H	2.08	0.47
1:A:130:HIS:ND1	6:A:636:HOH:O	2.35	0.47
1:A:159:PHE:CG	1:A:207:PRO:HA	2.50	0.47
1:D:220:THR:O	1:D:220:THR:HG22	2.16	0.46
1:B:82:ARG:NH1	1:B:82:ARG:HG2	2.19	0.46
1:C:36:PHE:HD1	1:C:36:PHE:O	1.98	0.46
1:D:80:ASP:OD2	1:D:83:ARG:HB2	2.16	0.46
1:D:299:HIS:ND1	6:D:629:HOH:O	2.35	0.45
1:B:139:GLU:C	1:B:141:ASP:H	2.20	0.45
1:C:154:HIS:CE1	5:C:403:ZZU:HG2C	2.51	0.45
1:D:36:PHE:CE1	1:D:108:MET:HG3	2.52	0.45
1:A:9:THR:HG21	1:A:71:HIS:CE1	2.52	0.45
1:A:222:GLU:N	1:A:222:GLU:OE1	2.49	0.45
1:B:136:ARG:O	1:B:139:GLU:HB2	2.18	0.44
1:C:169:LEU:HD23	1:C:321:ARG:CG	2.48	0.44
1:B:36:PHE:HA	1:B:41:LEU:HD23	1.98	0.44
1:B:100:GLU:HG3	1:B:320:LYS:HE3	1.99	0.44
1:C:91:TRP:CE2	1:C:124:GLN:HG2	2.53	0.44
1:D:157:ASP:OD1	1:D:211:HIS:CE1	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:119:GLY:O	1:D:342:LEU:HA	2.18	0.43
1:C:26:THR:HG23	1:C:102:PRO:CB	2.30	0.43
1:B:237:ARG:N	1:B:238:PRO:CD	2.75	0.43
1:A:333:GLU:HG2	6:A:657:HOH:O	2.18	0.43
1:C:101:PHE:HB3	1:C:102:PRO:HD3	2.00	0.43
1:A:22:VAL:O	1:A:26:THR:HB	2.19	0.43
1:D:165:ASP:OD1	1:D:299:HIS:HE1	2.01	0.43
1:C:156:GLU:OE2	5:C:403:ZZU:N	2.52	0.43
1:B:139:GLU:O	1:B:141:ASP:N	2.49	0.43
1:B:33:TYR:CD2	1:B:41:LEU:HB2	2.54	0.43
1:D:89:ASP:O	1:D:135:ILE:HG12	2.19	0.43
1:A:54:GLU:HG3	6:A:561:HOH:O	2.18	0.43
1:B:92:ARG:C	1:B:94:ARG:H	2.23	0.43
1:D:274:ALA:O	1:D:278:VAL:HG23	2.19	0.43
1:D:88:PRO:HG2	1:D:133:PHE:CE2	2.54	0.43
1:B:150:LEU:HB3	1:B:151:LEU:H	1.65	0.42
1:C:181:THR:O	1:C:303:HIS:HA	2.19	0.42
1:D:168:ILE:O	1:D:321:ARG:HA	2.18	0.42
1:A:26:THR:HG23	1:A:102:PRO:CB	2.40	0.42
1:B:311:ARG:HH11	1:B:311:ARG:HB2	1.84	0.42
1:A:35:SER:HB2	6:A:578:HOH:O	2.18	0.42
1:C:81:GLN:NE2	1:C:173:ARG:HH11	2.16	0.42
1:C:23:ALA:O	1:C:26:THR:HG22	2.19	0.42
1:A:226:ARG:HG3	1:A:334:MET:HA	2.01	0.42
1:A:213:PRO:HG3	1:A:227:PHE:HB3	2.00	0.42
1:C:81:GLN:HE22	1:C:173:ARG:HE	1.67	0.41
1:D:148:LYS:O	1:D:307:PRO:HB3	2.20	0.41
1:D:130:HIS:HD2	1:D:321:ARG:NH1	2.19	0.41
1:C:90:HIS:HD2	1:C:92:ARG:N	2.14	0.41
1:C:83:ARG:O	1:C:99:PRO:HB2	2.21	0.41
1:C:81:GLN:NE2	1:C:173:ARG:HE	2.18	0.41
1:D:93:GLY:O	1:D:94:ARG:O	2.39	0.40
1:B:135:ILE:HD12	1:B:145:MET:HG3	2.03	0.40
1:A:25:LEU:O	1:A:29:LEU:HG	2.21	0.40
1:B:90:HIS:CD2	1:B:92:ARG:HD2	2.56	0.40
1:D:143:LEU:HD21	1:D:209:GLU:HB2	2.03	0.40
1:B:233:MET:CG	1:B:234:ILE:H	2.31	0.40

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	335/364 (92%)	325 (97%)	9 (3%)	1 (0%)	41	36
1	B	311/364 (85%)	295 (95%)	9 (3%)	7 (2%)	6	2
1	C	328/364 (90%)	311 (95%)	11 (3%)	6 (2%)	8	3
1	D	334/364 (92%)	314 (94%)	14 (4%)	6 (2%)	8	3
All	All	1308/1456 (90%)	1245 (95%)	43 (3%)	20 (2%)	10	4

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	139	GLU
1	B	145	MET
1	D	94	ARG
1	B	140	ASN
1	B	234	ILE
1	B	235	ASP
1	C	224	ALA
1	D	218	ILE
1	D	219	ALA
1	B	150	LEU
1	C	147	SER
1	D	209	GLU
1	A	147	SER
1	B	237	ARG
1	C	122	THR
1	C	225	ALA
1	D	95	VAL
1	D	147	SER
1	C	93	GLY
1	C	124	GLN

5.3.2 Protein sidechains ⓘ

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	287/311 (92%)	278 (97%)	9 (3%)	40	38
1	B	269/311 (86%)	252 (94%)	17 (6%)	18	12
1	C	283/311 (91%)	271 (96%)	12 (4%)	30	26
1	D	286/311 (92%)	270 (94%)	16 (6%)	21	16
All	All	1125/1244 (90%)	1071 (95%)	54 (5%)	25	21

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	THR
1	A	42	LEU
1	A	48	LEU
1	A	143	LEU
1	A	191	SER
1	A	216	ASN
1	A	218	ILE
1	A	246	SER
1	A	321	ARG
1	B	29	LEU
1	B	45	LEU
1	B	82	ARG
1	B	92	ARG
1	B	125	ASP
1	B	130	HIS
1	B	140	ASN
1	B	151	LEU
1	B	169	LEU
1	B	185	LEU
1	B	189	SER
1	B	197	VAL
1	B	237	ARG
1	B	284	ARG
1	B	299	HIS

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Mol	Chain	Res	Type
1	B	311	ARG
1	B	321	ARG
1	C	26	THR
1	C	29	LEU
1	C	42	LEU
1	C	68	ARG
1	C	122	THR
1	C	139	GLU
1	C	143	LEU
1	C	231	GLN
1	C	254	LEU
1	C	284	ARG
1	C	299	HIS
1	C	311	ARG
1	D	26	THR
1	D	29	LEU
1	D	42	LEU
1	D	45	LEU
1	D	48	LEU
1	D	68	ARG
1	D	96	ARG
1	D	147	SER
1	D	182	VAL
1	D	185	LEU
1	D	187	LEU
1	D	226	ARG
1	D	232	ARG
1	D	299	HIS
1	D	306	LEU
1	D	311	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	57	GLN
1	A	81	GLN
1	A	90	HIS
1	A	138	HIS
1	A	177	HIS
1	A	231	GLN
1	B	57	GLN
1	B	81	GLN

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Mol	Chain	Res	Type
1	B	90	HIS
1	B	177	HIS
1	B	299	HIS
1	C	57	GLN
1	C	81	GLN
1	C	90	HIS
1	C	130	HIS
1	C	142	GLN
1	C	177	HIS
1	D	57	GLN
1	D	81	GLN
1	D	90	HIS
1	D	130	HIS
1	D	142	GLN
1	D	177	HIS
1	D	211	HIS
1	D	215	ASN
1	D	263	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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	SIN	D	402	2	1,7,7	0.14	0	2,8,8	1.62	1 (50%)
5	ZZU	C	403	2	8,12,12	0.93	0	6,15,15	0.66	0
5	ZZU	D	403	2	8,12,12	0.88	0	6,15,15	0.61	0
3	AKG	A	403	2	3,9,9	0.34	0	4,11,11	0.63	0
4	SIN	C	402	2	1,7,7	0.09	0	2,8,8	1.19	0
3	AKG	B	402	2	3,9,9	0.75	0	4,11,11	0.36	0

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	SIN	D	402	2	-	0/1/5/5	-
5	ZZU	C	403	2	-	1/10/14/14	-
5	ZZU	D	403	2	-	4/10/14/14	-
3	AKG	A	403	2	-	2/3/9/9	-
4	SIN	C	402	2	-	0/1/5/5	-
3	AKG	B	402	2	-	2/3/9/9	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	402	SIN	C3-C2-C1	2.28	116.50	112.67

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	403	ZZU	CA-CB-CG-CD
5	D	403	ZZU	NE-CD-CG-CB
5	C	403	ZZU	NE-CD-CG-CB
3	B	402	AKG	C1-C2-C3-C4
5	D	403	ZZU	OB-CB-CG-CD
3	B	402	AKG	O5-C2-C3-C4
3	A	403	AKG	C1-C2-C3-C4

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Mol	Chain	Res	Type	Atoms
5	D	403	ZZU	CG-CD-NE-CZ
3	A	403	AKG	O5-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	403	ZZU	2	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

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	336/364 (92%)	0.16	17 (5%) 28 27	22, 35, 63, 128	4 (1%)
1	B	314/364 (86%)	0.57	36 (11%) 4 4	26, 41, 83, 113	3 (0%)
1	C	332/364 (91%)	0.39	32 (9%) 8 7	22, 34, 93, 134	4 (1%)
1	D	336/364 (92%)	0.65	43 (12%) 3 3	24, 44, 81, 143	3 (0%)
All	All	1318/1456 (90%)	0.44	128 (9%) 7 7	22, 38, 82, 143	14 (1%)

All (128) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	224	ALA	11.2
1	A	217	THR	10.9
1	C	224	ALA	10.2
1	B	209	GLU	7.7
1	D	225	ALA	7.7
1	D	220	THR	7.1
1	C	218	ILE	6.9
1	C	95	VAL	6.8
1	D	219	ALA	6.7
1	B	37	GLY	6.1
1	C	216	ASN	5.9
1	B	146	GLY	5.8
1	A	218	ILE	5.8
1	C	225	ALA	5.8
1	B	143	LEU	5.7
1	A	216	ASN	5.7
1	B	95	VAL	5.6
1	D	95	VAL	5.5
1	D	228	ALA	5.4
1	D	226	ARG	5.3
1	B	151	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
1	B	148	LYS	5.3
1	D	222	GLU	5.3
1	B	192	ALA	5.3
1	C	223	GLU	5.0
1	B	142	GLN	5.0
1	D	230	ILE	4.9
1	C	214	LYS	4.9
1	D	218	ILE	4.8
1	D	214	LYS	4.8
1	C	213	PRO	4.7
1	B	237	ARG	4.7
1	C	230	ILE	4.6
1	D	216	ASN	4.5
1	D	213	PRO	4.5
1	C	231	GLN	4.3
1	D	227	PHE	4.3
1	C	217	THR	4.0
1	B	234	ILE	4.0
1	A	215	ASN	3.8
1	B	150	LEU	3.8
1	C	234	ILE	3.7
1	C	229	THR	3.7
1	B	90	HIS	3.6
1	D	217	THR	3.7
1	A	221	GLU	3.6
1	B	267	ASP	3.6
1	B	210	SER	3.5
1	D	229	THR	3.4
1	B	96	ARG	3.4
1	B	140	ASN	3.4
1	A	209	GLU	3.4
1	C	148	LYS	3.4
1	C	226	ARG	3.3
1	B	93	GLY	3.3
1	D	223	GLU	3.3
1	C	210	SER	3.2
1	C	215	ASN	3.2
1	C	235	ASP	3.2
1	C	227	PHE	3.2
1	C	93	GLY	3.1
1	B	207	PRO	3.1
1	D	212	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	233	MET	3.0
1	A	37	GLY	3.0
1	D	215	ASN	3.0
1	B	233	MET	2.9
1	A	222	GLU	2.9
1	A	219	ALA	2.9
1	B	248	LEU	2.9
1	C	96	ARG	2.8
1	D	248	LEU	2.8
1	D	82	ARG	2.8
1	C	232	ARG	2.8
1	C	168	ILE	2.8
1	C	82	ARG	2.8
1	B	188	SER	2.8
1	B	208	ASP	2.7
1	A	193	GLU	2.7
1	B	141	ASP	2.7
1	B	264	ASP	2.7
1	C	236	GLU	2.7
1	B	122	THR	2.7
1	C	149	GLN	2.6
1	A	257	TYR	2.6
1	B	82	ARG	2.5
1	D	168	ILE	2.5
1	B	144	GLY	2.5
1	A	213	PRO	2.5
1	D	148	LYS	2.5
1	C	284	ARG	2.4
1	B	137	SER	2.4
1	D	210	SER	2.4
1	D	169	LEU	2.4
1	D	93	GLY	2.4
1	D	132	ILE	2.4
1	C	169	LEU	2.3
1	C	322	VAL	2.3
1	C	237	ARG	2.3
1	D	233	MET	2.3
1	D	9	THR	2.3
1	D	242	LEU	2.3
1	B	139	GLU	2.3
1	A	167	LEU	2.3
1	A	212	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	107	LEU	2.3
1	D	221	GLU	2.3
1	B	344	GLY	2.3
1	D	167	LEU	2.3
1	C	68	ARG	2.3
1	B	247	ARG	2.2
1	D	106	LEU	2.2
1	B	257	TYR	2.2
1	D	266	THR	2.2
1	B	238	PRO	2.2
1	D	236	GLU	2.1
1	B	235	ASP	2.1
1	A	82	ARG	2.1
1	D	170	GLY	2.1
1	A	132	ILE	2.0
1	D	311	ARG	2.0
1	D	319	LEU	2.0
1	D	110	TYR	2.0
1	B	191	SER	2.0
1	A	223	GLU	2.0
1	D	344	GLY	2.0
1	D	231	GLN	2.0
1	D	309	GLN	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 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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	AKG	B	402	10/10	0.83	0.16	40,49,53,57	0
5	ZZU	D	403	13/13	0.90	0.14	39,46,49,52	0
4	SIN	C	402	8/8	0.92	0.23	31,32,39,39	0
5	ZZU	C	403	13/13	0.92	0.15	36,47,58,61	0
3	AKG	A	403	10/10	0.94	0.15	29,33,38,38	0
4	SIN	D	402	8/8	0.97	0.18	33,36,37,38	0
2	FE	B	401	1/1	0.97	0.07	40,40,40,40	0
2	FE	A	402	1/1	0.97	0.11	55,55,55,55	0
2	FE	C	401	1/1	0.99	0.12	30,30,30,30	0
2	FE	D	401	1/1	1.00	0.12	31,31,31,31	0
2	FE	A	401	1/1	1.00	0.09	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.