wwPDB X-ray Structure Validation Summary Report (i)

May 13, 2020 – 09:11 pm BST

PDB ID	:	5ZE2
Title	:	Hairpin Complex, RAG1/2-hairpin 12RSS/23RSS complex in 5mM Mn2+ for 2 min at 4'C
Authors	:	Kim, M.S.; Chuenchor, W.; Chen, X.; Gellert, M.; Yang, W.
Deposited on	:	2018-02-25
Resolution	:	3.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

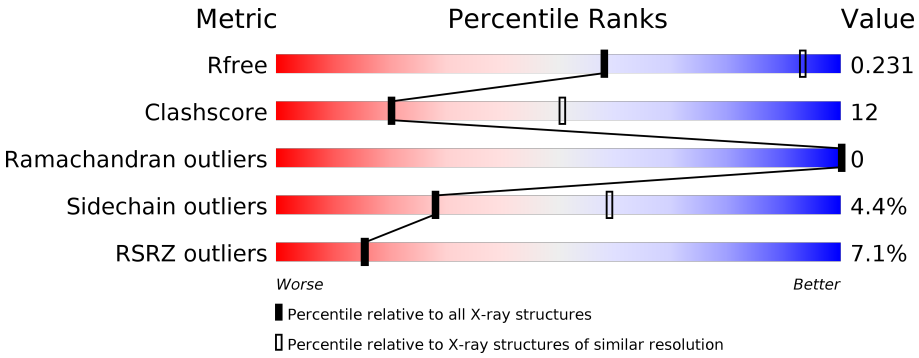
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 <=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	627	5% 68% 29%
1	C	627	8% 70% 28%
2	B	389	6% 62% 24% 12%
2	D	389	4% 60% 25% 13%
3	N	163	13% 60% 12% 28%
4	I	31	10% 39% 48% 13%

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Mol	Chain	Length	Quality of chain
5	J	31	6% 32% 68%
6	G	40	5% 28% 68% 5%
7	L	30	33% 50% 17%
8	M	40	13% 50% 50%
9	F	30	3% 43% 43% 13%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
12	EDO	C	2004	-	-	-	X

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 20278 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 mouse RAG1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	618	Total	C	N	O	S	0	0	0
			4964	3124	883	923	34			
1	C	623	Total	C	N	O	S	0	0	0
			5010	3152	897	927	34			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	382	GLY	-	cloning artifact	UNP P15919
A	383	PRO	-	cloning artifact	UNP P15919
C	382	GLY	-	cloning artifact	UNP P15919
C	383	PRO	-	cloning artifact	UNP P15919

- Molecule 2 is a protein called mouse RAG2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	341	Total	C	N	O	S	0	0	0
			2653	1695	449	491	18			
2	D	340	Total	C	N	O	S	0	1	0
			2657	1698	451	490	18			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-1	GLY	-	cloning artifact	UNP P21784
B	0	PRO	-	cloning artifact	UNP P21784
B	1	VAL	MET	engineered mutation	UNP P21784
D	-1	GLY	-	cloning artifact	UNP P21784
D	0	PRO	-	cloning artifact	UNP P21784
D	1	VAL	MET	engineered mutation	UNP P21784

- Molecule 3 is a protein called HMGB1 A-B box.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	N	117	Total	C	N	O	S	0	0	0
			833	529	141	156	7			

- Molecule 4 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	I	31	Total	C	N	O	P	0	0	0
			633	303	117	183	30			

- Molecule 5 is a DNA chain called DNA (31-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	J	31	Total	C	N	O	P	0	0	0
			632	303	114	185	30			

- Molecule 6 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	40	Total	C	N	O	P	0	0	0
			814	391	131	252	40			

- Molecule 7 is a DNA chain called DNA (30-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	L	30	Total	C	N	O	P	0	0	0
			611	290	118	173	30			

- Molecule 8 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	M	40	Total	C	N	O	P	0	0	0
			824	390	165	229	40			

- Molecule 9 is a DNA chain called DNA (30-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	F	30	Total	C	N	O	P	0	0	0
			617	296	106	186	29			

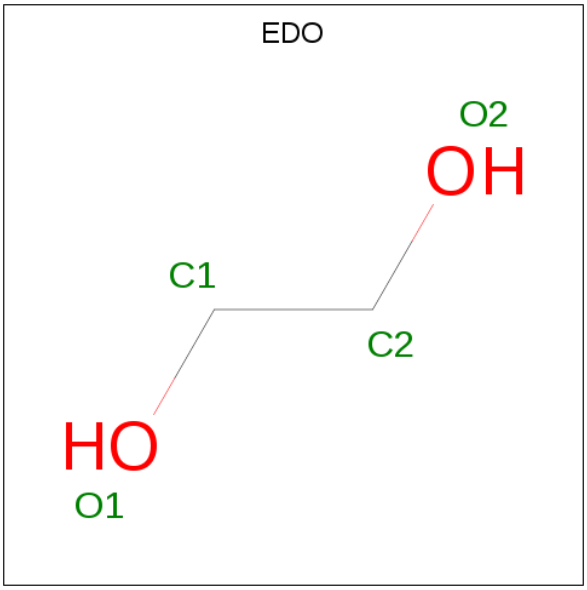
- Molecule 10 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total Zn 1 1	0	0
10	C	1	Total Zn 1 1	0	0

- Molecule 11 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	2	Total Mn 2 2	0	0
11	C	2	Total Mn 2 2	0	0

- Molecule 12 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	A	1	Total C O 4 2 2	0	0
12	A	1	Total C O 4 2 2	0	0
12	C	1	Total C O 4 2 2	0	0

- Molecule 13 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total K 1 1	0	0
13	C	1	Total K 1 1	0	0

- Molecule 14 is water.

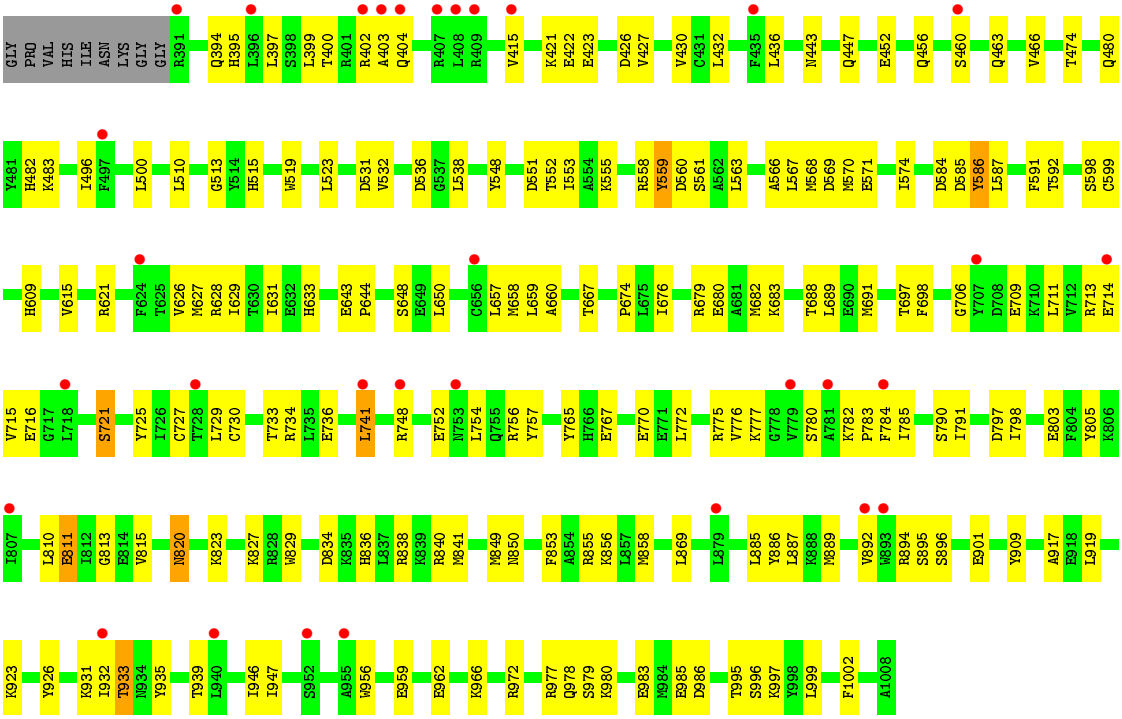
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	2	Total O 2 2	0	0
14	B	1	Total O 1 1	0	0
14	C	4	Total O 4 4	0	0
14	D	1	Total O 1 1	0	0
14	L	1	Total O 1 1	0	0
14	F	1	Total O 1 1	0	0

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.

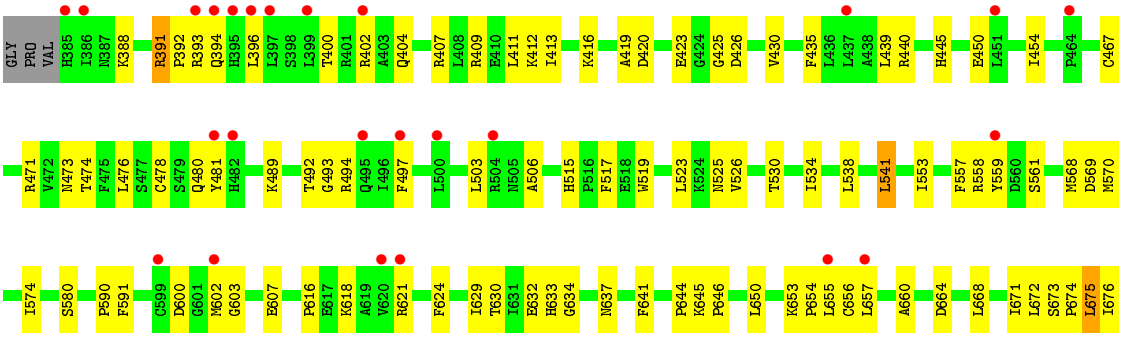
- Molecule 1: mouse RAG1

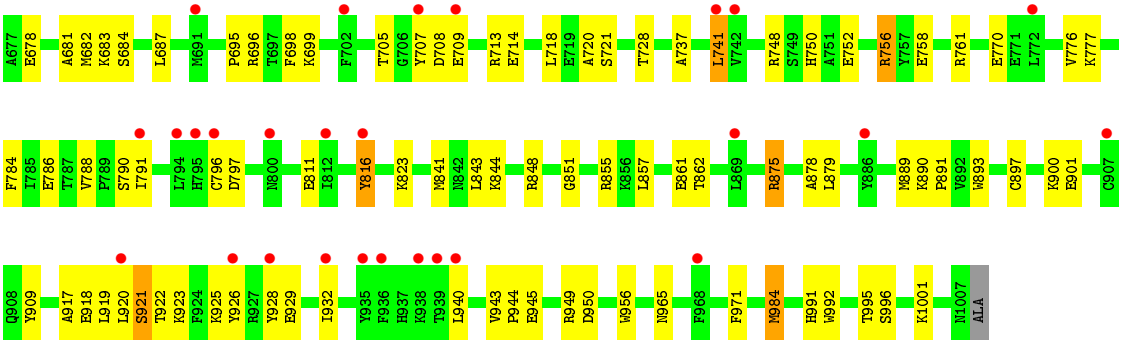
Chain A:



- Molecule 1: mouse RAG1

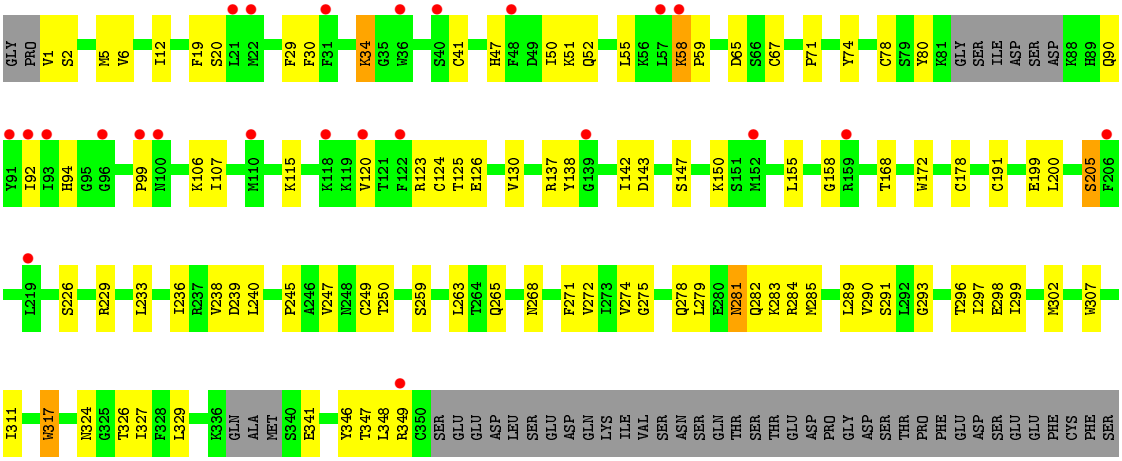
Chain C:





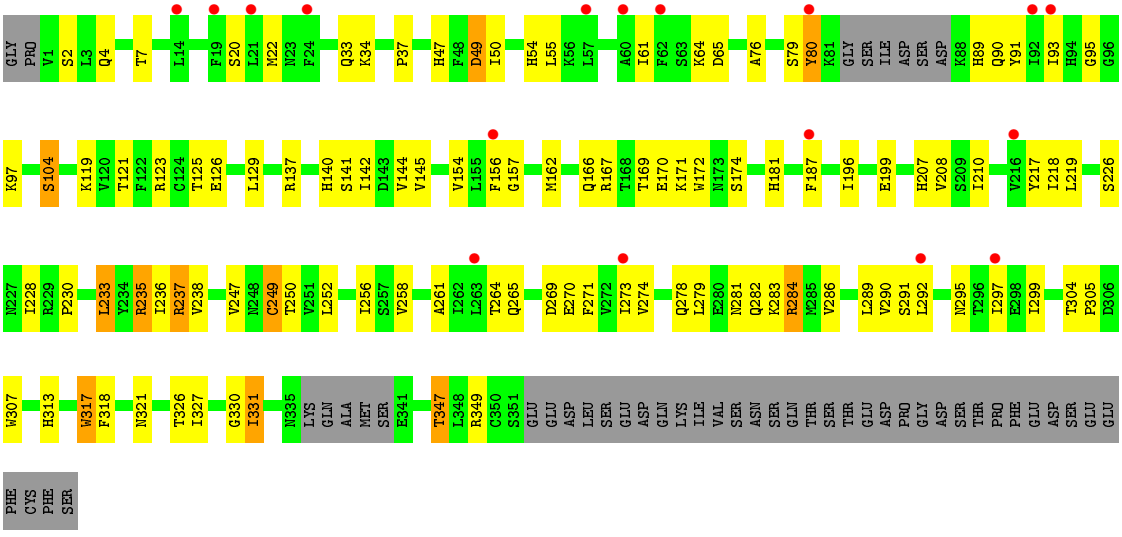
• Molecule 2: mouse RAG2

Chain B:



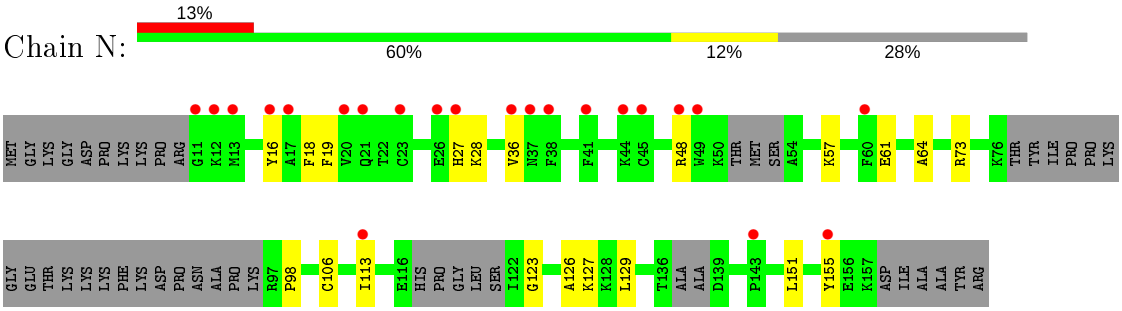
• Molecule 2: mouse RAG2

Chain D:



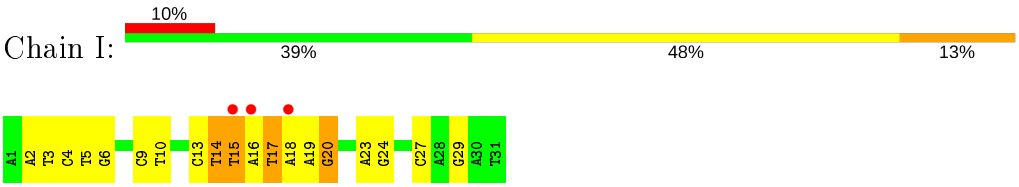
• Molecule 3: HMGB1 A-B box

Chain N:



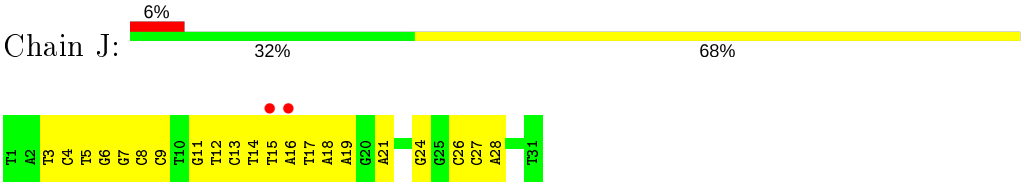
- Molecule 4: DNA (31-MER)

Chain I:



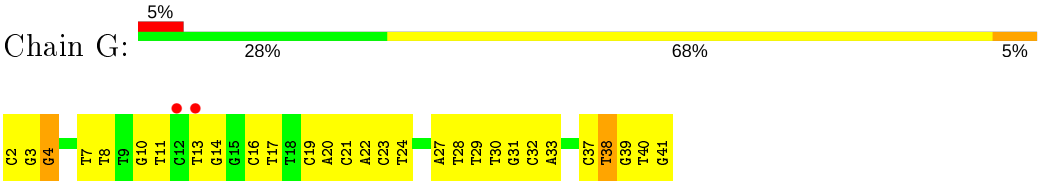
- Molecule 5: DNA (31-MER)

Chain J:



- Molecule 6: DNA (40-MER)

Chain G:

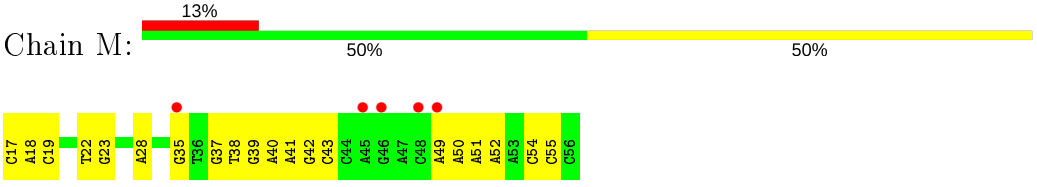


- Molecule 7: DNA (30-MER)

Chain L:

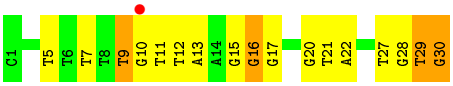
- Molecule 8: DNA (40-MER)

Chain M:



- Molecule 9: DNA (30-MER)

Chain F:


C1
T5
T6
T7
T8
T9
G10
T11
T12
A13
A14
G15
G16
G17
G20
T21
A22
T27
G28
T29
G30

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	132.77Å 108.12Å 155.74Å 90.00° 114.45° 90.00°	Depositor
Resolution (Å)	37.63 – 3.30 85.97 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.1 (37.63-3.30) 89.8 (85.97-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.07 (at 3.33Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.200 , 0.237 0.199 , 0.231	Depositor DCC
R_{free} test set	3003 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	92.7	Xtriage
Anisotropy	0.639	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 61.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.027 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	20278	wwPDB-VP
Average B, all atoms (Å^2)	123.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.78% 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

5.1 Standard geometry

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

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	0.51	1/5067 (0.0%)	0.66	1/6826 (0.0%)
1	C	0.51	1/5114 (0.0%)	0.65	4/6887 (0.1%)
2	B	0.45	0/2720	0.64	0/3690
2	D	0.46	0/2725	0.68	0/3697
3	N	0.36	0/847	0.46	0/1135
4	I	1.17	6/710 (0.8%)	1.18	6/1094 (0.5%)
5	J	0.90	0/708	1.07	1/1091 (0.1%)
6	G	0.96	3/907 (0.3%)	1.13	4/1398 (0.3%)
7	L	1.18	2/686 (0.3%)	1.15	7/1052 (0.7%)
8	M	0.97	2/928 (0.2%)	0.96	1/1427 (0.1%)
9	F	1.12	2/690 (0.3%)	1.25	6/1066 (0.6%)
All	All	0.65	17/21102 (0.1%)	0.79	30/29363 (0.1%)

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	M	17	DC	OP3-P	-10.77	1.48	1.61
7	L	17	DC	OP3-P	-10.57	1.48	1.61
4	I	17	DT	C3'-O3'	7.74	1.54	1.44
4	I	14	DT	C1'-N1	7.53	1.59	1.49
9	F	28	DG	C3'-O3'	-7.30	1.34	1.44

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
9	F	30	DG	O4'-C1'-N9	8.89	114.22	108.00
8	M	22	DT	O4'-C4'-C3'	-8.19	101.09	106.00
9	F	9	DT	O4'-C4'-C3'	-7.86	101.28	106.00
4	I	15	DT	N3-C4-O4	7.80	124.58	119.90
9	F	30	DG	O5'-P-OP2	7.11	119.23	110.70

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	4964	0	4933	129	0
1	C	5010	0	4988	128	0
2	B	2653	0	2587	57	0
2	D	2657	0	2588	65	0
3	N	833	0	706	13	0
4	I	633	0	351	20	0
5	J	632	0	352	20	0
6	G	814	0	457	25	0
7	L	611	0	335	22	0
8	M	824	0	446	20	0
9	F	617	0	343	18	0
10	A	1	0	0	0	0
10	C	1	0	0	0	0
11	A	2	0	0	0	0
11	C	2	0	0	0	0
12	A	8	0	12	0	0
12	C	4	0	6	0	0
13	A	1	0	0	0	0
13	C	1	0	0	0	0
14	A	2	0	0	0	0
14	B	1	0	0	0	0
14	C	4	0	0	0	0
14	D	1	0	0	0	0
14	F	1	0	0	0	0
14	L	1	0	0	0	0
All	All	20278	0	18104	472	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 12.

The worst 5 of 472 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:A:741:LEU:HG	1:A:917:ALA:HB1	1.62	0.81
6:G:10:DG:H2'	6:G:11:DT:C6	2.20	0.76
7:L:34:DT:H3	9:F:13:DA:H61	1.34	0.75
1:C:709:GLU:OE2	1:C:713:ARG:NH2	2.20	0.74
1:C:394:GLN:O	1:C:407:ARG:NH1	2.21	0.73

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	616/627 (98%)	578 (94%)	38 (6%)	0	100	100
1	C	621/627 (99%)	585 (94%)	36 (6%)	0	100	100
2	B	335/389 (86%)	328 (98%)	7 (2%)	0	100	100
2	D	335/389 (86%)	325 (97%)	10 (3%)	0	100	100
3	N	107/163 (66%)	107 (100%)	0	0	100	100
All	All	2014/2195 (92%)	1923 (96%)	91 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	542/550 (98%)	523 (96%)	19 (4%)	36	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	C	547/550 (100%)	524 (96%)	23 (4%)	30 60
2	B	294/344 (86%)	281 (96%)	13 (4%)	28 59
2	D	294/344 (86%)	273 (93%)	21 (7%)	14 42
3	N	69/139 (50%)	68 (99%)	1 (1%)	67 82
All	All	1746/1927 (91%)	1669 (96%)	77 (4%)	28 59

5 of 77 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	559	TYR
1	C	756	ARG
2	D	291	SER
1	C	561	SER
1	C	684	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	961	ASN
2	D	313	HIS
2	B	4	GLN
1	A	753	ASN
1	C	990	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 carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 8 are monoatomic - leaving 3 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	$\#\|Z\| > 2$
12	EDO	A	2005	-	3,3,3	0.67	0	2,2,2	0.18	0
12	EDO	C	2004	-	3,3,3	0.70	0	2,2,2	0.25	0
12	EDO	A	2004	-	3,3,3	0.58	0	2,2,2	0.55	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
12	EDO	A	2005	-	-	1/1/1/1	-
12	EDO	C	2004	-	-	1/1/1/1	-
12	EDO	A	2004	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	A	2005	EDO	O1-C1-C2-O2
12	A	2004	EDO	O1-C1-C2-O2
12	C	2004	EDO	O1-C1-C2-O2

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, 95^{th} 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	618/627 (98%)	0.51	32 (5%) 27 25	69, 98, 144, 196	0
1	C	623/627 (99%)	0.60	52 (8%) 11 11	65, 98, 143, 174	0
2	B	341/389 (87%)	0.44	24 (7%) 16 16	79, 117, 151, 170	0
2	D	340/389 (87%)	0.43	17 (5%) 28 27	78, 111, 157, 181	0
3	N	117/163 (71%)	0.64	22 (18%) 1 1	157, 205, 230, 235	0
4	I	31/31 (100%)	0.26	3 (9%) 7 8	124, 192, 247, 255	4 (12%)
5	J	31/31 (100%)	0.20	2 (6%) 18 18	108, 184, 244, 258	4 (12%)
6	G	40/40 (100%)	0.26	2 (5%) 28 27	79, 191, 264, 271	0
7	L	30/30 (100%)	0.04	0 100 100	81, 117, 165, 173	0
8	M	40/40 (100%)	0.44	5 (12%) 3 3	95, 182, 236, 253	0
9	F	30/30 (100%)	0.29	1 (3%) 46 44	77, 112, 162, 168	0
All	All	2241/2397 (93%)	0.50	160 (7%) 16 16	65, 107, 204, 271	8 (0%)

The worst 5 of 160 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	I	15	DT	5.5
5	J	16	DA	5.3
4	I	16	DA	5.1
3	N	13	MET	5.1
3	N	41	PHE	5.0

6.2 Non-standard residues in protein, DNA, RNA chains

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, 95^{th} 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
12	EDO	C	2004	4/4	0.41	0.91	111,112,113,120	0
11	MN	C	2002	1/1	0.78	0.36	93,93,93,93	0
12	EDO	A	2005	4/4	0.84	1.55	83,85,93,94	0
11	MN	C	2003	1/1	0.86	0.33	85,85,85,85	0
11	MN	A	2003	1/1	0.90	0.39	81,81,81,81	0
13	K	A	2006	1/1	0.90	0.15	95,95,95,95	0
12	EDO	A	2004	4/4	0.91	0.49	92,95,105,106	0
11	MN	A	2002	1/1	0.94	0.36	92,92,92,92	0
13	K	C	2005	1/1	0.95	0.10	92,92,92,92	0
10	ZN	A	2001	1/1	0.97	0.26	90,90,90,90	0
10	ZN	C	2001	1/1	0.98	0.26	89,89,89,89	0

6.5 Other polymers (i)

There are no such residues in this entry.