WORLDWIDE wwPDB PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Feb 1, 2016 – 07:29 AM GMT

PDB ID : 3AXY

Title : Structure of Florigen Activation Complex Consisting of Rice Florigen Hd3a, 14-3-3 Protein GF14 and Rice FD Homolog OsFD1

Authors : Ohki, I.; Furuita, K.; Hayashi, K.; Taoka, K.; Tsuji, H.; Nakagawa, A.; Shimamoto, K.; Kojima, C.

Deposited on : 2011-04-19

Resolution : 2.40 Å(reported)

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

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 2.40 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	Percentile Ranks	Value
Rfree		0.274
Clashscore		17
Ramachandran outliers		0.7%
Sidechain outliers		11.5%
RSRZ outliers		2.3%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution
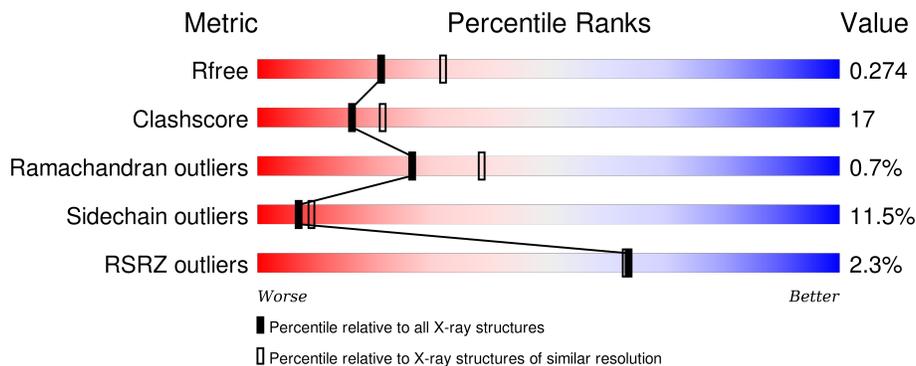
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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. 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	170	3% 74% 19% • •
1	B	170	2% 74% 22% • •
1	G	170	% 76% 18% • •
1	H	170	% 70% 24% • •
2	C	240	2% 65% 23% 8% ••

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Mol	Chain	Length	Quality of chain
2	D	240	3% 69% 24% 5% ·
2	I	240	3% 70% 21% 5% ··
2	J	240	3% 63% 27% 8% ·
3	E	9	33% 33% 11% 22%
3	F	9	33% 33% 11% 22%
3	K	9	33% 33% 11% 22%
3	L	9	11% 33% 22% 22% 22%
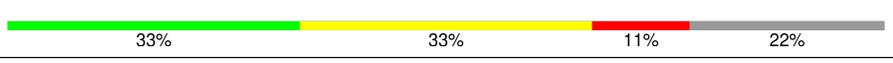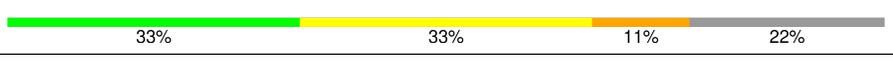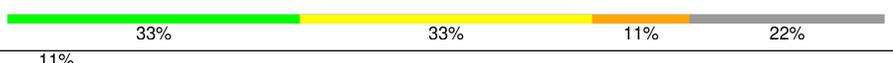
2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 13751 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 Protein HEADING DATE 3A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	166	Total	C	N	O	S	0	0	0
			1312	831	229	246	6			
1	B	166	Total	C	N	O	S	0	0	0
			1312	831	229	246	6			
1	G	165	Total	C	N	O	S	0	0	0
			1306	828	228	244	6			
1	H	166	Total	C	N	O	S	0	0	0
			1312	831	229	246	6			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	EXPRESSION TAG	UNP Q93WI9
A	2	PRO	-	EXPRESSION TAG	UNP Q93WI9
A	3	GLY	-	EXPRESSION TAG	UNP Q93WI9
A	4	HIS	-	EXPRESSION TAG	UNP Q93WI9
A	5	MET	-	EXPRESSION TAG	UNP Q93WI9
A	43	LEU	CYS	ENGINEERED MUTATION	UNP Q93WI9
A	109	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
A	166	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
B	1	GLY	-	EXPRESSION TAG	UNP Q93WI9
B	2	PRO	-	EXPRESSION TAG	UNP Q93WI9
B	3	GLY	-	EXPRESSION TAG	UNP Q93WI9
B	4	HIS	-	EXPRESSION TAG	UNP Q93WI9
B	5	MET	-	EXPRESSION TAG	UNP Q93WI9
B	43	LEU	CYS	ENGINEERED MUTATION	UNP Q93WI9
B	109	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
B	166	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
G	1	GLY	-	EXPRESSION TAG	UNP Q93WI9
G	2	PRO	-	EXPRESSION TAG	UNP Q93WI9
G	3	GLY	-	EXPRESSION TAG	UNP Q93WI9
G	4	HIS	-	EXPRESSION TAG	UNP Q93WI9
G	5	MET	-	EXPRESSION TAG	UNP Q93WI9

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Chain	Residue	Modelled	Actual	Comment	Reference
G	43	LEU	CYS	ENGINEERED MUTATION	UNP Q93WI9
G	109	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
G	166	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
H	1	GLY	-	EXPRESSION TAG	UNP Q93WI9
H	2	PRO	-	EXPRESSION TAG	UNP Q93WI9
H	3	GLY	-	EXPRESSION TAG	UNP Q93WI9
H	4	HIS	-	EXPRESSION TAG	UNP Q93WI9
H	5	MET	-	EXPRESSION TAG	UNP Q93WI9
H	43	LEU	CYS	ENGINEERED MUTATION	UNP Q93WI9
H	109	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9
H	166	SER	CYS	ENGINEERED MUTATION	UNP Q93WI9

- Molecule 2 is a protein called 14-3-3-like protein GF14-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	235	Total 1875	C 1181	N 312	O 373	S 9	0	0	0
2	D	235	Total 1875	C 1181	N 312	O 373	S 9	0	0	0
2	I	235	Total 1875	C 1181	N 312	O 373	S 9	0	0	0
2	J	234	Total 1867	C 1176	N 311	O 372	S 8	0	0	0

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
C	-3	PRO	-	EXPRESSION TAG	UNP Q6ZKC0
C	-2	LEU	-	EXPRESSION TAG	UNP Q6ZKC0
C	-1	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
C	0	SER	-	EXPRESSION TAG	UNP Q6ZKC0
D	-4	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
D	-3	PRO	-	EXPRESSION TAG	UNP Q6ZKC0
D	-2	LEU	-	EXPRESSION TAG	UNP Q6ZKC0
D	-1	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
D	0	SER	-	EXPRESSION TAG	UNP Q6ZKC0
I	-4	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
I	-3	PRO	-	EXPRESSION TAG	UNP Q6ZKC0
I	-2	LEU	-	EXPRESSION TAG	UNP Q6ZKC0
I	-1	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
I	0	SER	-	EXPRESSION TAG	UNP Q6ZKC0

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Chain	Residue	Modelled	Actual	Comment	Reference
J	-4	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
J	-3	PRO	-	EXPRESSION TAG	UNP Q6ZKC0
J	-2	LEU	-	EXPRESSION TAG	UNP Q6ZKC0
J	-1	GLY	-	EXPRESSION TAG	UNP Q6ZKC0
J	0	SER	-	EXPRESSION TAG	UNP Q6ZKC0

- Molecule 3 is a protein called Rice FD homolog OsFD1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	7	Total 60	C 37	N 10	O 12	P 1	0	0	0
3	F	7	Total 60	C 37	N 10	O 12	P 1	0	0	0
3	K	7	Total 60	C 37	N 10	O 12	P 1	0	0	0
3	L	7	Total 60	C 37	N 10	O 12	P 1	0	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	108	Total 108	O 108	0	0
4	B	68	Total 68	O 68	0	0
4	C	118	Total 118	O 118	0	0
4	D	92	Total 92	O 92	0	0
4	E	9	Total 9	O 9	0	0
4	F	4	Total 4	O 4	0	0
4	G	120	Total 120	O 120	0	0
4	H	68	Total 68	O 68	0	0
4	I	104	Total 104	O 104	0	0
4	J	74	Total 74	O 74	0	0
4	K	8	Total 8	O 8	0	0

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| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	L	4	Total O 4 4		0	0

3 Residue-property plots ⓘ

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Protein HEADING DATE 3A
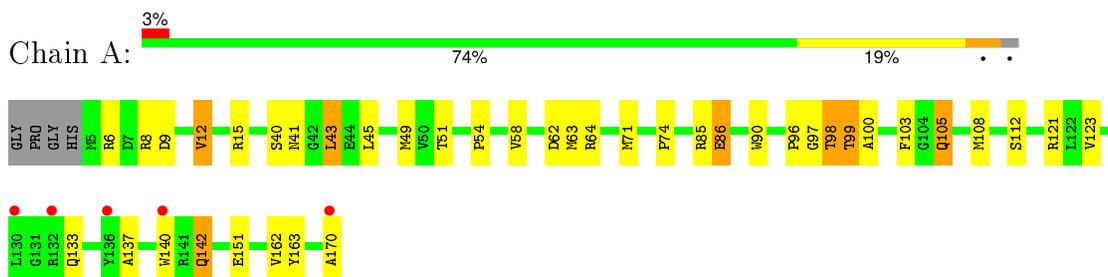
- Molecule 1: Protein HEADING DATE 3A
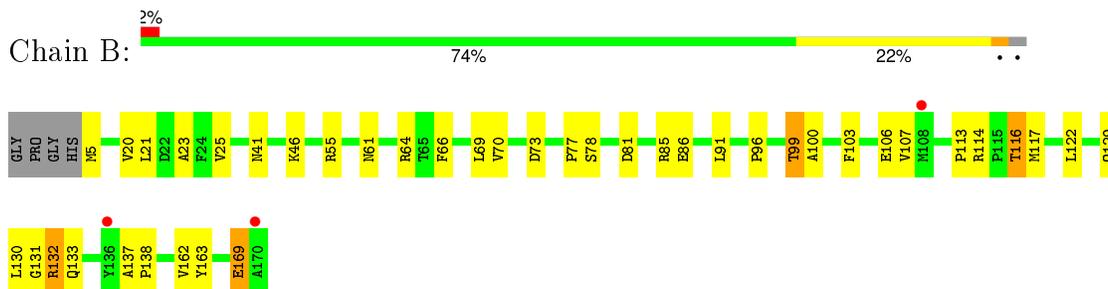
- Molecule 1: Protein HEADING DATE 3A
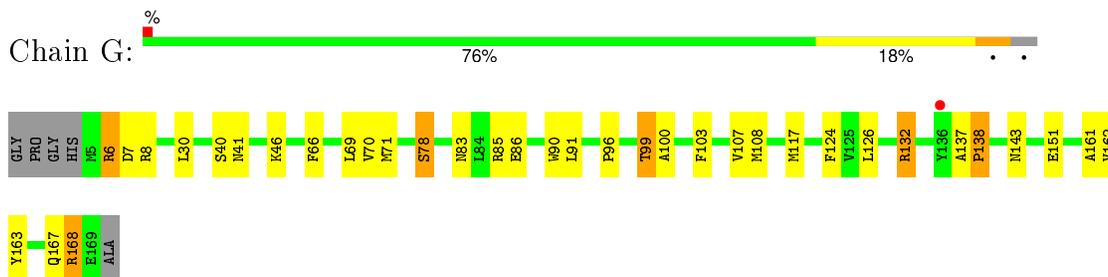
- Molecule 1: Protein HEADING DATE 3A
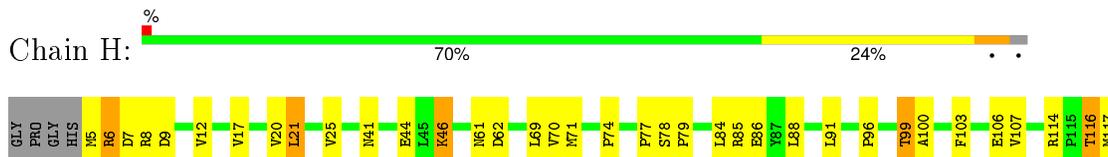
• Molecule 2: 14-3-3-like protein GF14-C
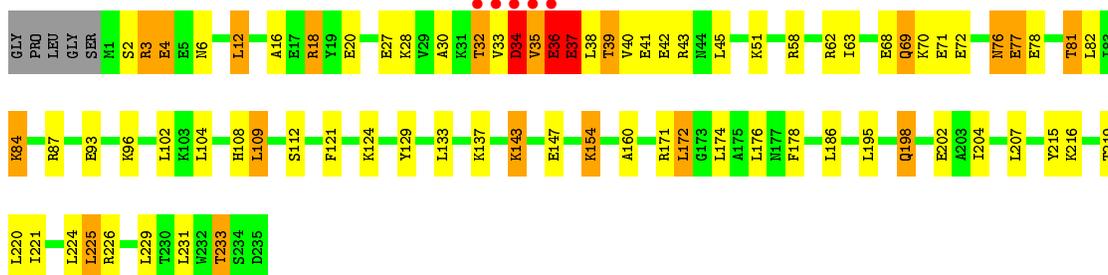
Chain C:

• Molecule 2: 14-3-3-like protein GF14-C
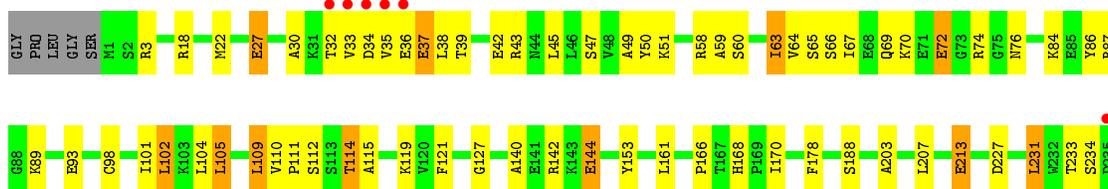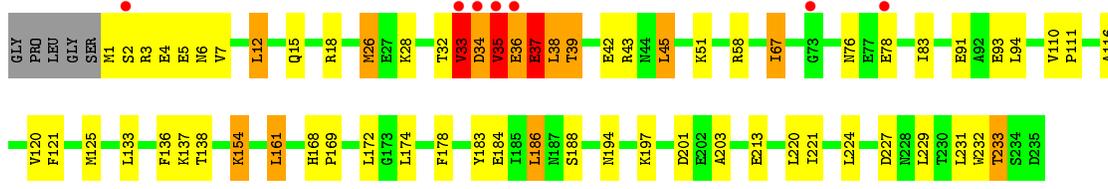
Chain D:

• Molecule 2: 14-3-3-like protein GF14-C

Chain I:

• Molecule 2: 14-3-3-like protein GF14-C
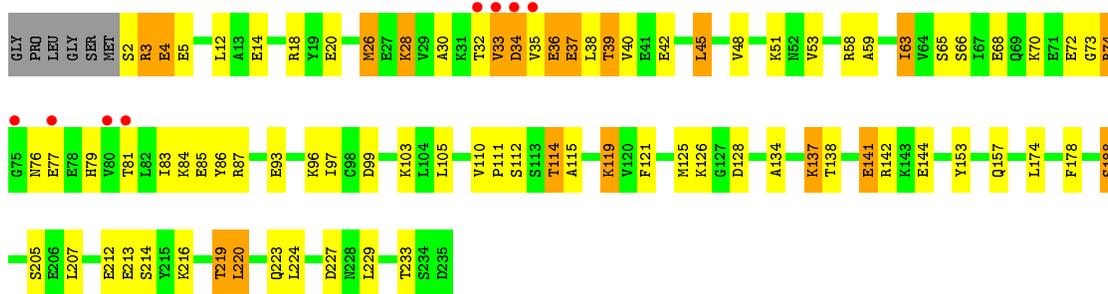
Chain J:

● Molecule 3: Rice FD homolog OsFD1
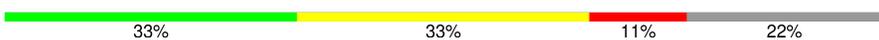
Chain E:

● Molecule 3: Rice FD homolog OsFD1

Chain F:
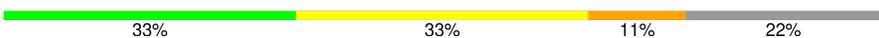
● Molecule 3: Rice FD homolog OsFD1

Chain K:
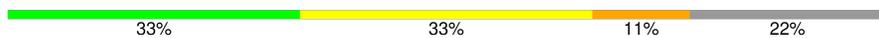
● Molecule 3: Rice FD homolog OsFD1

Chain L:

4 Data and refinement statistics ⓘ

| Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	76.73Å 96.65Å 99.51Å 68.23° 87.90° 77.94°	Depositor
Resolution (Å)	50.00 – 2.40 37.86 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.1 (50.00-2.40) 85.3 (37.86-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) >$ [1]	2.73 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.227 , 0.276 0.227 , 0.274	Depositor DCC
R_{free} test set	7276 reflections (7.88%)	DCC
Wilson B-factor (Å^2)	32.2	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 39.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Outliers	0 of 99449 reflections	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	13751	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 21.48 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 6.9501e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: SEP

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	0.39	0/1345	0.49	0/1831
1	B	0.33	0/1345	0.45	0/1831
1	G	0.37	0/1339	0.49	0/1824
1	H	0.34	0/1345	0.46	0/1831
2	C	0.38	0/1903	0.50	0/2563
2	D	0.35	0/1903	0.46	0/2563
2	I	0.37	0/1903	0.49	0/2563
2	J	0.34	0/1895	0.44	0/2553
3	E	0.43	0/50	0.92	1/64 (1.6%)
3	F	0.42	0/50	0.54	0/64
3	K	0.47	0/50	0.47	0/64
3	L	0.38	0/50	0.63	0/64
All	All	0.36	0/13178	0.48	1/17815 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	C	0	3
2	I	0	3
All	All	0	6

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	E	191	LEU	CA-CB-CG	5.19	127.23	115.30

There are no chirality outliers.

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	129	TYR	Sidechain
2	C	36	GLU	Peptide
2	C	37	GLU	Peptide
2	I	33	VAL	Peptide
2	I	34	ASP	Peptide

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	1312	0	1283	36	0
1	B	1312	0	1283	39	0
1	G	1306	0	1278	33	0
1	H	1312	0	1283	44	0
2	C	1875	0	1868	76	0
2	D	1875	0	1868	54	0
2	I	1875	0	1868	79	0
2	J	1867	0	1856	87	0
3	E	60	0	56	5	0
3	F	60	0	56	6	0
3	K	60	0	56	9	0
3	L	60	0	56	6	0
4	A	108	0	0	7	0
4	B	68	0	0	2	0
4	C	118	0	0	10	0
4	D	92	0	0	3	0
4	E	9	0	0	0	0
4	F	4	0	0	2	0
4	G	120	0	0	4	0
4	H	68	0	0	4	0
4	I	104	0	0	7	0
4	J	74	0	0	8	0
4	K	8	0	0	2	0
4	L	4	0	0	0	0
All	All	13751	0	12811	434	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 17.

The worst 5 of 434 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)
3:F:189:ARG:HG3	4:F:708:HOH:O	1.40	1.19
1:B:99:THR:CG2	1:B:100:ALA:H	1.54	1.17
1:G:6:ARG:HG2	1:G:6:ARG:HH11	1.13	1.13
2:I:39:THR:HG23	2:I:42:GLU:HG3	1.31	1.10
2:J:39:THR:HG21	4:J:574:HOH:O	1.50	1.09

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	164/170 (96%)	153 (93%)	11 (7%)	0	100	100
1	B	164/170 (96%)	159 (97%)	5 (3%)	0	100	100
1	G	163/170 (96%)	154 (94%)	7 (4%)	2 (1%)	16	23
1	H	164/170 (96%)	156 (95%)	8 (5%)	0	100	100
2	C	233/240 (97%)	224 (96%)	6 (3%)	3 (1%)	15	21
2	D	233/240 (97%)	221 (95%)	12 (5%)	0	100	100
2	I	233/240 (97%)	226 (97%)	3 (1%)	4 (2%)	11	14
2	J	232/240 (97%)	218 (94%)	12 (5%)	2 (1%)	21	30
3	E	4/9 (44%)	4 (100%)	0	0	100	100
3	F	4/9 (44%)	4 (100%)	0	0	100	100
3	K	4/9 (44%)	4 (100%)	0	0	100	100
3	L	4/9 (44%)	4 (100%)	0	0	100	100
All	All	1602/1676 (96%)	1527 (95%)	64 (4%)	11 (1%)	26	38

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	37	GLU
2	I	33	VAL
2	I	38	LEU
2	C	34	ASP
1	G	168	ARG

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	145/147 (99%)	132 (91%)	13 (9%)	12	17
1	B	145/147 (99%)	137 (94%)	8 (6%)	27	42
1	G	145/147 (99%)	137 (94%)	8 (6%)	27	42
1	H	145/147 (99%)	129 (89%)	16 (11%)	8	10
2	C	201/204 (98%)	166 (83%)	35 (17%)	2	2
2	D	201/204 (98%)	178 (89%)	23 (11%)	7	9
2	I	201/204 (98%)	182 (90%)	19 (10%)	11	15
2	J	200/204 (98%)	167 (84%)	33 (16%)	3	3
3	E	5/7 (71%)	4 (80%)	1 (20%)	1	1
3	F	5/7 (71%)	3 (60%)	2 (40%)	0	0
3	K	5/7 (71%)	4 (80%)	1 (20%)	1	1
3	L	5/7 (71%)	3 (60%)	2 (40%)	0	0
All	All	1403/1432 (98%)	1242 (88%)	161 (12%)	7	9

5 of 161 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	144	GLU
1	H	6	ARG
2	J	141	GLU
2	D	178	PHE

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Mol	Chain	Res	Type
3	F	190	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 28 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	223	GLN
2	D	194	ASN
2	I	194	ASN
2	D	52	ASN
2	D	76	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)

4 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	$\#|Z| > 2$
3	SEP	E	192	3	8,9,10	1.40	1 (12%)	8,12,14	2.30	1 (12%)
3	SEP	F	192	3	8,9,10	1.55	1 (12%)	8,12,14	1.78	3 (37%)
3	SEP	K	192	3	8,9,10	1.53	1 (12%)	8,12,14	2.11	2 (25%)
3	SEP	L	192	3	8,9,10	1.47	1 (12%)	8,12,14	1.49	1 (12%)

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
3	SEP	E	192	3	-	0/6/8/10	0/0/0/0
3	SEP	F	192	3	-	0/6/8/10	0/0/0/0
3	SEP	K	192	3	-	0/6/8/10	0/0/0/0
3	SEP	L	192	3	-	0/6/8/10	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	192	SEP	P-O1P	2.83	1.60	1.51
3	L	192	SEP	P-O1P	2.92	1.60	1.51
3	K	192	SEP	P-O1P	3.18	1.61	1.51
3	F	192	SEP	P-O1P	3.40	1.62	1.51

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	192	SEP	O-C-CA	-2.01	120.25	125.49
3	F	192	SEP	O3P-P-OG	2.35	113.33	106.56
3	K	192	SEP	O3P-P-OG	2.40	113.47	106.56
3	L	192	SEP	OG-CB-CA	2.98	110.82	108.27
3	F	192	SEP	OG-CB-CA	3.74	111.46	108.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	192	SEP	1	0
3	F	192	SEP	1	0
3	K	192	SEP	1	0
3	L	192	SEP	1	0

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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	166/170 (97%)	-0.28	5 (3%)	54	53	12, 25, 44, 60	0
1	B	166/170 (97%)	-0.06	3 (1%)	71	71	17, 32, 56, 68	0
1	G	165/170 (97%)	-0.15	1 (0%)	90	90	13, 23, 44, 60	0
1	H	166/170 (97%)	-0.31	1 (0%)	90	90	17, 32, 48, 69	0
2	C	235/240 (97%)	-0.18	5 (2%)	67	66	15, 27, 58, 76	0
2	D	235/240 (97%)	-0.05	6 (2%)	59	58	18, 33, 64, 80	0
2	I	235/240 (97%)	-0.05	7 (2%)	54	53	14, 27, 60, 75	0
2	J	234/240 (97%)	-0.04	8 (3%)	49	49	19, 35, 69, 77	0
3	E	6/9 (66%)	0.28	0	100	100	25, 31, 43, 53	0
3	F	6/9 (66%)	0.47	0	100	100	30, 37, 44, 57	0
3	K	6/9 (66%)	-0.29	0	100	100	22, 30, 41, 52	0
3	L	6/9 (66%)	0.87	1 (16%)	2	2	35, 41, 49, 58	0
All	All	1626/1676 (97%)	-0.12	37 (2%)	64	63	12, 29, 57, 80	0

The worst 5 of 37 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	35	VAL	8.0
2	D	35	VAL	6.7
2	I	33	VAL	6.0
2	I	35	VAL	5.6
2	D	34	ASP	5.4

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. LLDF column lists the quality of electron

density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å^2)	Q<0.9
3	SEP	E	192	10/11	0.98	0.14	-	18,27,30,32	0
3	SEP	L	192	10/11	0.99	0.12	-	19,28,33,36	0
3	SEP	F	192	10/11	0.98	0.11	-	16,27,29,31	0
3	SEP	K	192	10/11	0.98	0.12	-	10,21,23,26	0

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.