



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 7, 2026 – 02:17 AM UTC

PDB ID : 6YVH / pdb_00006yvh
Title : CWC22-CWC27-EIF4A3 Complex
Authors : Basquin, J.; Busetto, V.; LeHir, H.; Conti, E.
Deposited on : 2020-04-28
Resolution : 3.19 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

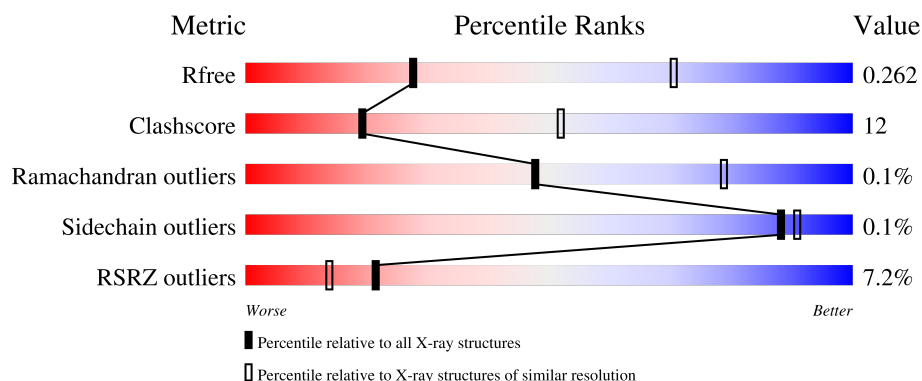
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.19 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}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)

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 $\leq 5\%$. 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	291	3% 73% 21% 6%
1	B	291	3% 74% 21% 6%
1	D	291	5% 68% 26% 6%
1	F	291	5% 70% 23% 7%
2	C	57	5% 63% 23% 14%

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Mol	Chain	Length	Quality of chain
2	E	57	
2	G	57	
2	I	57	
3	H	166	
3	J	166	
3	K	166	
3	L	166	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14536 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 Pre-mRNA-splicing factor CWC22 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	274	Total	C	N	O	S	0	1	0
			2074	1327	358	380	9			
1	B	274	Total	C	N	O	S	0	1	0
			2054	1318	348	380	8			
1	D	274	Total	C	N	O	S	0	1	0
			2068	1321	354	385	8			
1	F	272	Total	C	N	O	S	0	1	0
			2094	1338	353	393	10			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	116	ARG	-	expression tag	UNP Q9HCG8
A	117	SER	-	expression tag	UNP Q9HCG8
A	118	MET	-	expression tag	UNP Q9HCG8
B	116	ARG	-	expression tag	UNP Q9HCG8
B	117	SER	-	expression tag	UNP Q9HCG8
B	118	MET	-	expression tag	UNP Q9HCG8
D	116	ARG	-	expression tag	UNP Q9HCG8
D	117	SER	-	expression tag	UNP Q9HCG8
D	118	MET	-	expression tag	UNP Q9HCG8
F	116	ARG	-	expression tag	UNP Q9HCG8
F	117	SER	-	expression tag	UNP Q9HCG8
F	118	MET	-	expression tag	UNP Q9HCG8

- Molecule 2 is a protein called Spliceosome-associated protein CWC27 homolog.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	49	Total	C	N	O	S	0	0	0
			356	222	58	75	1			
2	I	49	Total	C	N	O	S	0	0	0
			349	220	57	71	1			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	49	Total	C	N	O	S	0	0	0
			347	218	56	72	1			
2	G	44	Total	C	N	O	S	0	0	0
			332	208	56	67	1			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	375	ARG	-	expression tag	UNP Q6UX04
C	376	SER	-	expression tag	UNP Q6UX04
C	377	MET	-	expression tag	UNP Q6UX04
I	375	ARG	-	expression tag	UNP Q6UX04
I	376	SER	-	expression tag	UNP Q6UX04
I	377	MET	-	expression tag	UNP Q6UX04
E	375	ARG	-	expression tag	UNP Q6UX04
E	376	SER	-	expression tag	UNP Q6UX04
E	377	MET	-	expression tag	UNP Q6UX04
G	375	ARG	-	expression tag	UNP Q6UX04
G	376	SER	-	expression tag	UNP Q6UX04
G	377	MET	-	expression tag	UNP Q6UX04

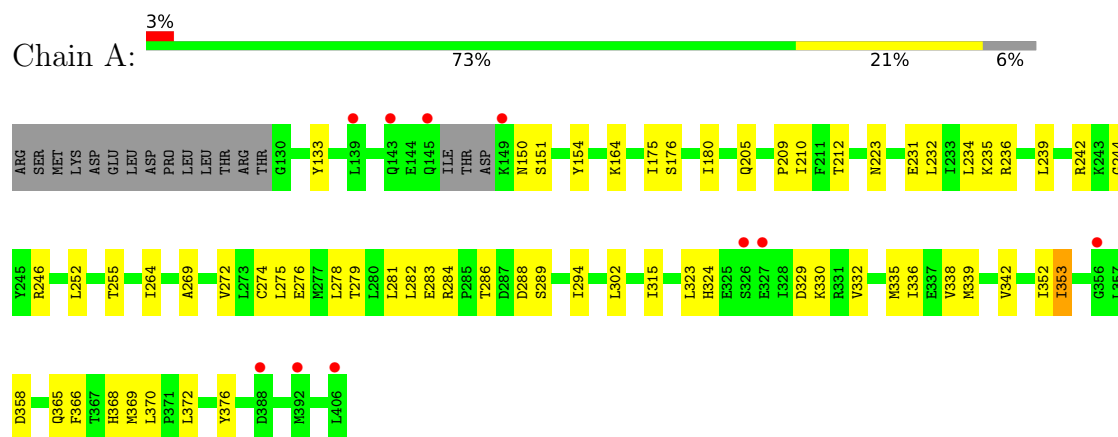
- Molecule 3 is a protein called Eukaryotic initiation factor 4A-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	162	Total	C	N	O	S	0	0	0
			1259	795	209	247	8			
3	J	162	Total	C	N	O	S	0	0	0
			1244	790	205	243	6			
3	K	164	Total	C	N	O	S	0	1	0
			1128	715	192	215	6			
3	L	162	Total	C	N	O	S	0	0	0
			1231	784	198	241	8			

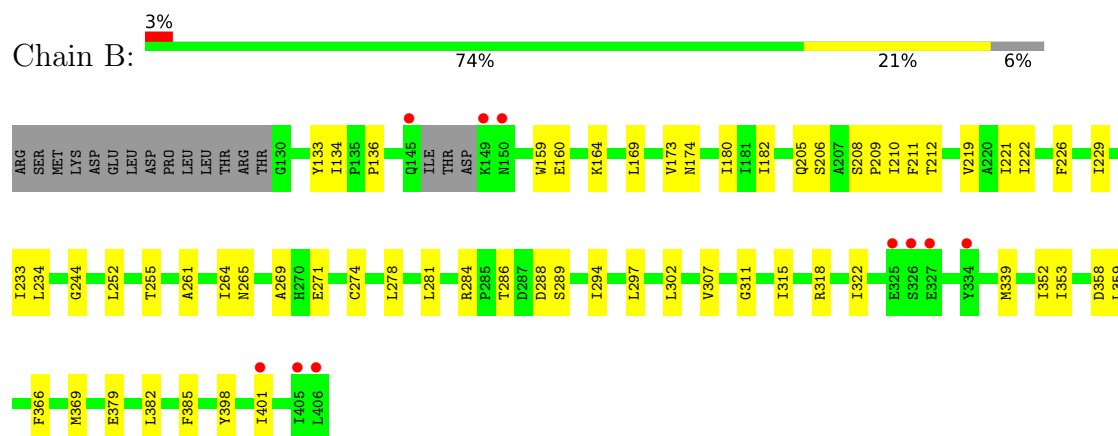
3 Residue-property plots [i](#)

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.

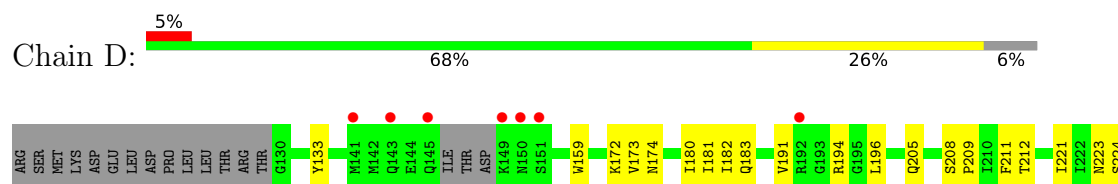
- Molecule 1: Pre-mRNA-splicing factor CWC22 homolog

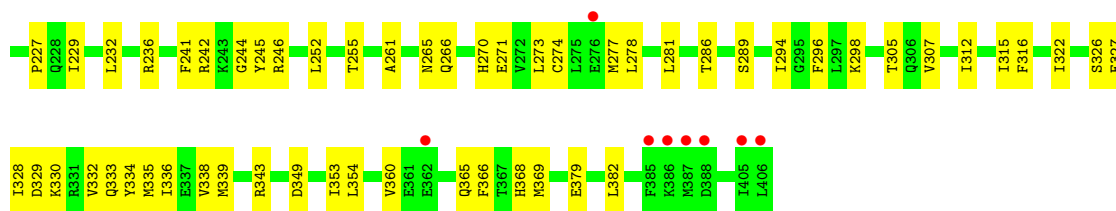


- Molecule 1: Pre-mRNA-splicing factor CWC22 homolog

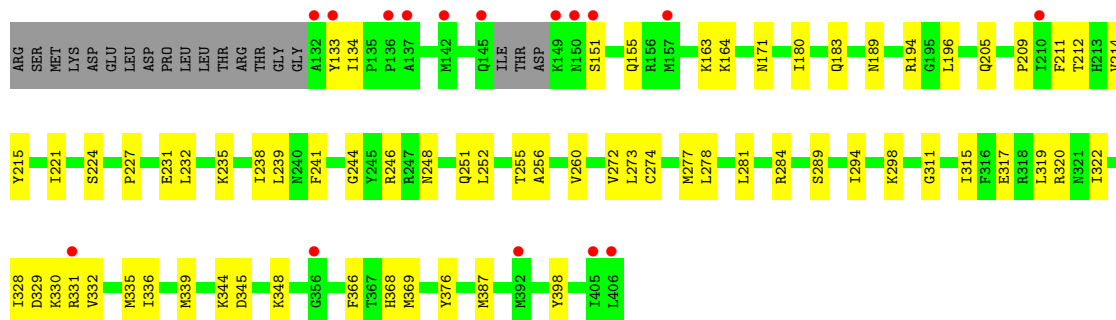


- Molecule 1: Pre-mRNA-splicing factor CWC22 homolog

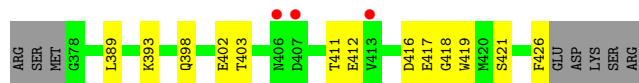




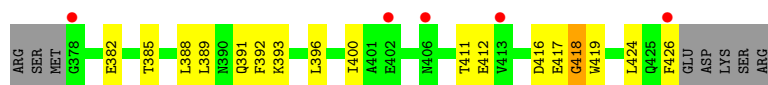
• Molecule 1: Pre-mRNA-splicing factor CWC22 homolog



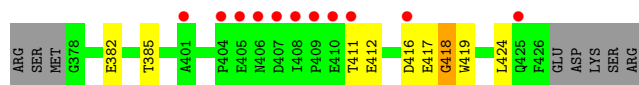
• Molecule 2: Spliceosome-associated protein CWC27 homolog



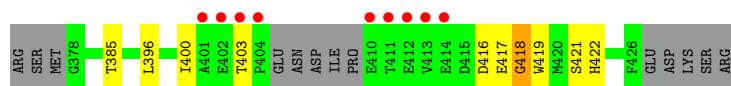
• Molecule 2: Spliceosome-associated protein CWC27 homolog



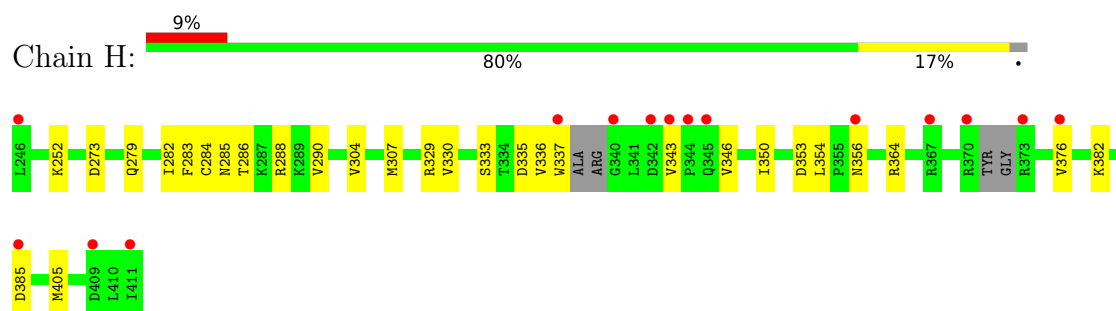
• Molecule 2: Spliceosome-associated protein CWC27 homolog



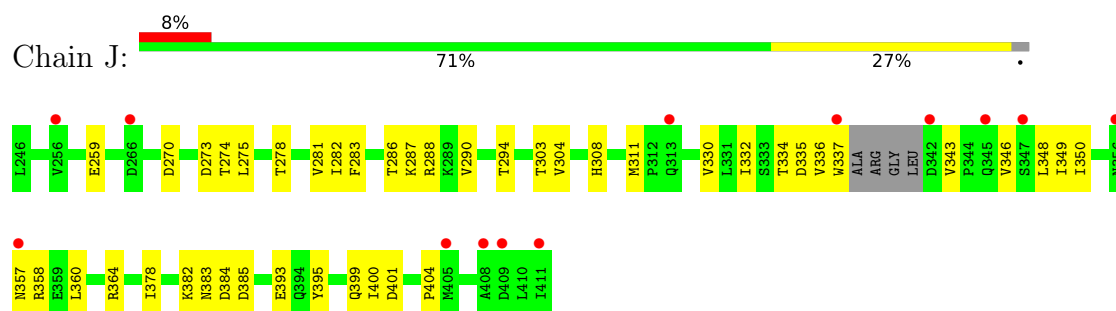
• Molecule 2: Spliceosome-associated protein CWC27 homolog



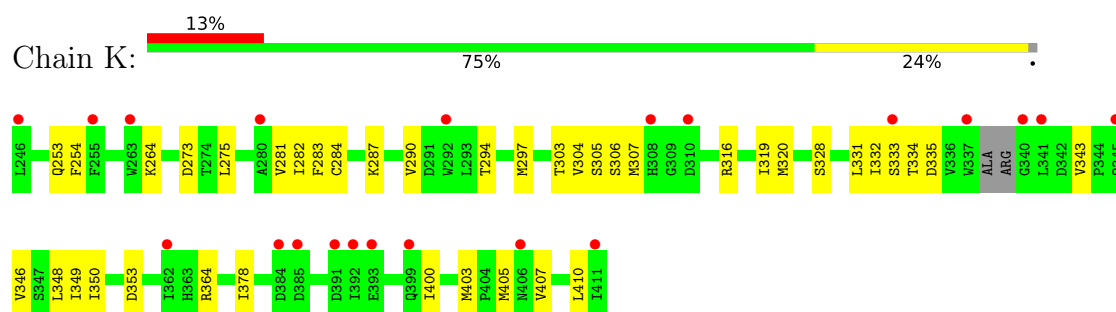
- Molecule 3: Eukaryotic initiation factor 4A-III



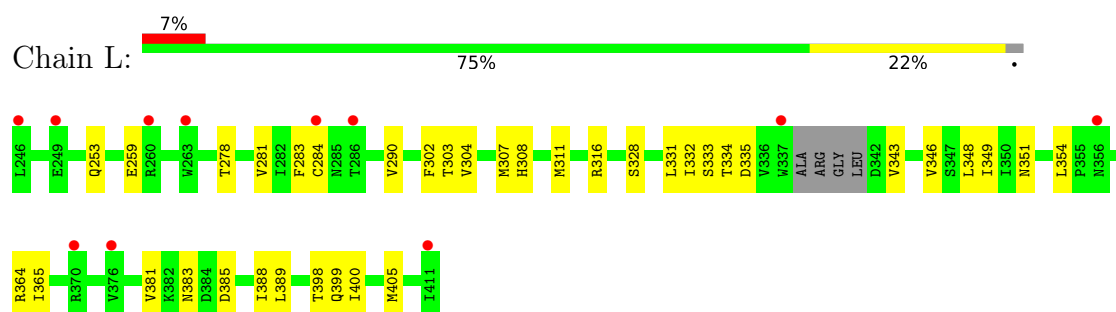
- Molecule 3: Eukaryotic initiation factor 4A-III



- Molecule 3: Eukaryotic initiation factor 4A-III



- Molecule 3: Eukaryotic initiation factor 4A-III



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	151.25Å 163.63Å 181.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	94.69 – 3.19 94.69 – 3.19	Depositor EDS
% Data completeness (in resolution range)	99.3 (94.69-3.19) 99.5 (94.69-3.19)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 3.19Å)	Xtriage
Refinement program	PHENIX dev_3758	Depositor
R, R_{free}	0.232 , 0.263 0.234 , 0.262	Depositor DCC
R_{free} test set	3895 reflections (5.17%)	wwPDB-VP
Wilson B-factor (Å ²)	111.5	Xtriage
Anisotropy	0.434	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 84.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14536	wwPDB-VP
Average B, all atoms (Å ²)	118.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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

5.1 Standard geometry

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	0.16	0/2111	0.41	0/2870
1	B	0.16	0/2091	0.39	0/2851
1	D	0.18	0/2104	0.42	0/2862
1	F	0.18	0/2131	0.44	0/2894
2	C	0.13	0/362	0.41	0/494
2	E	0.19	0/353	0.45	0/484
2	G	0.18	0/336	0.47	0/454
2	I	0.15	0/355	0.42	0/485
3	H	0.15	0/1279	0.37	0/1734
3	J	0.18	0/1266	0.44	0/1721
3	K	0.15	0/1147	0.38	0/1570
3	L	0.14	0/1253	0.39	0/1706
All	All	0.16	0/14788	0.41	0/20125

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	1
2	E	0	1
2	G	0	1
2	I	0	1
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	418	GLY	Peptide
2	E	418	GLY	Peptide
2	G	418	GLY	Peptide
2	I	418	GLY	Peptide

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	2074	0	2007	47	0
1	B	2054	0	1965	48	0
1	D	2068	0	1990	58	0
1	F	2094	0	2032	51	0
2	C	356	0	311	10	0
2	E	347	0	299	13	0
2	G	332	0	306	9	0
2	I	349	0	305	16	0
3	H	1259	0	1181	21	0
3	J	1244	0	1151	35	0
3	K	1128	0	969	29	0
3	L	1231	0	1133	31	0
All	All	14536	0	13649	329	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 329 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:F:284:ARG:NH2	2:G:421:SER:O	2.12	0.83
2:E:411:THR:HG22	2:E:412:GLU:H	1.43	0.83
1:F:246:ARG:HG3	2:G:418:GLY:H	1.44	0.82
1:D:294:ILE:HD11	1:D:335:MET:HE3	1.61	0.81
3:L:307:MET:HG3	3:L:316:ARG:HH11	1.46	0.80

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	271/291 (93%)	267 (98%)	3 (1%)	1 (0%)	30	62
1	B	271/291 (93%)	266 (98%)	5 (2%)	0	100	100
1	D	271/291 (93%)	268 (99%)	3 (1%)	0	100	100
1	F	269/291 (92%)	262 (97%)	7 (3%)	0	100	100
2	C	47/57 (82%)	40 (85%)	7 (15%)	0	100	100
2	E	47/57 (82%)	40 (85%)	7 (15%)	0	100	100
2	G	40/57 (70%)	36 (90%)	4 (10%)	0	100	100
2	I	47/57 (82%)	40 (85%)	7 (15%)	0	100	100
3	H	156/166 (94%)	151 (97%)	5 (3%)	0	100	100
3	J	158/166 (95%)	149 (94%)	9 (6%)	0	100	100
3	K	161/166 (97%)	154 (96%)	7 (4%)	0	100	100
3	L	158/166 (95%)	152 (96%)	6 (4%)	0	100	100
All	All	1896/2056 (92%)	1825 (96%)	70 (4%)	1 (0%)	48	79

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	151	SER

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	211/263 (80%)	210 (100%)	1 (0%)	81	85
1	B	207/263 (79%)	207 (100%)	0	100	100
1	D	210/263 (80%)	210 (100%)	0	100	100
1	F	219/263 (83%)	219 (100%)	0	100	100
2	C	35/52 (67%)	35 (100%)	0	100	100
2	E	33/52 (64%)	33 (100%)	0	100	100
2	G	34/52 (65%)	34 (100%)	0	100	100
2	I	33/52 (64%)	33 (100%)	0	100	100
3	H	133/151 (88%)	133 (100%)	0	100	100
3	J	128/151 (85%)	128 (100%)	0	100	100
3	K	98/151 (65%)	98 (100%)	0	100	100
3	L	127/151 (84%)	127 (100%)	0	100	100
All	All	1468/1864 (79%)	1467 (100%)	1 (0%)	88	91

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	353	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
3	J	301	ASN
3	L	383	ASN
3	L	406	ASN
3	L	363	HIS
1	D	205	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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(Å²)	Q<0.9
1	A	274/291 (94%)	0.22	10 (3%)	46	28	58, 107, 164, 258	1 (0%)
1	B	274/291 (94%)	0.21	10 (3%)	46	28	59, 106, 175, 307	1 (0%)
1	D	274/291 (94%)	0.34	15 (5%)	30	19	66, 105, 173, 286	1 (0%)
1	F	272/291 (93%)	0.29	16 (5%)	28	18	67, 97, 180, 216	1 (0%)
2	C	49/57 (85%)	0.67	3 (6%)	27	17	85, 127, 313, 347	0
2	E	49/57 (85%)	1.20	11 (22%)	2	2	93, 138, 303, 382	0
2	G	44/57 (77%)	1.08	9 (20%)	2	2	82, 122, 209, 276	0
2	I	49/57 (85%)	0.61	5 (10%)	12	8	87, 123, 241, 318	0
3	H	162/166 (97%)	0.51	15 (9%)	14	9	67, 99, 166, 213	0
3	J	162/166 (97%)	0.63	13 (8%)	18	12	78, 98, 166, 214	0
3	K	164/166 (98%)	0.97	21 (12%)	7	6	82, 140, 188, 224	1 (0%)
3	L	162/166 (97%)	0.63	11 (6%)	23	15	103, 150, 199, 215	0
All	All	1935/2056 (94%)	0.47	139 (7%)	21	14	58, 111, 191, 382	5 (0%)

The worst 5 of 139 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	H	411	ILE	6.4
2	G	414	GLU	5.7
1	D	150	ASN	5.4
1	F	150	ASN	5.4
3	H	340	GLY	5.4

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 oligosaccharides 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.