



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 11:27 am BST

PDB ID : 4B8C
Title : nuclease module of the yeast Ccr4-Not complex
Authors : Basquin, J.; Conti, E.
Deposited on : 2012-08-26
Resolution : 3.41 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
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

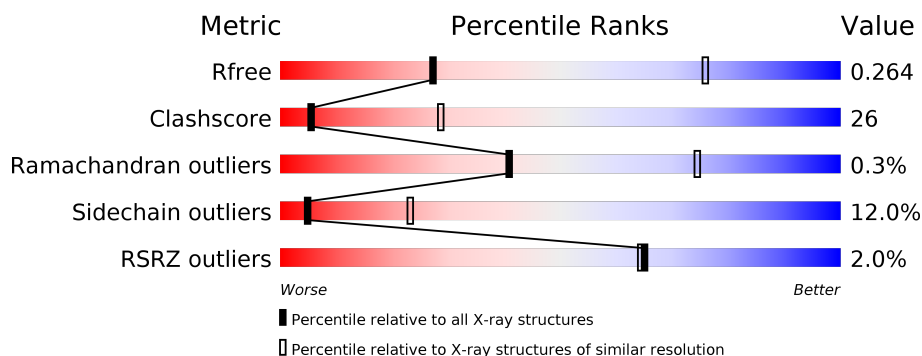
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.41 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	1486 (3.50-3.34)
Clashscore	141614	1572 (3.50-3.34)
Ramachandran outliers	138981	1534 (3.50-3.34)
Sidechain outliers	138945	1535 (3.50-3.34)
RSRZ outliers	127900	1395 (3.50-3.34)

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	288	
1	C	288	
1	E	288	
1	F	288	
2	B	249	
2	G	249	

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Mol	Chain	Length	Quality of chain
2	H	249	
2	I	249	
3	D	727	
3	J	727	
3	K	727	
3	L	727	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 24298 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 POLY(A) RIBONUCLEASE POP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	267	Total	C	N	O	S	0	0	0
			2170	1409	346	404	11			
1	C	267	Total	C	N	O	S	0	0	0
			2174	1412	347	404	11			
1	E	267	Total	C	N	O	S	0	0	0
			2174	1411	347	405	11			
1	F	267	Total	C	N	O	S	0	0	0
			2170	1409	346	404	11			

- Molecule 2 is a protein called GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	233	Total	C	N	O	S	0	0	0
			1869	1221	309	333	6			
2	G	233	Total	C	N	O	S	0	0	0
			1869	1221	309	333	6			
2	H	233	Total	C	N	O	S	0	0	0
			1869	1221	309	333	6			
2	I	233	Total	C	N	O	S	0	0	0
			1869	1221	309	333	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	752	ARG	-	expression tag	UNP P25655
B	753	SER	-	expression tag	UNP P25655
B	754	MET	-	expression tag	UNP P25655
G	752	ARG	-	expression tag	UNP P25655
G	753	SER	-	expression tag	UNP P25655
G	754	MET	-	expression tag	UNP P25655
H	752	ARG	-	expression tag	UNP P25655
H	753	SER	-	expression tag	UNP P25655

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Chain	Residue	Modelled	Actual	Comment	Reference
H	754	MET	-	expression tag	UNP P25655
I	752	ARG	-	expression tag	UNP P25655
I	753	SER	-	expression tag	UNP P25655
I	754	MET	-	expression tag	UNP P25655

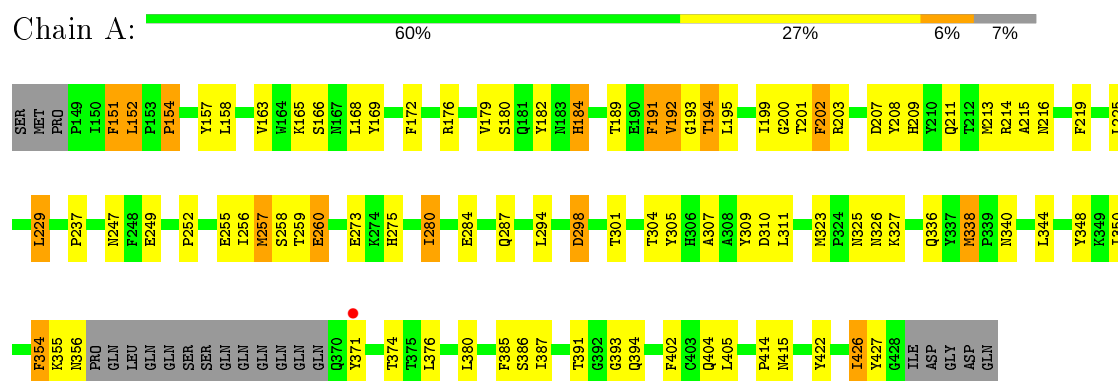
- Molecule 3 is a protein called GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	318	Total	C	N	O	S	0	0	0
			2456	1599	387	459	11			
3	J	210	Total	C	N	O	S	0	0	0
			1604	1034	266	298	6			
3	K	318	Total	C	N	O	S	0	0	0
			2470	1608	392	459	11			
3	L	210	Total	C	N	O	S	0	0	0
			1604	1034	266	298	6			

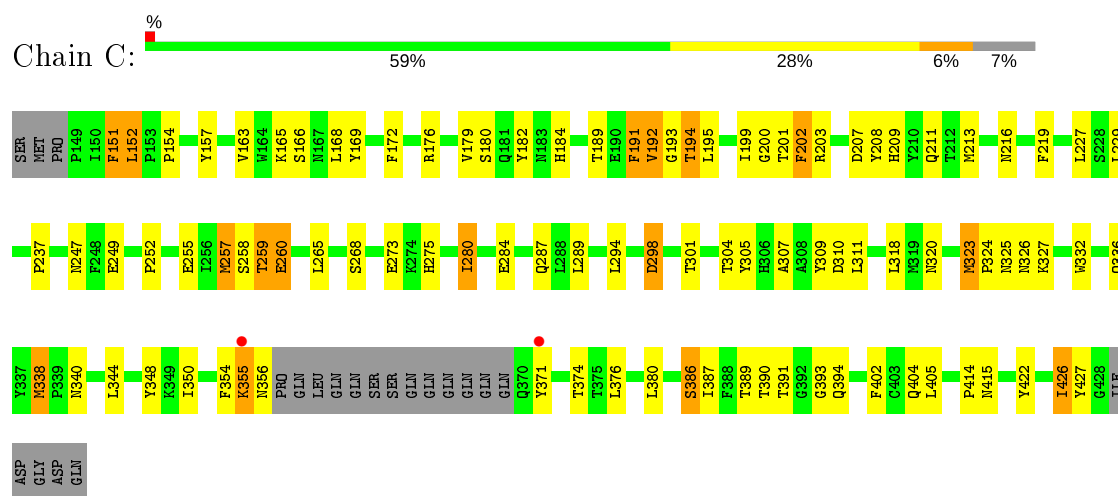
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

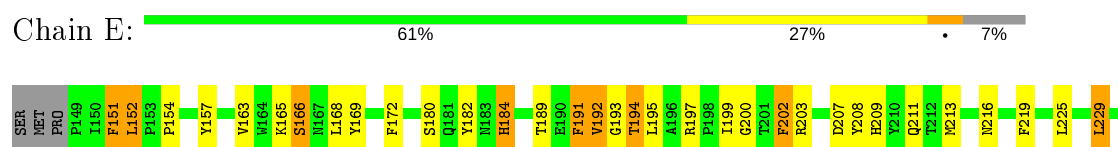
• Molecule 1: POLY(A) RIBONUCLEASE POP2

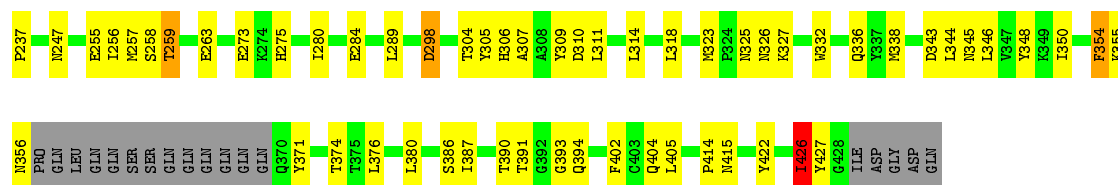


• Molecule 1: POLY(A) RIBONUCLEASE POP2



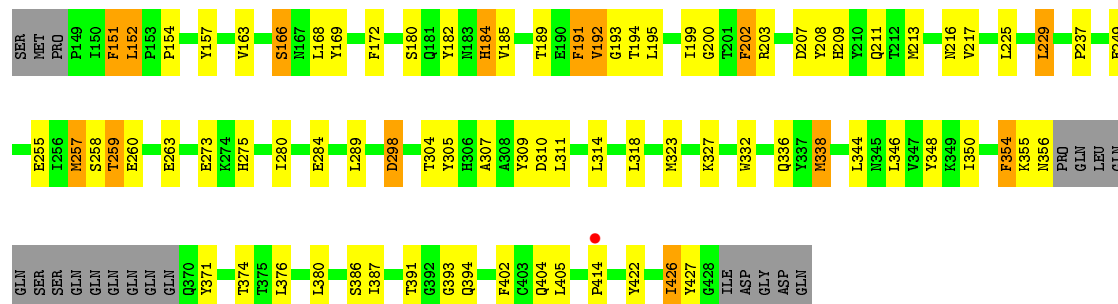
• Molecule 1: POLY(A) RIBONUCLEASE POP2





• Molecule 1: POLY(A) RIBONUCLEASE POP2

Chain F: 64% 24% 5% 7%



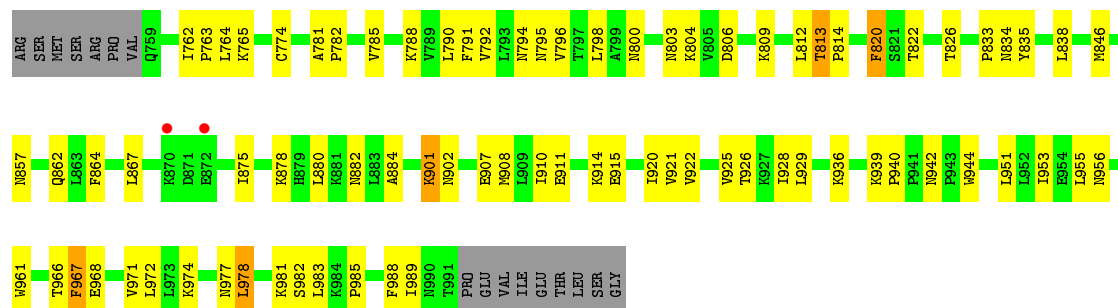
• Molecule 2: GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1

Chain B: 65% 27% 6%



• Molecule 2: GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1

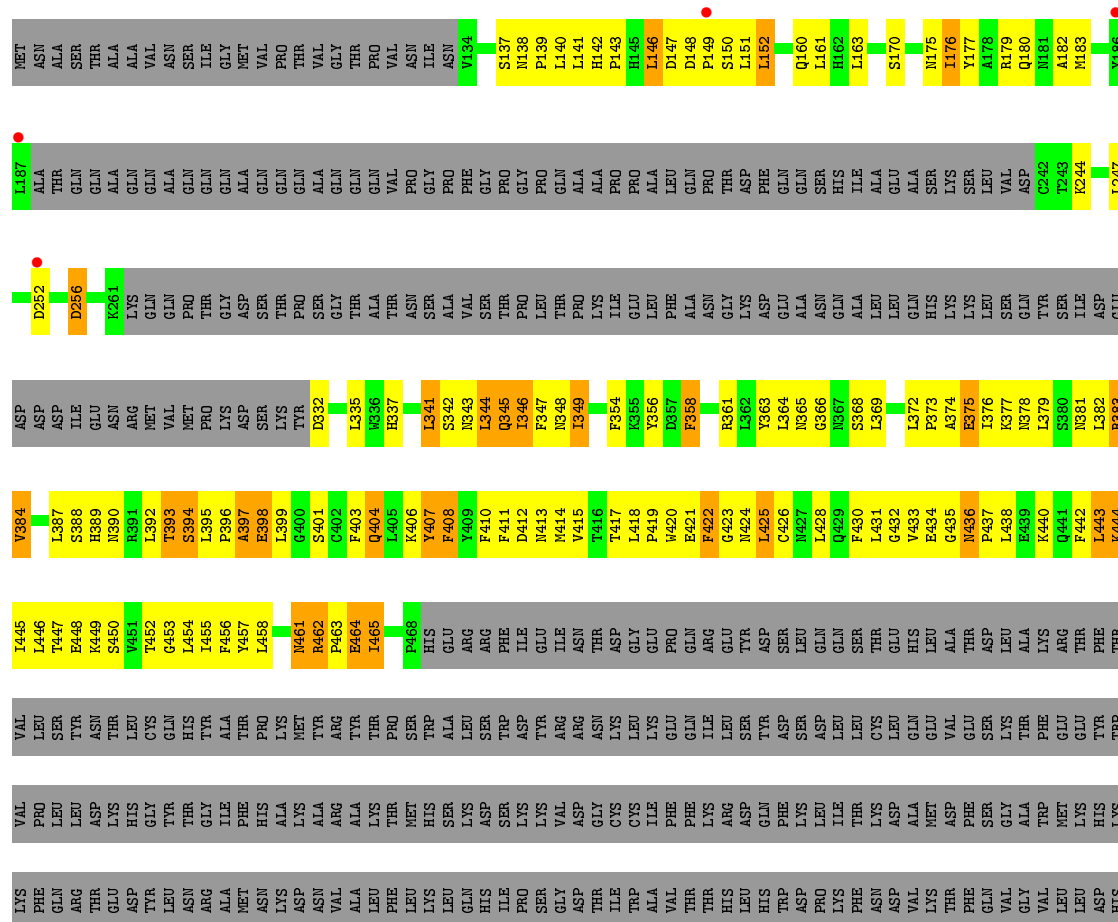
Chain G: 61% 30% 6%



• Molecule 2: GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1

Chain H: 61% 31% 6%





● Molecule 3: GLUCOSE-REPRESSIBLE ALCOHOL DEHYDROGENASE TRANSCRIPTIONAL EFFECTOR

P810	N811	D812	K813	F814	P815	S816	D817	H818	I819	P820	LEU	LEU	ALA	ARG	PHE	GLU	PHE	MET	LYS	THR	ASN	THR	THR	GLY	SER	LYS	LYS	VAL
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	122.65Å 122.91Å 126.42Å 89.47° 89.74° 64.22°	Depositor
Resolution (Å)	47.95 – 3.41 48.23 – 3.28	Depositor EDS
% Data completeness (in resolution range)	97.1 (47.95-3.41) 97.4 (48.23-3.28)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 3.25Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.1_743)	Depositor
R, R_{free}	0.233 , 0.270 0.226 , 0.264	Depositor DCC
R_{free} test set	4942 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	77.9	Xtriage
Anisotropy	0.333	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 72.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l 0.018 for k,h,-l 0.022 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	24298	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.27% 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	0.56	0/2231	0.67	0/3028
1	C	0.54	0/2235	0.67	0/3032
1	E	0.50	0/2235	0.66	0/3033
1	F	0.52	0/2231	0.66	0/3028
2	B	0.43	0/1908	0.58	0/2588
2	G	0.42	0/1908	0.57	0/2588
2	H	0.43	0/1908	0.58	0/2588
2	I	0.44	0/1908	0.58	0/2588
3	D	0.53	0/2520	0.76	2/3446 (0.1%)
3	J	0.62	1/1640 (0.1%)	0.94	4/2240 (0.2%)
3	K	0.54	1/2535 (0.0%)	0.76	1/3463 (0.0%)
3	L	0.63	2/1640 (0.1%)	0.94	3/2240 (0.1%)
All	All	0.52	4/24899 (0.0%)	0.71	10/33862 (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
1	A	0	1
1	C	0	1
1	E	0	1
3	D	0	1
3	J	0	1
3	K	0	1
3	L	0	2
All	All	0	8

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	L	462	ARG	C-N	8.80	1.50	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	J	462	ARG	C-N	8.53	1.50	1.34
3	L	332	ASP	CA-CB	5.73	1.66	1.53
3	K	426	CYS	CB-SG	5.22	1.91	1.82

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	L	462	ARG	O-C-N	13.09	145.96	121.10
3	J	462	ARG	O-C-N	12.95	145.70	121.10
3	J	462	ARG	CA-C-N	-9.27	91.15	117.10
3	L	462	ARG	CA-C-N	-9.18	91.41	117.10
3	J	397	ALA	N-CA-C	-6.26	94.10	111.00

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	194	THR	Peptide
1	C	194	THR	Peptide
3	D	344	LEU	Peptide
1	E	194	THR	Peptide
3	J	332	ASP	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	2170	0	2083	87	0
1	C	2174	0	2094	94	0
1	E	2174	0	2089	86	1
1	F	2170	0	2083	74	1
2	B	1869	0	1936	49	0
2	G	1869	0	1936	51	1
2	H	1869	0	1936	62	0
2	I	1869	0	1936	50	1
3	D	2456	0	2268	226	0
3	J	1604	0	1505	145	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	2470	0	2293	204	0
3	L	1604	0	1505	157	1
All	All	24298	0	23664	1240	3

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 26.

The worst 5 of 1240 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:D:176:ILE:HD11	3:D:343:ASN:HD22	1.20	1.04
3:J:422:PHE:HD1	3:J:422:PHE:O	1.42	1.00
3:K:176:ILE:HD11	3:K:343:ASN:HD22	1.21	1.00
3:K:567:VAL:HG13	3:K:568:PRO:HD3	1.41	0.99
3:D:424:ASN:HD21	3:D:807:ILE:HG21	1.29	0.98

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:166:SER:OG	3:L:146:LEU:O[1_554]	2.08	0.12
2:G:835:TYR:OH	2:I:800:ASN:CA[1_465]	2.10	0.10
1:E:166:SER:OG	3:J:146:LEU:O[1_455]	2.14	0.06

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	263/288 (91%)	250 (95%)	12 (5%)	1 (0%)	34 69
1	C	263/288 (91%)	250 (95%)	12 (5%)	1 (0%)	34 69

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	263/288 (91%)	249 (95%)	13 (5%)	1 (0%)	34	69
1	F	263/288 (91%)	250 (95%)	13 (5%)	0	100	100
2	B	231/249 (93%)	222 (96%)	9 (4%)	0	100	100
2	G	231/249 (93%)	222 (96%)	9 (4%)	0	100	100
2	H	231/249 (93%)	221 (96%)	10 (4%)	0	100	100
2	I	231/249 (93%)	222 (96%)	9 (4%)	0	100	100
3	D	300/727 (41%)	253 (84%)	46 (15%)	1 (0%)	41	74
3	J	204/727 (28%)	168 (82%)	34 (17%)	2 (1%)	15	51
3	K	300/727 (41%)	253 (84%)	46 (15%)	1 (0%)	41	74
3	L	204/727 (28%)	171 (84%)	31 (15%)	2 (1%)	15	51
All	All	2984/5056 (59%)	2731 (92%)	244 (8%)	9 (0%)	41	74

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	D	380	SER
3	K	380	SER
3	J	464	GLU
3	J	465	ILE
3	L	465	ILE

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	241/264 (91%)	216 (90%)	25 (10%)	7	30
1	C	242/264 (92%)	218 (90%)	24 (10%)	8	32
1	E	242/264 (92%)	220 (91%)	22 (9%)	9	35
1	F	241/264 (91%)	218 (90%)	23 (10%)	8	33
2	B	211/231 (91%)	199 (94%)	12 (6%)	20	53
2	G	211/231 (91%)	198 (94%)	13 (6%)	18	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	H	211/231 (91%)	199 (94%)	12 (6%)	20	53
2	I	211/231 (91%)	198 (94%)	13 (6%)	18	51
3	D	258/648 (40%)	206 (80%)	52 (20%)	1	5
3	J	165/648 (26%)	129 (78%)	36 (22%)	1	4
3	K	261/648 (40%)	208 (80%)	53 (20%)	1	5
3	L	165/648 (26%)	130 (79%)	35 (21%)	1	4
All	All	2659/4572 (58%)	2339 (88%)	320 (12%)	5	23

5 of 320 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	209	HIS
2	H	961	TRP
3	L	345	GLN
1	F	298	ASP
2	G	822	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
3	D	424	ASN
3	L	175	ASN
3	K	413	ASN
3	D	343	ASN
3	K	352	ASN

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 ⓘ

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 ⓘ

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	267/288 (92%)	-0.19	1 (0%) 92 91	36, 58, 98, 121	0
1	C	267/288 (92%)	-0.18	2 (0%) 87 86	36, 58, 99, 121	0
1	E	267/288 (92%)	-0.25	0 100 100	35, 58, 100, 121	0
1	F	267/288 (92%)	-0.20	1 (0%) 92 91	36, 59, 98, 124	0
2	B	233/249 (93%)	0.00	3 (1%) 77 75	48, 79, 115, 146	0
2	G	233/249 (93%)	-0.10	2 (0%) 84 83	49, 81, 112, 146	0
2	H	233/249 (93%)	0.04	5 (2%) 63 63	48, 80, 115, 145	0
2	I	233/249 (93%)	-0.06	5 (2%) 63 63	50, 81, 114, 145	0
3	D	318/727 (43%)	0.11	14 (4%) 34 34	50, 87, 136, 160	0
3	J	210/727 (28%)	-0.29	4 (1%) 66 66	35, 61, 101, 127	0
3	K	318/727 (43%)	0.19	22 (6%) 16 20	50, 87, 136, 160	0
3	L	210/727 (28%)	-0.23	3 (1%) 75 73	35, 62, 102, 131	0
All	All	3056/5056 (60%)	-0.08	62 (2%) 65 64	35, 72, 115, 160	0

The worst 5 of 62 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	K	597	ASP	5.4
3	K	135	ASN	4.1
2	H	801	LEU	3.8
2	B	991	THR	3.8
3	K	149	PRO	3.6

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.