



wwPDB X-ray Structure Validation Summary Report ⓘ

May 29, 2020 – 10:39 pm BST

PDB ID : 3SJA
Title : Crystal structure of *S. cerevisiae* Get3 in the open state in complex with Get1 cytosolic domain
Authors : Reitz, S.; Wild, K.; Sinning, I.
Deposited on : 2011-06-21
Resolution : 3.00 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
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

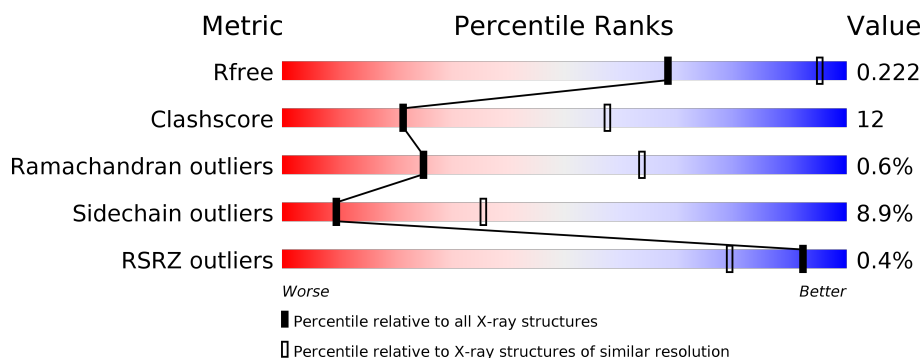
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	362	<div> <div></div> <div>62%28%7%</div> </div>
1	B	362	<div> <div>%</div> <div>67%24%6%</div> </div>
1	E	362	<div> <div></div> <div>67%23%7%</div> </div>
1	F	362	<div> <div></div> <div>65%25%6%</div> </div>
1	I	362	<div> <div>%</div> <div>65%25%6%</div> </div>
2	C	65	<div> <div></div> <div>78%14%6%</div> </div>

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Mol	Chain	Length	Quality of chain
2	D	65	<div><div></div><div>82%</div><div>11%6%</div></div>
2	G	65	<div><div></div><div>85%</div><div>9%6%</div></div>
2	H	65	<div><div></div><div>83%</div><div>11%6%</div></div>
2	J	65	<div><div></div><div>85%</div><div>9%6%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15873 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 ATPase GET3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2643	1667	441	516	19			
1	B	341	Total	C	N	O	S	0	0	0
			2663	1678	444	522	19			
1	E	338	Total	C	N	O	S	0	0	0
			2639	1665	441	514	19			
1	F	341	Total	C	N	O	S	0	0	0
			2663	1678	444	522	19			
1	I	339	Total	C	N	O	S	0	0	0
			2647	1669	442	517	19			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	355	LEU	-	EXPRESSION TAG	UNP Q12154
A	356	GLU	-	EXPRESSION TAG	UNP Q12154
A	357	HIS	-	EXPRESSION TAG	UNP Q12154
A	358	HIS	-	EXPRESSION TAG	UNP Q12154
A	359	HIS	-	EXPRESSION TAG	UNP Q12154
A	360	HIS	-	EXPRESSION TAG	UNP Q12154
A	361	HIS	-	EXPRESSION TAG	UNP Q12154
A	362	HIS	-	EXPRESSION TAG	UNP Q12154
B	355	LEU	-	EXPRESSION TAG	UNP Q12154
B	356	GLU	-	EXPRESSION TAG	UNP Q12154
B	357	HIS	-	EXPRESSION TAG	UNP Q12154
B	358	HIS	-	EXPRESSION TAG	UNP Q12154
B	359	HIS	-	EXPRESSION TAG	UNP Q12154
B	360	HIS	-	EXPRESSION TAG	UNP Q12154
B	361	HIS	-	EXPRESSION TAG	UNP Q12154
B	362	HIS	-	EXPRESSION TAG	UNP Q12154
E	355	LEU	-	EXPRESSION TAG	UNP Q12154
E	356	GLU	-	EXPRESSION TAG	UNP Q12154
E	357	HIS	-	EXPRESSION TAG	UNP Q12154

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Chain	Residue	Modelled	Actual	Comment	Reference
E	358	HIS	-	EXPRESSION TAG	UNP Q12154
E	359	HIS	-	EXPRESSION TAG	UNP Q12154
E	360	HIS	-	EXPRESSION TAG	UNP Q12154
E	361	HIS	-	EXPRESSION TAG	UNP Q12154
E	362	HIS	-	EXPRESSION TAG	UNP Q12154
F	355	LEU	-	EXPRESSION TAG	UNP Q12154
F	356	GLU	-	EXPRESSION TAG	UNP Q12154
F	357	HIS	-	EXPRESSION TAG	UNP Q12154
F	358	HIS	-	EXPRESSION TAG	UNP Q12154
F	359	HIS	-	EXPRESSION TAG	UNP Q12154
F	360	HIS	-	EXPRESSION TAG	UNP Q12154
F	361	HIS	-	EXPRESSION TAG	UNP Q12154
F	362	HIS	-	EXPRESSION TAG	UNP Q12154
I	355	LEU	-	EXPRESSION TAG	UNP Q12154
I	356	GLU	-	EXPRESSION TAG	UNP Q12154
I	357	HIS	-	EXPRESSION TAG	UNP Q12154
I	358	HIS	-	EXPRESSION TAG	UNP Q12154
I	359	HIS	-	EXPRESSION TAG	UNP Q12154
I	360	HIS	-	EXPRESSION TAG	UNP Q12154
I	361	HIS	-	EXPRESSION TAG	UNP Q12154
I	362	HIS	-	EXPRESSION TAG	UNP Q12154

- Molecule 2 is a protein called Golgi to ER traffic protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	61	Total	C	N	O	S	0	0	0
			515	317	95	102	1			
2	D	61	Total	C	N	O	S	0	0	0
			515	317	95	102	1			
2	G	61	Total	C	N	O	S	0	0	0
			515	317	95	102	1			
2	H	61	Total	C	N	O	S	0	0	0
			515	317	95	102	1			
2	J	61	Total	C	N	O	S	0	0	0
			515	317	95	102	1			

There are 35 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	35	MET	-	EXPRESSION TAG	UNP P53192
C	94	HIS	-	EXPRESSION TAG	UNP P53192
C	95	HIS	-	EXPRESSION TAG	UNP P53192

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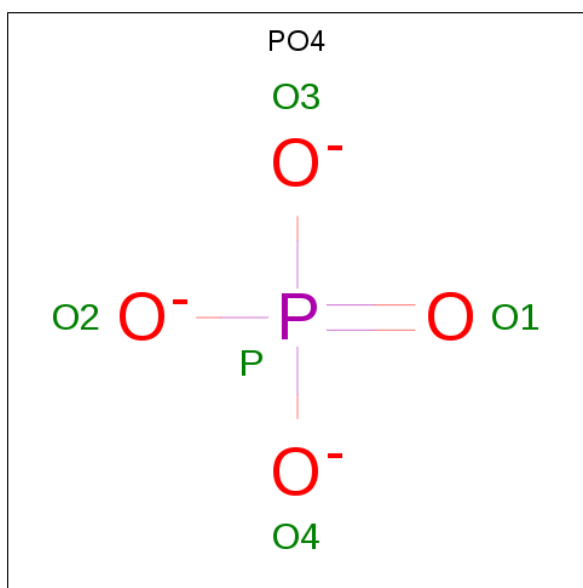
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Chain	Residue	Modelled	Actual	Comment	Reference
C	96	HIS	-	EXPRESSION TAG	UNP P53192
C	97	HIS	-	EXPRESSION TAG	UNP P53192
C	98	HIS	-	EXPRESSION TAG	UNP P53192
C	99	HIS	-	EXPRESSION TAG	UNP P53192
D	35	MET	-	EXPRESSION TAG	UNP P53192
D	94	HIS	-	EXPRESSION TAG	UNP P53192
D	95	HIS	-	EXPRESSION TAG	UNP P53192
D	96	HIS	-	EXPRESSION TAG	UNP P53192
D	97	HIS	-	EXPRESSION TAG	UNP P53192
D	98	HIS	-	EXPRESSION TAG	UNP P53192
D	99	HIS	-	EXPRESSION TAG	UNP P53192
G	35	MET	-	EXPRESSION TAG	UNP P53192
G	94	HIS	-	EXPRESSION TAG	UNP P53192
G	95	HIS	-	EXPRESSION TAG	UNP P53192
G	96	HIS	-	EXPRESSION TAG	UNP P53192
G	97	HIS	-	EXPRESSION TAG	UNP P53192
G	98	HIS	-	EXPRESSION TAG	UNP P53192
G	99	HIS	-	EXPRESSION TAG	UNP P53192
H	35	MET	-	EXPRESSION TAG	UNP P53192
H	94	HIS	-	EXPRESSION TAG	UNP P53192
H	95	HIS	-	EXPRESSION TAG	UNP P53192
H	96	HIS	-	EXPRESSION TAG	UNP P53192
H	97	HIS	-	EXPRESSION TAG	UNP P53192
H	98	HIS	-	EXPRESSION TAG	UNP P53192
H	99	HIS	-	EXPRESSION TAG	UNP P53192
J	35	MET	-	EXPRESSION TAG	UNP P53192
J	94	HIS	-	EXPRESSION TAG	UNP P53192
J	95	HIS	-	EXPRESSION TAG	UNP P53192
J	96	HIS	-	EXPRESSION TAG	UNP P53192
J	97	HIS	-	EXPRESSION TAG	UNP P53192
J	98	HIS	-	EXPRESSION TAG	UNP P53192
J	99	HIS	-	EXPRESSION TAG	UNP P53192

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	I	1	Total Zn 1 1	0	0
3	A	1	Total Zn 1 1	0	0
3	E	1	Total Zn 1 1	0	0

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		
4	B	1	Total	O	P	0	0
			5	4	1		
4	D	1	Total	O	P	0	0
			5	4	1		
4	E	1	Total	O	P	0	0
			5	4	1		
4	F	1	Total	O	P	0	0
			5	4	1		
4	I	1	Total	O	P	0	0
			5	4	1		

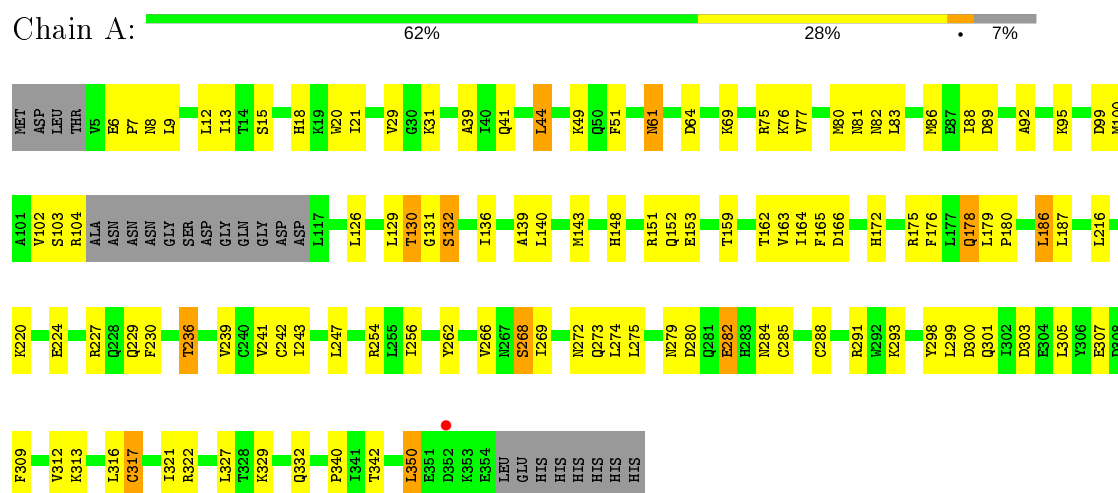
- Molecule 5 is water.

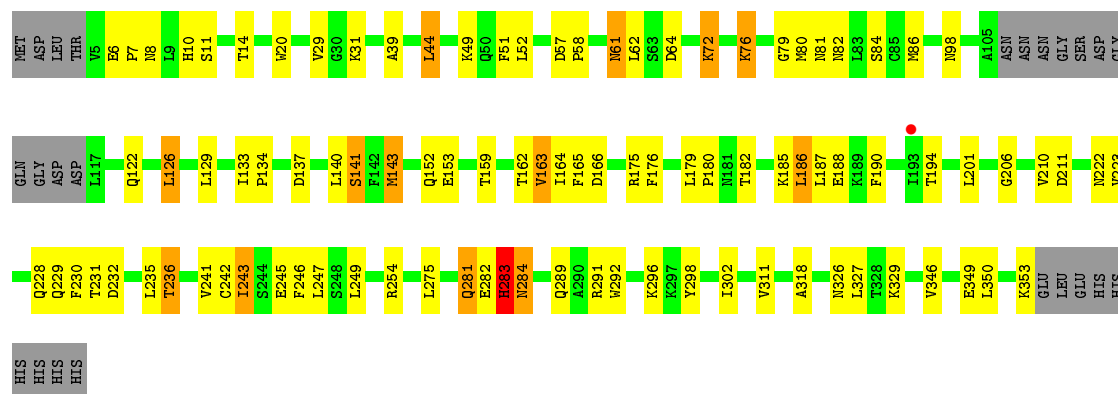
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	O	0	0
			1	1		
5	B	1	Total	O	0	0
			1	1		
5	F	2	Total	O	0	0
			2	2		
5	I	1	Total	O	0	0
			1	1		

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.

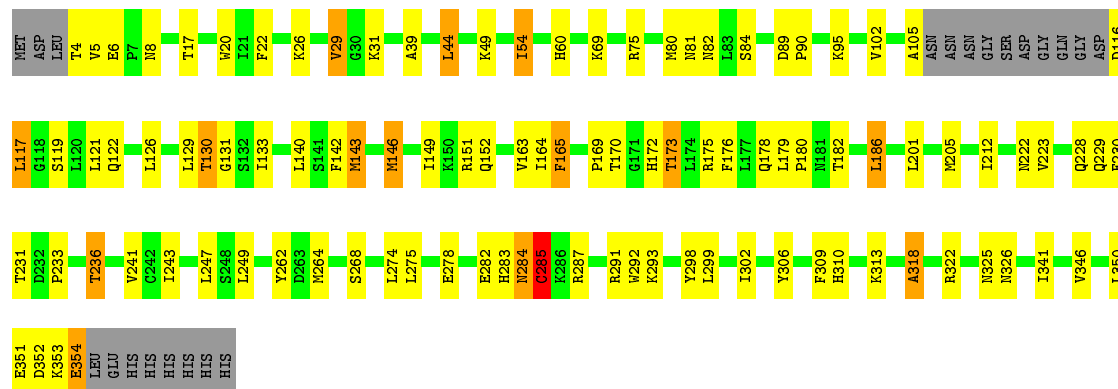
• Molecule 1: ATPase GET3





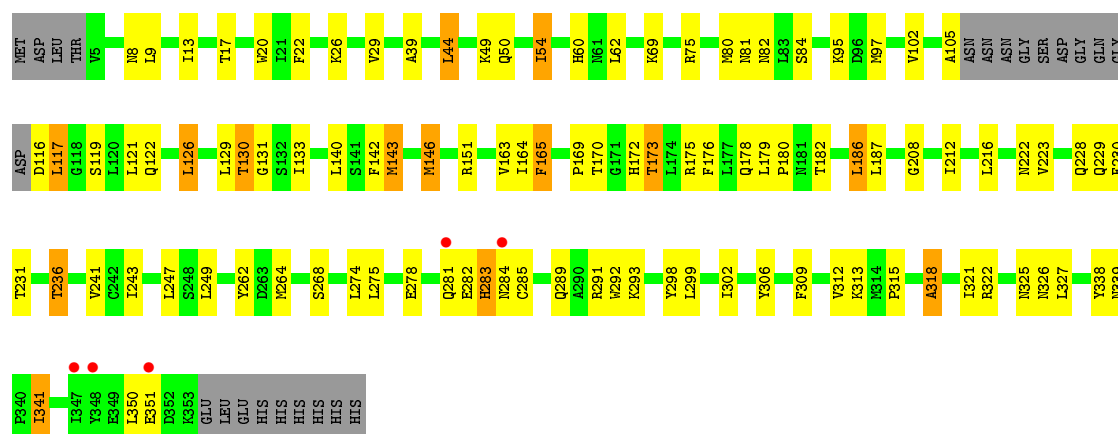
• Molecule 1: ATPase GET3

Chain F: 65% 25% 6%



• Molecule 1: ATPase GET3

Chain I: 65% 25% 6%

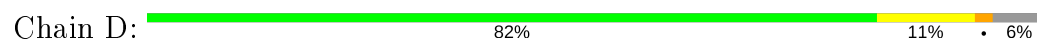


• Molecule 2: Golgi to ER traffic protein 1

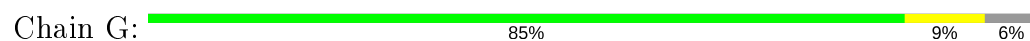
Chain C: 78% 14% 6%



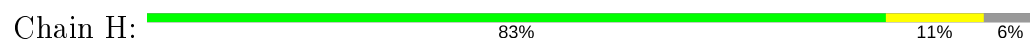
- Molecule 2: Golgi to ER traffic protein 1



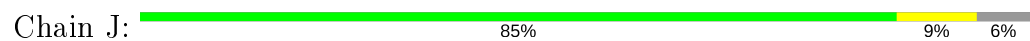
- Molecule 2: Golgi to ER traffic protein 1



- Molecule 2: Golgi to ER traffic protein 1



- Molecule 2: Golgi to ER traffic protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	204.12Å 91.46Å 149.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.30 – 3.00 51.27 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (51.30-3.00) 99.5 (51.27-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.52 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6 _289)	Depositor
R, R_{free}	0.181 , 0.231 0.173 , 0.222	Depositor DCC
R_{free} test set	2857 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	76.6	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 73.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15873	wwPDB-VP
Average B, all atoms (Å ²)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PO4

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	0.44	0/2686	0.61	0/3621
1	B	0.46	0/2706	0.60	0/3649
1	E	0.45	0/2682	0.62	0/3616
1	F	0.40	0/2706	0.56	0/3649
1	I	0.40	0/2690	0.57	0/3627
2	C	0.40	0/522	0.49	0/696
2	D	0.40	0/522	0.48	0/696
2	G	0.39	0/522	0.48	0/696
2	H	0.38	0/522	0.48	0/696
2	J	0.37	0/522	0.50	0/696
All	All	0.43	0/16080	0.58	0/21642

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	B	0	2
1	F	0	1
All	All	0	3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	26	LYS	Peptide

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Mol	Chain	Res	Type	Group
1	B	284	ASN	Peptide
1	F	284	ASN	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	2643	0	2628	81	0
1	B	2663	0	2645	79	0
1	E	2639	0	2627	80	0
1	F	2663	0	2644	67	0
1	I	2647	0	2631	74	0
2	C	515	0	505	4	0
2	D	515	0	505	3	0
2	G	515	0	505	1	0
2	H	515	0	505	2	0
2	J	515	0	505	1	0
3	A	1	0	0	0	0
3	E	1	0	0	0	0
3	I	1	0	0	0	0
4	A	10	0	0	0	0
4	B	5	0	0	0	0
4	D	5	0	0	0	0
4	E	5	0	0	0	0
4	F	5	0	0	1	0
4	I	5	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	F	2	0	0	0	0
5	I	1	0	0	0	0
All	All	15873	0	15700	378	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 378 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:352:ASP:HB3	1:I:69:LYS:HB3	1.36	1.03
1:A:9:LEU:O	1:A:13:ILE:HG13	1.68	0.94
1:A:230:PHE:HA	1:A:236:THR:HG21	1.49	0.93
1:A:239:VAL:HG13	1:A:268:SER:HB2	1.53	0.89
1:I:281:GLN:HA	1:I:283:HIS:ND1	1.87	0.89

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	334/362 (92%)	317 (95%)	16 (5%)	1 (0%)	41	76
1	B	337/362 (93%)	322 (96%)	14 (4%)	1 (0%)	41	76
1	E	334/362 (92%)	321 (96%)	10 (3%)	3 (1%)	17	55
1	F	337/362 (93%)	321 (95%)	12 (4%)	4 (1%)	13	48
1	I	335/362 (92%)	318 (95%)	14 (4%)	3 (1%)	17	55
2	C	59/65 (91%)	56 (95%)	3 (5%)	0	100	100
2	D	59/65 (91%)	57 (97%)	2 (3%)	0	100	100
2	G	59/65 (91%)	57 (97%)	2 (3%)	0	100	100
2	H	59/65 (91%)	58 (98%)	1 (2%)	0	100	100
2	J	59/65 (91%)	56 (95%)	3 (5%)	0	100	100
All	All	1972/2135 (92%)	1883 (96%)	77 (4%)	12 (1%)	25	64

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	285	CYS
1	F	173	THR
1	F	285	CYS

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Mol	Chain	Res	Type
1	F	318	ALA
1	I	173	THR

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	297/317 (94%)	270 (91%)	27 (9%)	9	34
1	B	299/317 (94%)	274 (92%)	25 (8%)	11	38
1	E	296/317 (93%)	272 (92%)	24 (8%)	11	40
1	F	299/317 (94%)	266 (89%)	33 (11%)	6	25
1	I	297/317 (94%)	266 (90%)	31 (10%)	7	27
2	C	58/62 (94%)	54 (93%)	4 (7%)	15	48
2	D	58/62 (94%)	54 (93%)	4 (7%)	15	48
2	G	58/62 (94%)	54 (93%)	4 (7%)	15	48
2	H	58/62 (94%)	55 (95%)	3 (5%)	23	59
2	J	58/62 (94%)	54 (93%)	4 (7%)	15	48
All	All	1778/1895 (94%)	1619 (91%)	159 (9%)	9	35

5 of 159 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	143	MET
1	F	60	HIS
1	I	186	LEU
1	E	182	THR
1	E	283	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	326	ASN

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Mol	Chain	Res	Type
1	F	222	ASN
1	I	289	GLN
1	F	122	GLN
1	F	228	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 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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	PO4	A	365	-	4,4,4	0.95	0	6,6,6	0.98	0
4	PO4	D	7	-	4,4,4	0.96	0	6,6,6	0.66	0
4	PO4	I	364	-	4,4,4	1.00	0	6,6,6	0.54	0
4	PO4	E	364	-	4,4,4	0.98	0	6,6,6	0.83	0
4	PO4	A	364	-	4,4,4	0.92	0	6,6,6	0.61	0
4	PO4	B	363	-	4,4,4	0.76	0	6,6,6	0.91	0
4	PO4	F	363	-	4,4,4	0.81	0	6,6,6	0.65	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	F	363	PO4	1	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	338/362 (93%)	-0.47	1 (0%) 94 84	36, 70, 124, 198	0
1	B	341/362 (94%)	-0.35	2 (0%) 89 72	35, 68, 118, 168	0
1	E	338/362 (93%)	-0.35	1 (0%) 94 84	41, 70, 120, 214	0
1	F	341/362 (94%)	-0.37	0 100 100	41, 75, 117, 154	0
1	I	339/362 (93%)	-0.25	5 (1%) 73 46	43, 76, 126, 249	0
2	C	61/65 (93%)	-0.55	0 100 100	42, 69, 106, 134	0
2	D	61/65 (93%)	-0.41	0 100 100	47, 70, 105, 135	0
2	G	61/65 (93%)	-0.49	0 100 100	46, 71, 108, 137	0
2	H	61/65 (93%)	-0.49	0 100 100	49, 73, 107, 133	0
2	J	61/65 (93%)	-0.37	0 100 100	47, 71, 105, 133	0
All	All	2002/2135 (93%)	-0.37	9 (0%) 92 79	35, 72, 119, 249	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	347	ILE	3.4
1	I	281	GLN	3.2
1	I	348	TYR	3.0
1	I	284	ASN	2.5
1	A	352	ASP	2.4

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, 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	B-factors(Å ²)	Q<0.9
4	PO4	A	365	5/5	0.82	0.31	111,163,169,181	0
4	PO4	B	363	5/5	0.86	0.24	94,120,148,162	0
4	PO4	F	363	5/5	0.86	0.23	117,125,165,167	0
4	PO4	E	364	5/5	0.87	0.26	112,142,147,153	0
4	PO4	I	364	5/5	0.90	0.16	133,136,154,167	0
4	PO4	D	7	5/5	0.92	0.37	121,126,132,137	0
4	PO4	A	364	5/5	0.96	0.23	111,115,127,129	0
3	ZN	I	363	1/1	0.98	0.04	107,107,107,107	1
3	ZN	E	363	1/1	0.99	0.15	82,82,82,82	0
3	ZN	A	363	1/1	0.99	0.15	79,79,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.