



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:11 PM GMT

PDB ID : 5C73
Title : ATP-driven lipid-linked oligosaccharide flippase PglK in outward-occluded conformation
Authors : Perez, C.; Locher, K.P.
Deposited on : 2015-06-24
Resolution : 5.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/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 : unknown
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

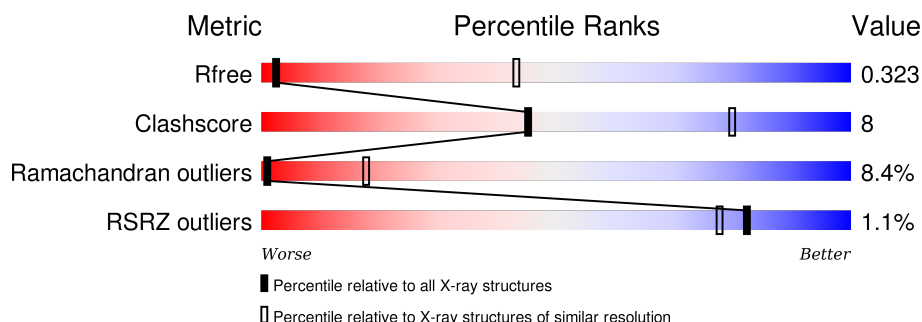
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 5.90 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}	91344	1000 (8.00-3.66)
Clashscore	102246	1048 (8.00-3.70)
Ramachandran outliers	100387	1021 (8.00-3.66)
RSRZ outliers	91569	1015 (8.00-3.64)

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 $\leq 5\%$. 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	564	<div> <div></div> <div>82%15%.</div> </div>
1	B	564	<div> <div></div> <div>82%16%.</div> </div>
1	C	564	<div> <div></div> <div>83%15%.</div> </div>
1	F	564	<div> <div></div> <div>85%14%.</div> </div>
1	G	564	<div> <div></div> <div>82%16%.</div> </div>
1	K	564	<div> <div>3%</div> <div>85%13%.</div> </div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 16752 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 glycosylation K.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	C	564	Total	C	N	O	0	0	0
			2792	1664	564	564			
1	K	564	Total	C	N	O	0	0	0
			2792	1664	564	564			
1	A	564	Total	C	N	O	0	0	0
			2792	1664	564	564			
1	B	564	Total	C	N	O	0	0	0
			2792	1664	564	564			
1	G	564	Total	C	N	O	0	0	0
			2792	1664	564	564			
1	F	564	Total	C	N	O	0	0	0
			2792	1664	564	564			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	2	VAL	LEU	conflict	UNP Q0P9C4
C	27	VAL	ILE	conflict	UNP Q0P9C4
C	105	LYS	TYR	conflict	UNP Q0P9C4
C	202	LEU	VAL	conflict	UNP Q0P9C4
C	325	ASN	ASP	conflict	UNP Q0P9C4
C	341	GLY	GLU	conflict	UNP Q0P9C4
C	410	LYS	GLU	conflict	UNP Q0P9C4
C	416	SER	ASN	conflict	UNP Q0P9C4
C	418	ALA	THR	conflict	UNP Q0P9C4
C	456	LYS	ARG	conflict	UNP Q0P9C4
C	505	ILE	MET	conflict	UNP Q0P9C4
C	510	GLN	GLU	conflict	UNP Q0P9C4
K	2	VAL	LEU	conflict	UNP Q0P9C4
K	27	VAL	ILE	conflict	UNP Q0P9C4
K	105	LYS	TYR	conflict	UNP Q0P9C4
K	202	LEU	VAL	conflict	UNP Q0P9C4
K	325	ASN	ASP	conflict	UNP Q0P9C4

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Chain	Residue	Modelled	Actual	Comment	Reference
K	341	GLY	GLU	conflict	UNP Q0P9C4
K	410	LYS	GLU	conflict	UNP Q0P9C4
K	416	SER	ASN	conflict	UNP Q0P9C4
K	418	ALA	THR	conflict	UNP Q0P9C4
K	456	LYS	ARG	conflict	UNP Q0P9C4
K	505	ILE	MET	conflict	UNP Q0P9C4
K	510	GLN	GLU	conflict	UNP Q0P9C4
A	2	VAL	LEU	conflict	UNP Q0P9C4
A	27	VAL	ILE	conflict	UNP Q0P9C4
A	105	LYS	TYR	conflict	UNP Q0P9C4
A	202	LEU	VAL	conflict	UNP Q0P9C4
A	325	ASN	ASP	conflict	UNP Q0P9C4
A	341	GLY	GLU	conflict	UNP Q0P9C4
A	410	LYS	GLU	conflict	UNP Q0P9C4
A	416	SER	ASN	conflict	UNP Q0P9C4
A	418	ALA	THR	conflict	UNP Q0P9C4
A	456	LYS	ARG	conflict	UNP Q0P9C4
A	505	ILE	MET	conflict	UNP Q0P9C4
A	510	GLN	GLU	conflict	UNP Q0P9C4
B	2	VAL	LEU	conflict	UNP Q0P9C4
B	27	VAL	ILE	conflict	UNP Q0P9C4
B	105	LYS	TYR	conflict	UNP Q0P9C4
B	202	LEU	VAL	conflict	UNP Q0P9C4
B	325	ASN	ASP	conflict	UNP Q0P9C4
B	341	GLY	GLU	conflict	UNP Q0P9C4
B	410	LYS	GLU	conflict	UNP Q0P9C4
B	416	SER	ASN	conflict	UNP Q0P9C4
B	418	ALA	THR	conflict	UNP Q0P9C4
B	456	LYS	ARG	conflict	UNP Q0P9C4
B	505	ILE	MET	conflict	UNP Q0P9C4
B	510	GLN	GLU	conflict	UNP Q0P9C4
G	2	VAL	LEU	conflict	UNP Q0P9C4
G	27	VAL	ILE	conflict	UNP Q0P9C4
G	105	LYS	TYR	conflict	UNP Q0P9C4
G	202	LEU	VAL	conflict	UNP Q0P9C4
G	325	ASN	ASP	conflict	UNP Q0P9C4
G	341	GLY	GLU	conflict	UNP Q0P9C4
G	410	LYS	GLU	conflict	UNP Q0P9C4
G	416	SER	ASN	conflict	UNP Q0P9C4
G	418	ALA	THR	conflict	UNP Q0P9C4
G	456	LYS	ARG	conflict	UNP Q0P9C4
G	505	ILE	MET	conflict	UNP Q0P9C4

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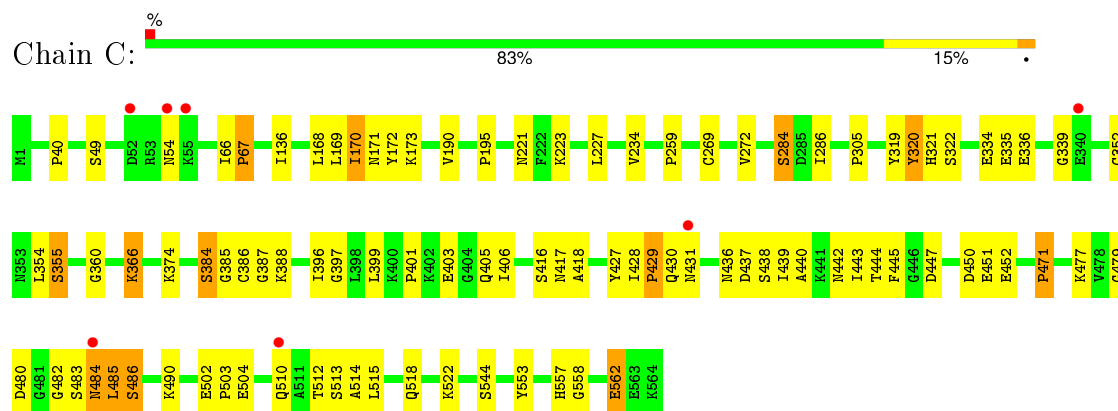
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Chain	Residue	Modelled	Actual	Comment	Reference
G	510	GLN	GLU	conflict	UNP Q0P9C4
F	2	VAL	LEU	conflict	UNP Q0P9C4
F	27	VAL	ILE	conflict	UNP Q0P9C4
F	105	LYS	TYR	conflict	UNP Q0P9C4
F	202	LEU	VAL	conflict	UNP Q0P9C4
F	325	ASN	ASP	conflict	UNP Q0P9C4
F	341	GLY	GLU	conflict	UNP Q0P9C4
F	410	LYS	GLU	conflict	UNP Q0P9C4
F	416	SER	ASN	conflict	UNP Q0P9C4
F	418	ALA	THR	conflict	UNP Q0P9C4
F	456	LYS	ARG	conflict	UNP Q0P9C4
F	505	ILE	MET	conflict	UNP Q0P9C4
F	510	GLN	GLU	conflict	UNP Q0P9C4

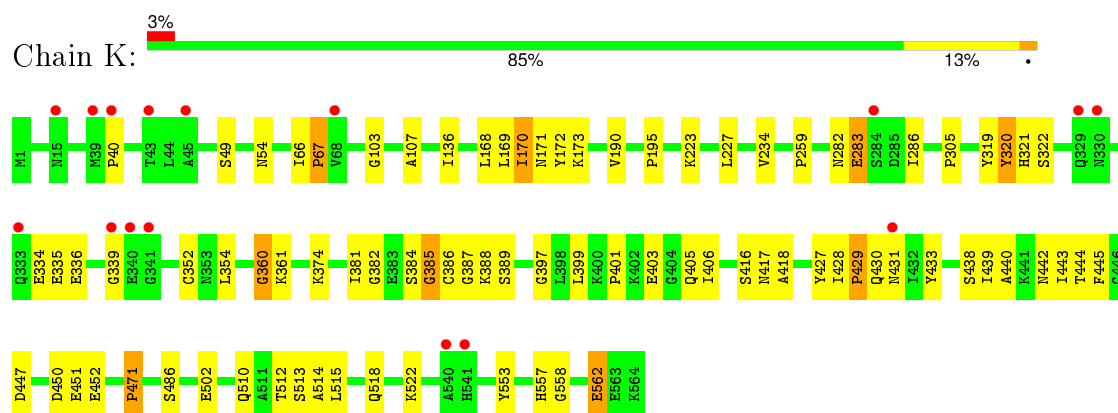
3 Residue-property plots

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.

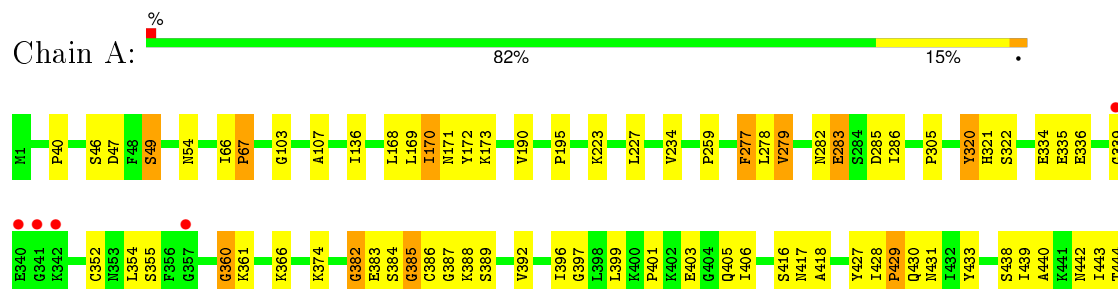
• Molecule 1: Protein glycosylation K



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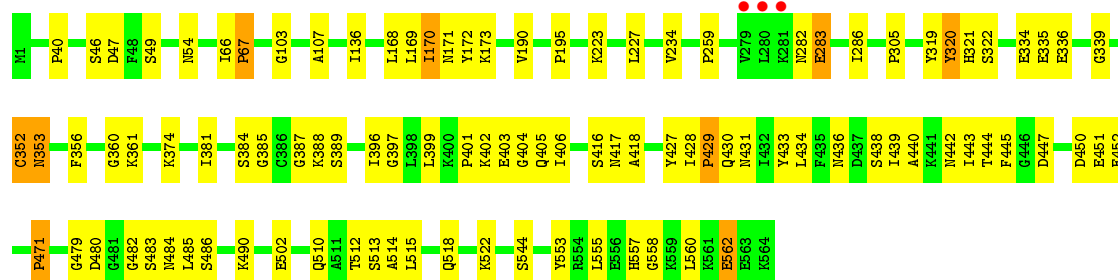
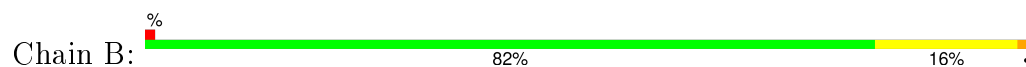


• Molecule 1: Protein glycosylation K

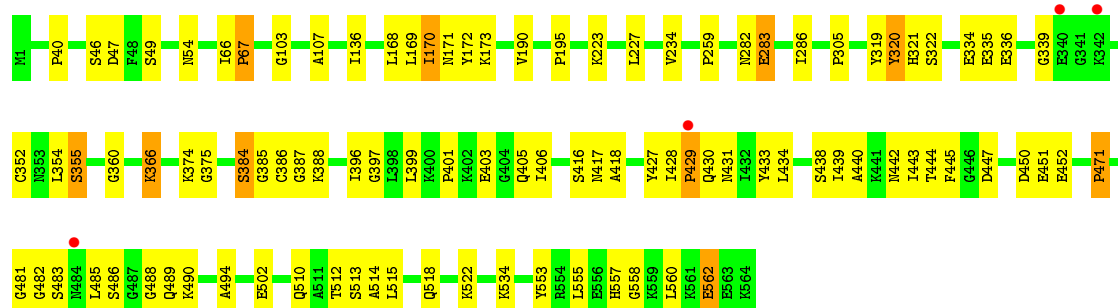
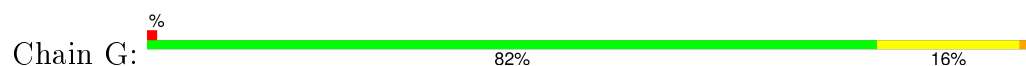




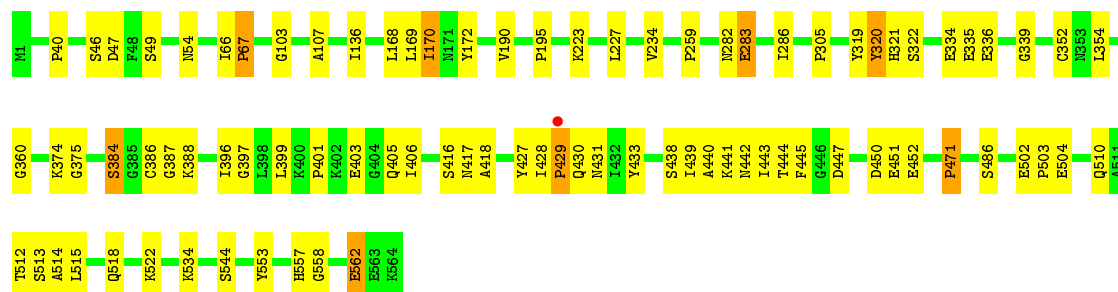
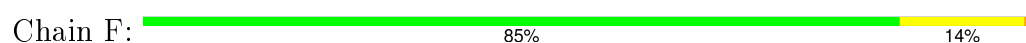
• Molecule 1: Protein glycosylation K



• Molecule 1: Protein glycosylation K



• Molecule 1: Protein glycosylation K



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	200.03Å 200.03Å 693.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.94 – 5.90 29.94 – 5.50	Depositor EDS
% Data completeness (in resolution range)	84.5 (29.94-5.90) 70.7 (29.94-5.50)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 5.67Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.284 , 0.317 0.290 , 0.323	Depositor DCC
R_{free} test set	1622 reflections (5.07%)	DCC
Wilson B-factor (Å ²)	319.2	Xtriage
Anisotropy	0.122	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	1.00 , 2394.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 32880 reflections	Xtriage
F_o, F_c correlation	0.72	EDS
Total number of atoms	16752	wwPDB-VP
Average B, all atoms (Å ²)	368.0	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.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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](#)

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	0/2791	0.49	8/3889 (0.2%)
1	B	0.38	0/2791	0.49	8/3889 (0.2%)
1	C	0.38	0/2791	0.50	8/3889 (0.2%)
1	F	0.39	0/2791	0.51	8/3889 (0.2%)
1	G	0.39	0/2791	0.50	8/3889 (0.2%)
1	K	0.37	0/2791	0.49	8/3889 (0.2%)
All	All	0.38	0/16746	0.50	48/23334 (0.2%)

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	C	0	1

There are no bond length outliers.

All (48) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	305	PRO	N-CA-CB	6.10	110.62	103.30
1	C	305	PRO	N-CA-CB	6.04	110.55	103.30
1	K	305	PRO	N-CA-CB	6.01	110.51	103.30
1	K	40	PRO	N-CA-CB	5.99	110.48	103.30
1	B	401	PRO	N-CA-CB	5.96	110.45	103.30
1	F	305	PRO	N-CA-CB	5.95	110.43	103.30
1	C	471	PRO	N-CA-CB	5.94	110.43	103.30
1	K	401	PRO	N-CA-CB	5.94	110.42	103.30
1	A	471	PRO	N-CA-CB	5.93	110.42	103.30
1	B	471	PRO	N-CA-CB	5.92	110.41	103.30
1	F	471	PRO	N-CA-CB	5.90	110.38	103.30
1	G	471	PRO	N-CA-CB	5.90	110.38	103.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	40	PRO	N-CA-CB	5.89	110.37	103.30
1	G	305	PRO	N-CA-CB	5.89	110.37	103.30
1	B	305	PRO	N-CA-CB	5.87	110.34	103.30
1	C	401	PRO	N-CA-CB	5.85	110.32	103.30
1	G	401	PRO	N-CA-CB	5.85	110.32	103.30
1	A	401	PRO	N-CA-CB	5.84	110.31	103.30
1	K	471	PRO	N-CA-CB	5.78	110.23	103.30
1	C	40	PRO	N-CA-CB	5.73	110.17	103.30
1	G	40	PRO	N-CA-CB	5.72	110.16	103.30
1	B	40	PRO	N-CA-CB	5.70	110.14	103.30
1	F	401	PRO	N-CA-CB	5.69	110.13	103.30
1	A	40	PRO	N-CA-CB	5.68	110.12	103.30
1	B	259	PRO	N-CA-CB	5.55	109.96	103.30
1	K	67	PRO	N-CA-CB	5.54	109.95	103.30
1	C	67	PRO	N-CA-CB	5.52	109.93	103.30
1	G	67	PRO	N-CA-CB	5.51	109.92	103.30
1	A	67	PRO	N-CA-CB	5.50	109.91	103.30
1	F	195	PRO	N-CA-CB	5.46	109.85	103.30
1	B	67	PRO	N-CA-CB	5.44	109.83	103.30
1	F	67	PRO	N-CA-CB	5.44	109.83	103.30
1	K	259	PRO	N-CA-CB	5.43	109.81	103.30
1	C	429	PRO	N-CA-CB	5.37	109.75	103.30
1	G	429	PRO	N-CA-CB	5.33	109.70	103.30
1	K	429	PRO	N-CA-CB	5.32	109.69	103.30
1	C	259	PRO	N-CA-CB	5.32	109.68	103.30
1	B	429	PRO	N-CA-CB	5.30	109.67	103.30
1	A	429	PRO	N-CA-CB	5.30	109.66	103.30
1	F	429	PRO	N-CA-CB	5.29	109.65	103.30
1	B	195	PRO	N-CA-CB	5.29	109.65	103.30
1	K	195	PRO	N-CA-CB	5.29	109.64	103.30
1	F	259	PRO	N-CA-CB	5.27	109.63	103.30
1	C	195	PRO	N-CA-CB	5.23	109.58	103.30
1	G	259	PRO	N-CA-CB	5.22	109.56	103.30
1	A	195	PRO	N-CA-CB	5.14	109.47	103.30
1	G	195	PRO	N-CA-CB	5.14	109.47	103.30
1	A	259	PRO	N-CA-CB	5.11	109.43	103.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	284	SER	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	2792	0	1242	34	0
1	B	2792	0	1242	36	0
1	C	2792	0	1242	36	0
1	F	2792	0	1242	24	0
1	G	2792	0	1242	35	0
1	K	2792	0	1242	25	0
All	All	16752	0	7452	188	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 8.

All (188) 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:G:434:LEU:CB	1:G:481:GLY:HA2	1.79	1.13
1:C:486:SER:O	1:C:490:LYS:CB	2.07	1.01
1:B:356:PHE:HA	1:B:402:LYS:CB	1.97	0.94
1:C:482:GLY:HA2	1:C:483:SER:O	1.76	0.86
1:C:486:SER:O	1:C:490:LYS:N	2.14	0.81
1:B:436:ASN:HA	1:B:479:GLY:O	1.83	0.78
1:B:360:GLY:HA2	1:B:361:LYS:CB	2.16	0.76
1:F:169:LEU:N	1:F:170:ILE:O	2.20	0.75
1:G:169:LEU:N	1:G:170:ILE:O	2.19	0.75
1:K:169:LEU:N	1:K:170:ILE:O	2.20	0.75
1:A:169:LEU:N	1:A:170:ILE:O	2.20	0.74
1:A:485:LEU:HA	1:A:489:GLN:CB	2.16	0.74
1:B:384:SER:HA	1:B:388:LYS:CB	2.17	0.74
1:C:169:LEU:N	1:C:170:ILE:O	2.20	0.74
1:B:169:LEU:N	1:B:170:ILE:O	2.21	0.73
1:C:269:CYS:O	1:C:272:VAL:N	2.23	0.72
1:K:385:GLY:H	1:K:389:SER:CB	2.03	0.71
1:G:485:LEU:HA	1:G:489:GLN:CB	2.22	0.69
1:B:482:GLY:HA2	1:B:483:SER:C	2.12	0.69
1:A:384:SER:O	1:A:386:CYS:N	2.25	0.69
1:A:482:GLY:H	1:A:483:SER:CB	2.05	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:438:SER:O	1:G:440:ALA:N	2.26	0.69
1:B:450:ASP:O	1:B:452:GLU:N	2.27	0.68
1:G:482:GLY:HA2	1:G:483:SER:C	2.12	0.68
1:K:450:ASP:O	1:K:452:GLU:N	2.27	0.68
1:A:438:SER:O	1:A:440:ALA:N	2.26	0.68
1:G:450:ASP:O	1:G:452:GLU:N	2.27	0.68
1:B:438:SER:O	1:B:440:ALA:N	2.27	0.68
1:G:320:TYR:O	1:G:322:SER:N	2.27	0.67
1:A:450:ASP:O	1:A:452:GLU:N	2.28	0.67
1:C:450:ASP:O	1:C:452:GLU:N	2.27	0.67
1:C:438:SER:O	1:C:440:ALA:N	2.28	0.66
1:A:277:PHE:O	1:A:279:VAL:N	2.28	0.66
1:K:438:SER:O	1:K:440:ALA:N	2.27	0.66
1:F:450:ASP:O	1:F:452:GLU:N	2.28	0.66
1:B:486:SER:O	1:B:490:LYS:N	2.25	0.66
1:K:429:PRO:O	1:K:431:ASN:N	2.29	0.66
1:A:429:PRO:O	1:A:431:ASN:N	2.30	0.65
1:G:429:PRO:O	1:G:431:ASN:N	2.30	0.65
1:F:438:SER:O	1:F:440:ALA:N	2.30	0.65
1:B:429:PRO:O	1:B:431:ASN:N	2.30	0.65
1:C:429:PRO:O	1:C:431:ASN:N	2.29	0.65
1:F:429:PRO:O	1:F:431:ASN:N	2.30	0.64
1:G:490:LYS:O	1:G:494:ALA:HB2	1.96	0.64
1:F:320:TYR:O	1:F:322:SER:N	2.31	0.64
1:C:442:ASN:O	1:C:444:THR:N	2.32	0.63
1:C:320:TYR:O	1:C:322:SER:N	2.31	0.63
1:A:320:TYR:O	1:A:322:SER:N	2.32	0.62
1:B:320:TYR:O	1:B:322:SER:N	2.32	0.62
1:F:442:ASN:O	1:F:444:THR:N	2.32	0.62
1:A:442:ASN:O	1:A:444:THR:N	2.31	0.62
1:B:334:GLU:O	1:B:336:GLU:N	2.33	0.62
1:B:442:ASN:O	1:B:444:THR:N	2.32	0.62
1:G:282:ASN:HA	1:G:283:GLU:O	1.99	0.62
1:K:334:GLU:O	1:K:336:GLU:N	2.34	0.61
1:K:320:TYR:O	1:K:322:SER:N	2.33	0.61
1:G:490:LYS:O	1:G:494:ALA:CB	2.48	0.61
1:K:442:ASN:O	1:K:444:THR:N	2.34	0.61
1:B:486:SER:O	1:B:490:LYS:CB	2.49	0.61
1:G:442:ASN:O	1:G:444:THR:N	2.33	0.60
1:B:282:ASN:HA	1:B:283:GLU:O	2.01	0.60
1:A:382:GLY:HA2	1:A:555:LEU:H	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:513:SER:O	1:F:515:LEU:N	2.34	0.59
1:C:334:GLU:O	1:C:336:GLU:N	2.35	0.59
1:A:482:GLY:HA2	1:A:483:SER:C	2.22	0.59
1:B:352:CYS:O	1:B:353:ASN:O	2.20	0.59
1:G:334:GLU:O	1:G:336:GLU:N	2.36	0.59
1:C:485:LEU:O	1:C:490:LYS:CB	2.52	0.58
1:C:484:ASN:O	1:C:486:SER:N	2.30	0.58
1:F:334:GLU:O	1:F:336:GLU:N	2.36	0.58
1:A:392:VAL:O	1:A:396:ILE:N	2.36	0.57
1:C:384:SER:H	1:C:388:LYS:H	1.51	0.57
1:B:513:SER:O	1:B:515:LEU:N	2.37	0.57
1:A:334:GLU:O	1:A:336:GLU:N	2.36	0.57
1:C:513:SER:O	1:C:515:LEU:N	2.38	0.57
1:K:384:SER:O	1:K:386:CYS:N	2.35	0.57
1:C:486:SER:O	1:C:490:LYS:CA	2.53	0.57
1:F:282:ASN:HA	1:F:283:GLU:O	2.04	0.56
1:G:513:SER:O	1:G:515:LEU:N	2.39	0.56
1:K:513:SER:O	1:K:515:LEU:N	2.39	0.56
1:B:484:ASN:O	1:B:486:SER:N	2.40	0.55
1:G:384:SER:H	1:G:388:LYS:H	1.55	0.55
1:K:384:SER:HA	1:K:388:LYS:CB	2.37	0.54
1:C:482:GLY:CA	1:C:483:SER:CB	2.86	0.54
1:K:360:GLY:CA	1:K:361:LYS:CB	2.86	0.54
1:B:385:GLY:H	1:B:389:SER:CB	2.20	0.54
1:F:384:SER:H	1:F:388:LYS:H	1.55	0.54
1:A:513:SER:O	1:A:515:LEU:N	2.41	0.53
1:C:484:ASN:C	1:C:486:SER:H	2.12	0.53
1:G:434:LEU:CB	1:G:481:GLY:CA	2.72	0.53
1:B:360:GLY:CA	1:B:361:LYS:CB	2.86	0.52
1:G:385:GLY:HA3	1:F:486:SER:CB	2.38	0.52
1:C:482:GLY:N	1:C:483:SER:CB	2.73	0.51
1:C:482:GLY:HA2	1:C:483:SER:C	2.29	0.51
1:B:384:SER:CA	1:B:388:LYS:CB	2.88	0.51
1:K:360:GLY:N	1:K:361:LYS:CB	2.73	0.51
1:C:170:ILE:O	1:C:172:TYR:N	2.39	0.50
1:C:436:ASN:CB	1:C:479:GLY:O	2.59	0.50
1:B:384:SER:HA	1:B:389:SER:H	1.76	0.50
1:G:170:ILE:O	1:G:172:TYR:N	2.37	0.50
1:G:384:SER:C	1:G:386:CYS:H	2.15	0.49
1:G:518:GLN:O	1:G:522:LYS:N	2.46	0.49
1:F:170:ILE:O	1:F:172:TYR:N	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:LYS:O	1:A:227:LEU:N	2.46	0.49
1:A:482:GLY:N	1:A:483:SER:CB	2.73	0.49
1:G:486:SER:O	1:G:490:LYS:N	2.46	0.49
1:G:486:SER:N	1:G:490:LYS:H	2.11	0.49
1:F:223:LYS:O	1:F:227:LEU:N	2.46	0.49
1:K:282:ASN:HA	1:K:283:GLU:O	2.13	0.48
1:K:416:SER:C	1:K:418:ALA:H	2.16	0.48
1:A:282:ASN:HA	1:A:283:GLU:O	2.14	0.48
1:B:518:GLN:O	1:B:522:LYS:N	2.47	0.48
1:B:434:LEU:O	1:B:480:ASP:O	2.31	0.48
1:C:518:GLN:O	1:C:522:LYS:N	2.46	0.48
1:F:416:SER:C	1:F:418:ALA:H	2.15	0.48
1:A:355:SER:HA	1:A:366:LYS:H	1.78	0.48
1:A:518:GLN:O	1:A:522:LYS:N	2.46	0.48
1:A:384:SER:HA	1:A:388:LYS:CB	2.44	0.48
1:K:518:GLN:O	1:K:522:LYS:N	2.47	0.48
1:A:482:GLY:CA	1:A:483:SER:CB	2.92	0.47
1:A:46:SER:HA	1:A:47:ASP:HA	1.64	0.47
1:B:46:SER:HA	1:B:47:ASP:HA	1.59	0.47
1:A:170:ILE:O	1:A:172:TYR:N	2.38	0.47
1:G:46:SER:HA	1:G:47:ASP:HA	1.59	0.47
1:B:436:ASN:CA	1:B:479:GLY:O	2.59	0.47
1:F:518:GLN:O	1:F:522:LYS:N	2.48	0.47
1:B:416:SER:C	1:B:418:ALA:H	2.17	0.47
1:G:557:HIS:HA	1:G:558:GLY:HA2	1.57	0.47
1:B:171:ASN:O	1:B:173:LYS:N	2.46	0.47
1:F:557:HIS:HA	1:F:558:GLY:HA2	1.56	0.47
1:B:353:ASN:O	1:B:404:GLY:HA2	2.14	0.47
1:G:416:SER:C	1:G:418:ALA:H	2.19	0.47
1:A:416:SER:C	1:A:418:ALA:H	2.19	0.47
1:G:171:ASN:O	1:G:173:LYS:N	2.46	0.46
1:B:170:ILE:O	1:B:172:TYR:N	2.38	0.46
1:C:416:SER:C	1:C:418:ALA:H	2.18	0.46
1:C:384:SER:C	1:C:386:CYS:H	2.17	0.46
1:K:557:HIS:HA	1:K:558:GLY:HA2	1.58	0.46
1:C:223:LYS:O	1:C:227:LEU:N	2.48	0.46
1:K:223:LYS:O	1:K:227:LEU:N	2.49	0.46
1:G:169:LEU:H	1:G:170:ILE:C	2.19	0.46
1:F:384:SER:C	1:F:386:CYS:H	2.18	0.46
1:B:223:LYS:O	1:B:227:LEU:N	2.49	0.45
1:C:385:GLY:HA3	1:K:486:SER:CB	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:171:ASN:O	1:A:173:LYS:N	2.48	0.45
1:A:360:GLY:CA	1:A:361:LYS:CB	2.94	0.45
1:K:170:ILE:O	1:K:172:TYR:N	2.38	0.45
1:B:557:HIS:HA	1:B:558:GLY:HA2	1.56	0.45
1:C:553:TYR:HA	1:C:562:GLU:HA	1.99	0.44
1:C:169:LEU:H	1:C:170:ILE:C	2.21	0.44
1:C:355:SER:HA	1:C:366:LYS:H	1.83	0.44
1:B:103:GLY:O	1:B:107:ALA:N	2.51	0.44
1:K:553:TYR:HA	1:K:562:GLU:HA	1.99	0.44
1:A:169:LEU:H	1:A:170:ILE:C	2.21	0.44
1:B:553:TYR:HA	1:B:562:GLU:HA	2.00	0.44
1:G:355:SER:HA	1:G:366:LYS:H	1.82	0.43
1:F:169:LEU:H	1:F:170:ILE:C	2.21	0.43
1:C:557:HIS:HA	1:C:558:GLY:HA2	1.57	0.43
1:K:169:LEU:H	1:K:170:ILE:C	2.21	0.43
1:K:103:GLY:O	1:K:107:ALA:N	2.52	0.43
1:C:171:ASN:O	1:C:173:LYS:N	2.47	0.42
1:F:553:TYR:HA	1:F:562:GLU:HA	2.01	0.42
1:G:553:TYR:HA	1:G:562:GLU:HA	2.00	0.42
1:F:46:SER:HA	1:F:47:ASP:HA	1.58	0.42
1:F:103:GLY:O	1:F:107:ALA:N	2.52	0.42
1:A:103:GLY:O	1:A:107:ALA:N	2.53	0.42
1:G:375:GLY:HA2	1:G:534:LYS:O	2.20	0.42
1:C:483:SER:C	1:C:485:LEU:N	2.73	0.42
1:A:385:GLY:HA2	1:A:389:SER:CB	2.49	0.42
1:A:553:TYR:HA	1:A:562:GLU:HA	2.02	0.42
1:K:171:ASN:O	1:K:173:LYS:N	2.47	0.42
1:B:169:LEU:H	1:B:170:ILE:C	2.22	0.42
1:K:385:GLY:N	1:K:389:SER:CB	2.79	0.42
1:A:557:HIS:HA	1:A:558:GLY:HA2	1.57	0.42
1:F:441:LYS:HA	1:F:442:ASN:HA	1.85	0.42
1:G:223:LYS:O	1:G:227:LEU:N	2.52	0.42
1:G:103:GLY:O	1:G:107:ALA:N	2.54	0.41
1:G:486:SER:C	1:G:488:GLY:N	2.73	0.41
1:A:47:ASP:C	1:A:49:SER:H	2.24	0.41
1:B:555:LEU:HA	1:B:560:LEU:HA	2.03	0.41
1:C:221:ASN:C	1:C:223:LYS:H	2.23	0.41
1:G:555:LEU:HA	1:G:560:LEU:HA	2.02	0.41
1:F:503:PRO:HA	1:F:504:GLU:HA	1.91	0.41
1:A:170:ILE:C	1:A:172:TYR:H	2.23	0.40
1:C:503:PRO:HA	1:C:504:GLU:HA	1.90	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:483:SER:O	1:C:485:LEU:N	2.54	0.40
1:G:486:SER:O	1:G:488:GLY:N	2.54	0.40
1:F:375:GLY:HA2	1:F:534:LYS:O	2.22	0.40

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	562/564 (100%)	423 (75%)	89 (16%)	50 (9%)	1	17
1	B	562/564 (100%)	421 (75%)	96 (17%)	45 (8%)	1	19
1	C	562/564 (100%)	424 (75%)	86 (15%)	52 (9%)	1	16
1	F	562/564 (100%)	425 (76%)	92 (16%)	45 (8%)	1	19
1	G	562/564 (100%)	427 (76%)	89 (16%)	46 (8%)	1	18
1	K	562/564 (100%)	424 (75%)	93 (16%)	45 (8%)	1	19
All	All	3372/3384 (100%)	2544 (75%)	545 (16%)	283 (8%)	1	18

All (283) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	66	ILE
1	C	67	PRO
1	C	284	SER
1	C	321	HIS
1	C	335	GLU
1	C	354	LEU
1	C	396	ILE
1	C	430	GLN
1	C	443	ILE

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Mol	Chain	Res	Type
1	C	451	GLU
1	C	480	ASP
1	C	502	GLU
1	C	514	ALA
1	K	66	ILE
1	K	67	PRO
1	K	335	GLU
1	K	430	GLN
1	K	443	ILE
1	K	451	GLU
1	K	502	GLU
1	K	514	ALA
1	A	66	ILE
1	A	67	PRO
1	A	278	LEU
1	A	279	VAL
1	A	335	GLU
1	A	430	GLN
1	A	443	ILE
1	A	451	GLU
1	A	502	GLU
1	A	514	ALA
1	B	66	ILE
1	B	67	PRO
1	B	335	GLU
1	B	353	ASN
1	B	396	ILE
1	B	430	GLN
1	B	443	ILE
1	B	451	GLU
1	B	485	LEU
1	B	502	GLU
1	B	514	ALA
1	G	66	ILE
1	G	67	PRO
1	G	335	GLU
1	G	396	ILE
1	G	430	GLN
1	G	443	ILE
1	G	451	GLU
1	G	502	GLU
1	G	514	ALA

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Mol	Chain	Res	Type
1	F	66	ILE
1	F	67	PRO
1	F	321	HIS
1	F	335	GLU
1	F	354	LEU
1	F	396	ILE
1	F	430	GLN
1	F	443	ILE
1	F	451	GLU
1	F	502	GLU
1	F	514	ALA
1	C	170	ILE
1	C	286	ILE
1	C	320	TYR
1	C	384	SER
1	C	437	ASP
1	C	439	ILE
1	C	447	ASP
1	C	485	LEU
1	C	510	GLN
1	K	170	ILE
1	K	286	ILE
1	K	320	TYR
1	K	321	HIS
1	K	382	GLY
1	K	403	GLU
1	K	433	TYR
1	K	439	ILE
1	K	447	ASP
1	K	510	GLN
1	A	49	SER
1	A	170	ILE
1	A	277	PHE
1	A	286	ILE
1	A	320	TYR
1	A	321	HIS
1	A	354	LEU
1	A	385	GLY
1	A	433	TYR
1	A	439	ILE
1	A	447	ASP
1	A	480	ASP

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Mol	Chain	Res	Type
1	A	510	GLN
1	B	49	SER
1	B	170	ILE
1	B	283	GLU
1	B	286	ILE
1	B	320	TYR
1	B	321	HIS
1	B	439	ILE
1	B	447	ASP
1	B	510	GLN
1	G	170	ILE
1	G	283	GLU
1	G	286	ILE
1	G	320	TYR
1	G	321	HIS
1	G	354	LEU
1	G	384	SER
1	G	433	TYR
1	G	439	ILE
1	G	447	ASP
1	G	510	GLN
1	F	49	SER
1	F	170	ILE
1	F	286	ILE
1	F	320	TYR
1	F	384	SER
1	F	433	TYR
1	F	439	ILE
1	F	447	ASP
1	F	510	GLN
1	F	512	THR
1	C	49	SER
1	C	54	ASN
1	C	352	CYS
1	C	374	LYS
1	C	403	GLU
1	C	406	ILE
1	C	512	THR
1	K	49	SER
1	K	54	ASN
1	K	283	GLU
1	K	352	CYS

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Mol	Chain	Res	Type
1	K	354	LEU
1	K	406	ILE
1	K	512	THR
1	A	54	ASN
1	A	283	GLU
1	A	285	ASP
1	A	360	GLY
1	A	403	GLU
1	A	406	ILE
1	A	512	THR
1	B	54	ASN
1	B	403	GLU
1	B	406	ILE
1	B	512	THR
1	G	49	SER
1	G	54	ASN
1	G	403	GLU
1	G	406	ILE
1	G	512	THR
1	F	54	ASN
1	F	283	GLU
1	F	352	CYS
1	F	403	GLU
1	F	406	ILE
1	C	168	LEU
1	C	417	ASN
1	C	445	PHE
1	C	471	PRO
1	C	477	LYS
1	C	486	SER
1	C	562	GLU
1	K	168	LEU
1	K	360	GLY
1	K	417	ASN
1	K	445	PHE
1	K	471	PRO
1	A	168	LEU
1	A	352	CYS
1	A	399	LEU
1	A	405	GLN
1	A	417	ASN
1	A	445	PHE

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Mol	Chain	Res	Type
1	A	471	PRO
1	A	481	GLY
1	A	562	GLU
1	B	168	LEU
1	B	352	CYS
1	B	417	ASN
1	B	433	TYR
1	B	445	PHE
1	B	471	PRO
1	G	168	LEU
1	G	352	CYS
1	G	355	SER
1	G	366	LYS
1	G	417	ASN
1	G	445	PHE
1	G	471	PRO
1	F	168	LEU
1	F	399	LEU
1	F	417	ASN
1	F	445	PHE
1	F	471	PRO
1	F	562	GLU
1	C	136	ILE
1	C	319	TYR
1	C	355	SER
1	C	366	LYS
1	C	399	LEU
1	C	405	GLN
1	C	427	TYR
1	C	544	SER
1	K	136	ILE
1	K	319	TYR
1	K	374	LYS
1	K	399	LEU
1	K	405	GLN
1	K	427	TYR
1	K	562	GLU
1	A	374	LYS
1	A	383	GLU
1	A	427	TYR
1	B	136	ILE
1	B	374	LYS

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Mol	Chain	Res	Type
1	B	399	LEU
1	B	405	GLN
1	B	427	TYR
1	B	544	SER
1	B	562	GLU
1	G	136	ILE
1	G	374	LYS
1	G	399	LEU
1	G	405	GLN
1	G	427	TYR
1	F	319	TYR
1	F	360	GLY
1	F	374	LYS
1	F	405	GLN
1	F	427	TYR
1	F	544	SER
1	C	428	ILE
1	C	484	ASN
1	K	385	GLY
1	K	397	GLY
1	K	428	ILE
1	A	136	ILE
1	A	382	GLY
1	A	428	ILE
1	B	319	TYR
1	B	428	ILE
1	G	319	TYR
1	G	360	GLY
1	G	387	GLY
1	G	428	ILE
1	G	562	GLU
1	F	136	ILE
1	F	387	GLY
1	F	428	ILE
1	C	339	GLY
1	C	360	GLY
1	C	387	GLY
1	K	339	GLY
1	A	234	VAL
1	A	339	GLY
1	B	234	VAL
1	B	339	GLY

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Mol	Chain	Res	Type
1	G	234	VAL
1	G	339	GLY
1	F	339	GLY
1	C	397	GLY
1	K	190	VAL
1	K	234	VAL
1	K	381	ILE
1	A	190	VAL
1	A	397	GLY
1	B	190	VAL
1	G	397	GLY
1	F	190	VAL
1	F	234	VAL
1	F	397	GLY
1	C	190	VAL
1	C	234	VAL
1	A	387	GLY
1	B	387	GLY
1	B	397	GLY
1	G	190	VAL
1	B	381	ILE
1	K	387	GLY

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	564/564 (100%)	-0.76	6 (1%)	82	78	116, 317, 563, 807	0
1	B	564/564 (100%)	-0.77	3 (0%)	91	88	122, 325, 612, 815	0
1	C	564/564 (100%)	-0.59	7 (1%)	81	75	149, 400, 655, 817	0
1	F	564/564 (100%)	-0.83	1 (0%)	95	94	157, 328, 571, 841	0
1	G	564/564 (100%)	-0.74	4 (0%)	89	85	143, 309, 602, 820	0
1	K	564/564 (100%)	-0.55	16 (2%)	56	52	176, 393, 663, 826	0
All	All	3384/3384 (100%)	-0.71	37 (1%)	82	78	116, 342, 622, 841	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	340	GLU	7.8
1	A	340	GLU	5.1
1	A	341	GLY	5.0
1	B	280	LEU	4.7
1	C	340	GLU	3.8
1	C	54	ASN	3.4
1	A	357	GLY	3.3
1	K	339	GLY	3.2
1	C	431	ASN	3.1
1	K	431	ASN	3.0
1	K	541	HIS	3.0
1	K	68	VAL	2.9
1	C	484	ASN	2.8
1	C	510	GLN	2.8
1	A	541	HIS	2.8
1	G	342	LYS	2.8
1	B	281	LYS	2.7
1	G	340	GLU	2.7
1	K	43	THR	2.6

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Mol	Chain	Res	Type	RSRZ
1	K	39	MET	2.6
1	C	55	LYS	2.6
1	G	429	PRO	2.6
1	K	540	ALA	2.5
1	K	15	ASN	2.5
1	K	341	GLY	2.4
1	K	284	SER	2.4
1	A	339	GLY	2.4
1	F	429	PRO	2.4
1	K	330	ASN	2.3
1	C	52	ASP	2.3
1	K	40	PRO	2.3
1	G	484	ASN	2.2
1	B	279	VAL	2.2
1	A	342	LYS	2.1
1	K	329	GLN	2.1
1	K	45	ALA	2.0
1	K	333	GLN	2.0

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 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.