



Full wwPDB X-ray Structure Validation Report ⓘ

May 31, 2021 – 02:07 PM JST

PDB ID : 7D5Q
Title : Structure of NorC transporter (K398A mutant) in an outward-open conformation in complex with a single-chain Indian camelid antibody
Authors : Kumar, S.; Athreya, A.; Penmatsa, A.
Deposited on : 2020-09-27
Resolution : 3.60 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

<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 : 2.19
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) : 2.19

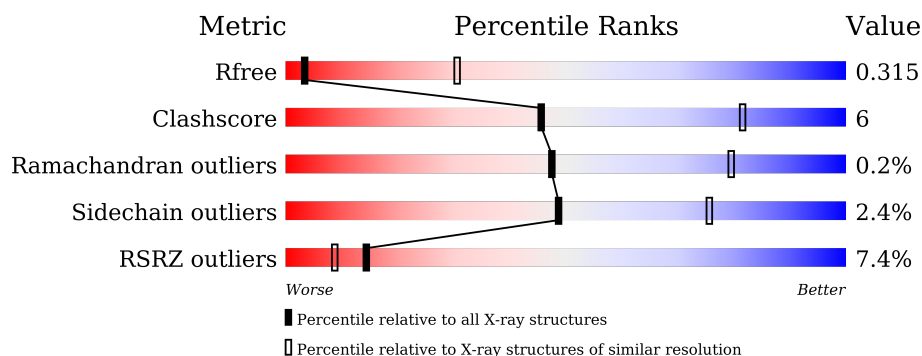
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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	1257 (3.70-3.50)
Clashscore	141614	1353 (3.70-3.50)
Ramachandran outliers	138981	1307 (3.70-3.50)
Sidechain outliers	138945	1307 (3.70-3.50)
RSRZ outliers	127900	1161 (3.70-3.50)

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	479	<div> <div>8%</div> <div>70% 13% 16%</div> </div>
1	B	479	<div> <div>5%</div> <div>73% 13% 14%</div> </div>
2	C	131	<div> <div>2%</div> <div>96% .</div> </div>
2	D	131	<div> <div>11%</div> <div>97% .</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7489 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 Drug transporter, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	403	Total	C	N	O	S	0	0	0
			2775	1825	441	490	19			
1	B	411	Total	C	N	O	S	0	0	0
			2808	1845	447	498	18			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	398	ALA	LYS	engineered mutation	UNP A0A0H2WZS4
A	463	GLY	-	expression tag	UNP A0A0H2WZS4
A	464	THR	-	expression tag	UNP A0A0H2WZS4
A	465	LEU	-	expression tag	UNP A0A0H2WZS4
A	466	VAL	-	expression tag	UNP A0A0H2WZS4
A	467	PRO	-	expression tag	UNP A0A0H2WZS4
A	468	ARG	-	expression tag	UNP A0A0H2WZS4
A	469	GLY	-	expression tag	UNP A0A0H2WZS4
A	470	SER	-	expression tag	UNP A0A0H2WZS4
A	471	GLY	-	expression tag	UNP A0A0H2WZS4
A	472	HIS	-	expression tag	UNP A0A0H2WZS4
A	473	HIS	-	expression tag	UNP A0A0H2WZS4
A	474	HIS	-	expression tag	UNP A0A0H2WZS4
A	475	HIS	-	expression tag	UNP A0A0H2WZS4
A	476	HIS	-	expression tag	UNP A0A0H2WZS4
A	477	HIS	-	expression tag	UNP A0A0H2WZS4
A	478	HIS	-	expression tag	UNP A0A0H2WZS4
A	479	HIS	-	expression tag	UNP A0A0H2WZS4
B	398	ALA	LYS	engineered mutation	UNP A0A0H2WZS4
B	463	GLY	-	expression tag	UNP A0A0H2WZS4
B	464	THR	-	expression tag	UNP A0A0H2WZS4
B	465	LEU	-	expression tag	UNP A0A0H2WZS4
B	466	VAL	-	expression tag	UNP A0A0H2WZS4
B	467	PRO	-	expression tag	UNP A0A0H2WZS4
B	468	ARG	-	expression tag	UNP A0A0H2WZS4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	469	GLY	-	expression tag	UNP A0A0H2WZS4
B	470	SER	-	expression tag	UNP A0A0H2WZS4
B	471	GLY	-	expression tag	UNP A0A0H2WZS4
B	472	HIS	-	expression tag	UNP A0A0H2WZS4
B	473	HIS	-	expression tag	UNP A0A0H2WZS4
B	474	HIS	-	expression tag	UNP A0A0H2WZS4
B	475	HIS	-	expression tag	UNP A0A0H2WZS4
B	476	HIS	-	expression tag	UNP A0A0H2WZS4
B	477	HIS	-	expression tag	UNP A0A0H2WZS4
B	478	HIS	-	expression tag	UNP A0A0H2WZS4
B	479	HIS	-	expression tag	UNP A0A0H2WZS4

- Molecule 2 is a protein called ICab.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	131	Total	C	N	O	S	0	0	0
			952	596	160	190	6			
2	D	131	Total	C	N	O	S	0	0	0
			952	596	160	190	6			

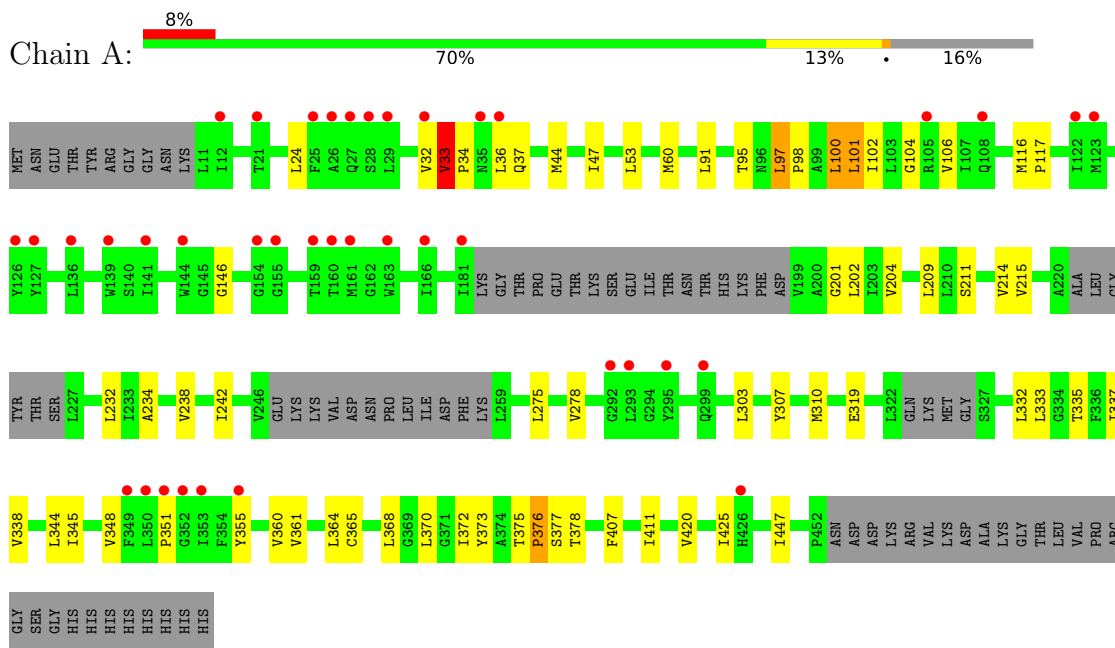
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

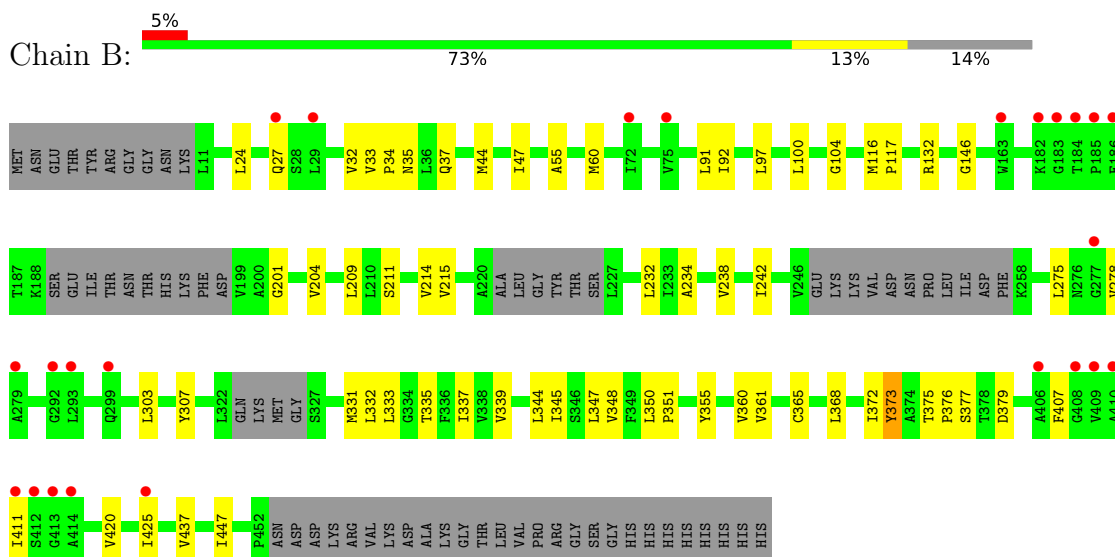
3 Residue-property plots

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.

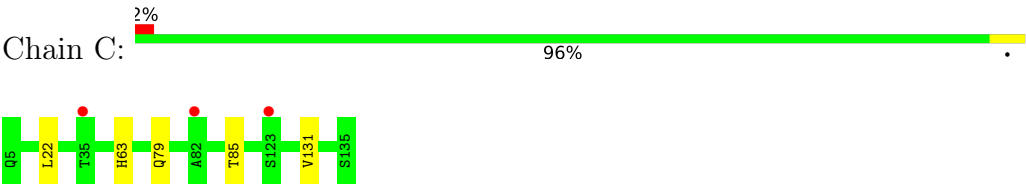
• Molecule 1: Drug transporter, putative



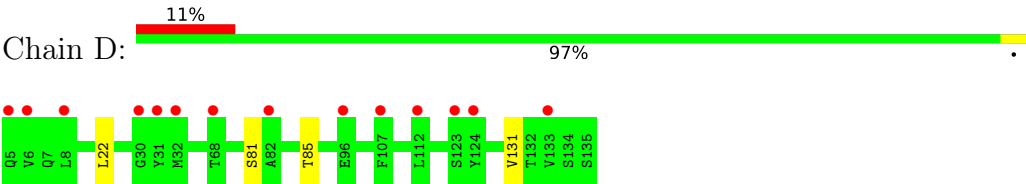
• Molecule 1: Drug transporter, putative



● Molecule 2: ICab



● Molecule 2: ICab



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	70.07Å 139.15Å 115.56Å 90.00° 105.66° 90.00°	Depositor
Resolution (Å)	111.52 – 3.60 111.27 – 3.60	Depositor EDS
% Data completeness (in resolution range)	99.9 (111.52-3.60) 100.0 (111.27-3.60)	Depositor EDS
R_{merge}	0.18	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.58Å)	Xtriage
Refinement program	REFMAC 5.8.0253	Depositor
R, R_{free}	0.308 , 0.315 0.310 , 0.315	Depositor DCC
R_{free} test set	1231 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	166.6	Xtriage
Anisotropy	0.065	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 127.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.056 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	7489	wwPDB-VP
Average B, all atoms (Å ²)	175.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.75	1/2817 (0.0%)	0.78	0/3847
1	B	0.72	0/2851	0.76	0/3898
2	C	0.69	0/975	0.76	0/1326
2	D	0.69	0/975	0.74	0/1326
All	All	0.72	1/7618 (0.0%)	0.76	0/10397

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	33	VAL	C-N	8.73	1.50	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2775	0	2798	43	0
1	B	2808	0	2803	41	0
2	C	952	0	844	7	0
2	D	952	0	844	4	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	7489	0	7289	95	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 6.

All (95) 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:A:344:LEU:HD13	1:A:361:VAL:HG23	1.62	0.82
1:B:337:ILE:HD13	1:B:368:LEU:HD11	1.69	0.75
1:A:375:THR:CG2	1:A:376:PRO:HD3	2.17	0.75
1:A:337:ILE:HD13	1:A:368:LEU:HD11	1.69	0.73
1:A:375:THR:HG22	1:A:376:PRO:HD3	1.70	0.73
1:A:97:LEU:HD12	1:A:98:PRO:HD2	1.72	0.72
1:B:344:LEU:HD23	1:B:361:VAL:HG23	1.76	0.67
1:A:345:ILE:O	1:A:348:VAL:HG12	1.99	0.63
1:B:32:VAL:HG12	1:B:32:VAL:O	1.99	0.63
2:C:63:HIS:CD2	2:C:79:GLN:HE21	2.16	0.63
1:B:97:LEU:N	1:B:97:LEU:HD23	2.14	0.63
1:A:32:VAL:HG12	1:A:32:VAL:O	2.00	0.62
1:B:345:ILE:O	1:B:348:VAL:HG12	1.99	0.61
1:A:44:MET:HA	1:A:47:ILE:HG22	1.84	0.59
1:B:44:MET:HA	1:B:47:ILE:HG22	1.83	0.59
1:A:97:LEU:HD12	1:A:98:PRO:CD	2.33	0.59
1:B:350:LEU:HD12	1:B:350:LEU:O	2.03	0.58
1:B:214:VAL:HG23	1:B:232:LEU:HD21	1.86	0.57
1:A:214:VAL:HG23	1:A:232:LEU:HD21	1.87	0.56
1:A:332:LEU:HG	1:A:447:ILE:HG21	1.88	0.56
1:B:347:LEU:CD1	1:B:350:LEU:HD11	2.36	0.56
1:B:32:VAL:HG12	1:B:35:ASN:HB2	1.88	0.54
1:B:332:LEU:HG	1:B:447:ILE:HG21	1.88	0.54
1:B:373:TYR:CE1	1:B:377:SER:OG	2.55	0.54
1:A:319:GLU:N	1:A:375:THR:HG21	2.23	0.53
1:B:24:LEU:HD23	1:B:24:LEU:C	2.29	0.53
1:A:24:LEU:C	1:A:24:LEU:HD23	2.29	0.53
2:C:79:GLN:O	2:C:79:GLN:HG3	2.07	0.52
1:B:33:VAL:N	1:B:34:PRO:CD	2.73	0.52
1:B:234:ALA:O	1:B:238:VAL:HG23	2.10	0.52
1:A:102:ILE:O	1:A:106:VAL:HG23	2.11	0.51
1:A:234:ALA:O	1:A:238:VAL:HG23	2.10	0.51
2:C:63:HIS:NE2	2:C:79:GLN:NE2	2.50	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:116:MET:HB2	1:B:117:PRO:HD3	1.94	0.50
1:A:116:MET:HB2	1:A:117:PRO:HD3	1.94	0.50
1:A:33:VAL:N	1:A:34:PRO:CD	2.74	0.50
2:C:22:LEU:HD13	2:C:131:VAL:HG23	1.94	0.49
2:D:22:LEU:HD13	2:D:131:VAL:HG23	1.95	0.48
1:B:420:VAL:HG23	1:B:425:ILE:HA	1.95	0.48
1:A:375:THR:HG23	1:A:376:PRO:HD3	1.93	0.48
1:A:337:ILE:O	1:A:365:CYS:SG	2.71	0.48
1:A:91:LEU:HG	1:A:100:LEU:HD21	1.95	0.47
1:B:337:ILE:O	1:B:365:CYS:SG	2.71	0.47
1:A:333:LEU:HD22	1:A:372:ILE:HG21	1.97	0.47
1:A:420:VAL:HG23	1:A:425:ILE:HA	1.96	0.47
2:C:63:HIS:CD2	2:C:79:GLN:NE2	2.83	0.47
1:A:91:LEU:HD23	1:A:104:GLY:CA	2.45	0.47
2:D:85:THR:O	2:D:85:THR:HG23	2.13	0.47
1:A:24:LEU:HD12	1:A:146:GLY:HA2	1.96	0.46
1:B:24:LEU:HD12	1:B:146:GLY:HA2	1.97	0.46
1:B:373:TYR:C	1:B:373:TYR:CD1	2.89	0.46
1:B:333:LEU:HD22	1:B:372:ILE:HG21	1.98	0.46
1:B:91:LEU:HD22	1:B:104:GLY:HA3	1.97	0.46
1:A:211:SER:O	1:A:215:VAL:HG23	2.17	0.45
1:B:211:SER:O	1:B:215:VAL:HG23	2.16	0.45
1:B:91:LEU:HD22	1:B:104:GLY:CA	2.47	0.45
1:B:204:VAL:HG21	1:B:242:ILE:CG2	2.46	0.45
1:B:303:LEU:HD21	1:B:360:VAL:HG22	1.97	0.45
1:A:204:VAL:HG21	1:A:242:ILE:CG2	2.47	0.45
1:A:91:LEU:HD23	1:A:104:GLY:HA2	1.98	0.45
1:A:377:SER:O	1:A:377:SER:OG	2.29	0.45
2:D:22:LEU:CD1	2:D:131:VAL:HG23	2.47	0.45
2:C:85:THR:O	2:C:85:THR:HG23	2.16	0.44
1:A:36:LEU:HD11	1:A:101:LEU:HD21	1.99	0.44
1:A:303:LEU:HD21	1:A:360:VAL:HG22	1.99	0.44
2:C:22:LEU:CD1	2:C:131:VAL:HG23	2.47	0.44
1:A:275:LEU:O	1:A:278:VAL:HG22	2.19	0.43
1:A:407:PHE:O	1:A:411:ILE:HD13	2.17	0.43
1:A:310:MET:HE3	1:A:364:LEU:HD12	2.01	0.43
1:B:407:PHE:O	1:B:411:ILE:HD13	2.18	0.43
1:A:201:GLY:O	1:A:204:VAL:HG12	2.19	0.43
1:B:92:ILE:HD11	1:B:104:GLY:HA3	2.00	0.43
1:A:53:LEU:HD13	1:A:106:VAL:HG22	2.00	0.42
1:A:204:VAL:HG21	1:A:242:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:331:MET:CE	1:B:377:SER:HB3	2.48	0.42
1:B:91:LEU:HD21	1:B:100:LEU:HD22	2.00	0.42
1:B:97:LEU:N	1:B:97:LEU:CD2	2.82	0.42
1:B:201:GLY:O	1:B:204:VAL:HG12	2.19	0.42
1:B:27:GLN:HE22	1:B:55:ALA:HB2	1.84	0.42
1:A:275:LEU:HD23	1:A:335:THR:HG22	2.01	0.42
1:B:275:LEU:HD23	1:B:335:THR:HG22	2.01	0.42
1:A:97:LEU:HG	1:A:100:LEU:HB3	2.02	0.42
1:B:275:LEU:O	1:B:278:VAL:HG22	2.19	0.42
1:A:373:TYR:C	1:A:373:TYR:CD1	2.93	0.41
1:B:32:VAL:CG1	1:B:35:ASN:HB2	2.50	0.41
1:B:204:VAL:HG21	1:B:242:ILE:HG21	2.01	0.41
1:A:202:LEU:C	1:A:202:LEU:HD13	2.40	0.41
1:A:338:VAL:HG11	1:A:370:LEU:HD12	2.03	0.41
1:A:344:LEU:HD23	1:A:344:LEU:HA	1.96	0.40
1:B:339:VAL:HG13	1:B:437:VAL:HG13	2.03	0.40
1:B:100:LEU:HD13	1:B:100:LEU:C	2.42	0.40
1:A:60:MET:HA	1:A:209:LEU:HD13	2.03	0.40
1:B:132:ARG:NH1	1:B:379:ASP:OD1	2.54	0.40
1:B:60:MET:HA	1:B:209:LEU:HD13	2.03	0.40
2:D:85:THR:O	2:D:85:THR:CG2	2.69	0.40

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	393/479 (82%)	356 (91%)	36 (9%)	1 (0%)	41	75
1	B	401/479 (84%)	365 (91%)	35 (9%)	1 (0%)	47	79
2	C	129/131 (98%)	121 (94%)	8 (6%)	0	100	100
2	D	129/131 (98%)	121 (94%)	8 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1052/1220 (86%)	963 (92%)	87 (8%)	2 (0%)	47 79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	351	PRO
1	B	351	PRO

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	266/379 (70%)	256 (96%)	10 (4%)	33 66
1	B	265/379 (70%)	259 (98%)	6 (2%)	50 76
2	C	93/105 (89%)	93 (100%)	0	100 100
2	D	93/105 (89%)	92 (99%)	1 (1%)	73 88
All	All	717/968 (74%)	700 (98%)	17 (2%)	49 75

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	33	VAL
1	A	37	GLN
1	A	95	THR
1	A	97	LEU
1	A	100	LEU
1	A	101	LEU
1	A	307	TYR
1	A	355	TYR
1	A	376	PRO
1	A	378	THR
1	B	37	GLN
1	B	307	TYR
1	B	355	TYR

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Mol	Chain	Res	Type
1	B	373	TYR
1	B	375	THR
1	B	376	PRO
2	D	81	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	272	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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.

No monomer is involved in short contacts.

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	403/479 (84%)	0.23	39 (9%) 7 4	118, 174, 212, 233	0
1	B	411/479 (85%)	0.02	24 (5%) 23 13	137, 197, 228, 253	0
2	C	131/131 (100%)	-0.07	3 (2%) 60 44	114, 142, 180, 209	0
2	D	131/131 (100%)	0.50	14 (10%) 6 3	117, 150, 182, 194	0
All	All	1076/1220 (88%)	0.14	80 (7%) 14 9	114, 176, 220, 253	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	412	SER	8.0
2	D	124	TYR	7.2
1	A	25	PHE	6.8
1	A	26	ALA	6.4
1	A	29	LEU	6.0
2	D	5	GLN	6.0
1	A	27	GLN	5.7
1	B	184	THR	5.3
1	A	351	PRO	5.2
2	D	123	SER	5.2
1	A	123	MET	5.1
2	D	6	VAL	5.1
1	B	185	PRO	4.5
1	A	426	HIS	4.3
1	A	352	GLY	4.2
1	B	410	ALA	4.0
2	D	31	TYR	3.9
1	B	411	ILE	3.9
2	D	30	GLY	3.9
1	A	293	LEU	3.8
2	D	68	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	350	LEU	3.8
1	B	72	ILE	3.8
1	A	353	ILE	3.6
1	A	161	MET	3.6
2	C	82	ALA	3.6
1	A	28	SER	3.6
1	A	160	THR	3.5
1	B	413	GLY	3.5
2	D	107	PHE	3.4
1	A	159	THR	3.4
1	B	182	LYS	3.3
2	D	32	MET	3.3
1	A	163	TRP	3.1
1	A	155	GLY	3.1
1	B	409	VAL	3.0
2	D	82	ALA	3.0
1	B	279	ALA	2.9
1	A	12	ILE	2.9
1	A	136	LEU	2.9
1	B	75	VAL	2.8
1	A	295	TYR	2.8
1	B	293	LEU	2.8
1	B	292	GLY	2.7
1	A	105	ARG	2.7
1	B	406	ALA	2.7
1	A	32	VAL	2.6
1	A	349	PHE	2.6
1	B	27	GLN	2.5
1	A	181	ILE	2.5
1	B	186	GLU	2.5
1	A	355	TYR	2.4
1	B	183	GLY	2.4
2	D	133	VAL	2.4
1	A	36	LEU	2.4
1	A	126	TYR	2.4
1	A	108	GLN	2.3
1	B	299	GLN	2.3
1	A	292	GLY	2.3
1	B	425	ILE	2.3
1	A	144	TRP	2.3
1	B	414	ALA	2.3
1	A	122	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	163	TRP	2.2
2	D	112	LEU	2.2
1	A	139	TRP	2.2
2	D	96	GLU	2.2
2	C	35	THR	2.2
1	A	299	GLN	2.1
1	A	127	TYR	2.1
1	B	29	LEU	2.1
2	C	123	SER	2.1
1	A	166	ILE	2.1
1	A	21	THR	2.1
1	B	277	GLY	2.1
1	A	35	ASN	2.1
1	A	141	ILE	2.1
1	A	154	GLY	2.0
1	B	408	GLY	2.0
2	D	8	LEU	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 monosaccharides 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
3	ZN	C	201	1/1	0.98	0.22	122,122,122,122	0
3	ZN	D	201	1/1	0.99	0.21	126,126,126,126	0

6.5 Other polymers [i](#)

There are no such residues in this entry.