



Full wwPDB X-ray Structure Validation Report ⓘ

May 10, 2017 – 07:55 PM EDT

PDB ID : 5ULD
Title : Structure and function of the divalent anion/Na⁺ symporter from *Vibrio cholerae* and a humanized variant
Authors : Lu, M.
Deposited on : 2017-01-24
Resolution : 2.78 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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-20029077

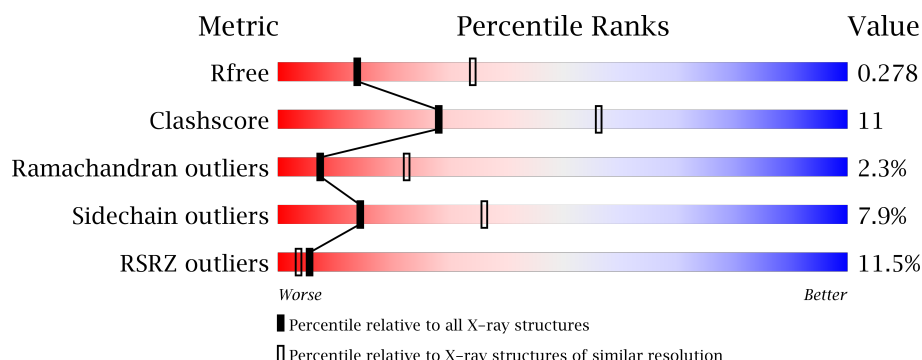
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.78 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}	100719	3276 (2.80-2.76)
Clashscore	112137	3771 (2.80-2.76)
Ramachandran outliers	110173	3707 (2.80-2.76)
Sidechain outliers	110143	3709 (2.80-2.76)
RSRZ outliers	101464	3307 (2.80-2.76)

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	445	<div> <div>13%</div> <div> <div></div> <div>72%</div> <div>24%</div> <div>.</div> </div> </div>
1	B	445	<div> <div>14%</div> <div> <div></div> <div>72%</div> <div>24%</div> <div>.</div> </div> </div>
1	C	445	<div> <div>9%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>.</div> </div> </div>
1	D	445	<div> <div>11%</div> <div> <div></div> <div>73%</div> <div>23%</div> <div>.</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NA	A	502	-	-	-	X
2	NA	D	501	-	-	-	X
3	CIT	B	503	-	-	-	X
3	CIT	C	503	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13456 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 Transporter, NadC family.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	445	Total	C	N	O	S	0	0	0
			3349	2234	523	566	26			
1	B	445	Total	C	N	O	S	0	0	0
			3349	2234	523	566	26			
1	C	445	Total	C	N	O	S	0	0	0
			3349	2234	523	566	26			
1	D	445	Total	C	N	O	S	0	0	0
			3349	2234	523	566	26			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	200	THR	SER	conflict	UNP Q9KNE0
A	201	GLY	PRO	conflict	UNP Q9KNE0
A	322	ILE	VAL	conflict	UNP Q9KNE0
A	376	THR	ALA	conflict	UNP Q9KNE0
A	379	VAL	THR	conflict	UNP Q9KNE0
A	381	THR	SER	conflict	UNP Q9KNE0
A	382	THR	ALA	conflict	UNP Q9KNE0
A	383	THR	ALA	conflict	UNP Q9KNE0
B	200	THR	SER	conflict	UNP Q9KNE0
B	201	GLY	PRO	conflict	UNP Q9KNE0
B	322	ILE	VAL	conflict	UNP Q9KNE0
B	376	THR	ALA	conflict	UNP Q9KNE0
B	379	VAL	THR	conflict	UNP Q9KNE0
B	381	THR	SER	conflict	UNP Q9KNE0
B	382	THR	ALA	conflict	UNP Q9KNE0
B	383	THR	ALA	conflict	UNP Q9KNE0
C	200	THR	SER	conflict	UNP Q9KNE0
C	201	GLY	PRO	conflict	UNP Q9KNE0
C	322	ILE	VAL	conflict	UNP Q9KNE0
C	376	THR	ALA	conflict	UNP Q9KNE0
C	379	VAL	THR	conflict	UNP Q9KNE0

Continued on next page...

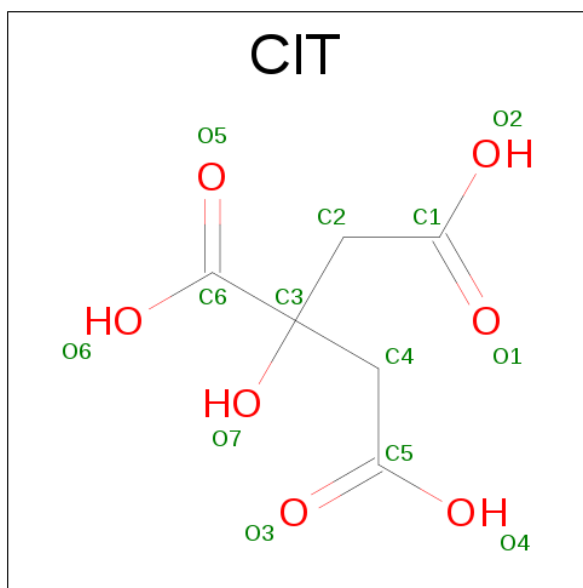
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	381	THR	SER	conflict	UNP Q9KNE0
C	382	THR	ALA	conflict	UNP Q9KNE0
C	383	THR	ALA	conflict	UNP Q9KNE0
D	200	THR	SER	conflict	UNP Q9KNE0
D	201	GLY	PRO	conflict	UNP Q9KNE0
D	322	ILE	VAL	conflict	UNP Q9KNE0
D	376	THR	ALA	conflict	UNP Q9KNE0
D	379	VAL	THR	conflict	UNP Q9KNE0
D	381	THR	SER	conflict	UNP Q9KNE0
D	382	THR	ALA	conflict	UNP Q9KNE0
D	383	THR	ALA	conflict	UNP Q9KNE0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Na 2 2	0	0
2	A	2	Total Na 2 2	0	0
2	D	2	Total Na 2 2	0	0
2	C	2	Total Na 2 2	0	0

- Molecule 3 is CITRIC ACID (three-letter code: CIT) (formula: C₆H₈O₇).

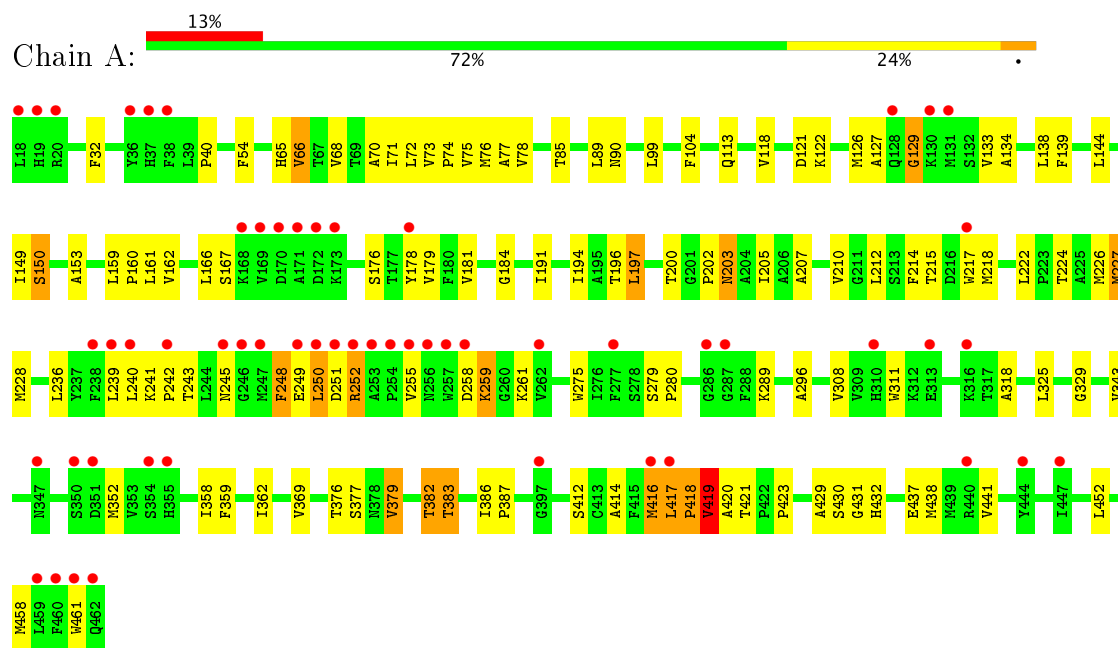


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 13	C 6	O 7	0	0
3	B	1	Total 13	C 6	O 7	0	0
3	C	1	Total 13	C 6	O 7	0	0
3	D	1	Total 13	C 6	O 7	0	0

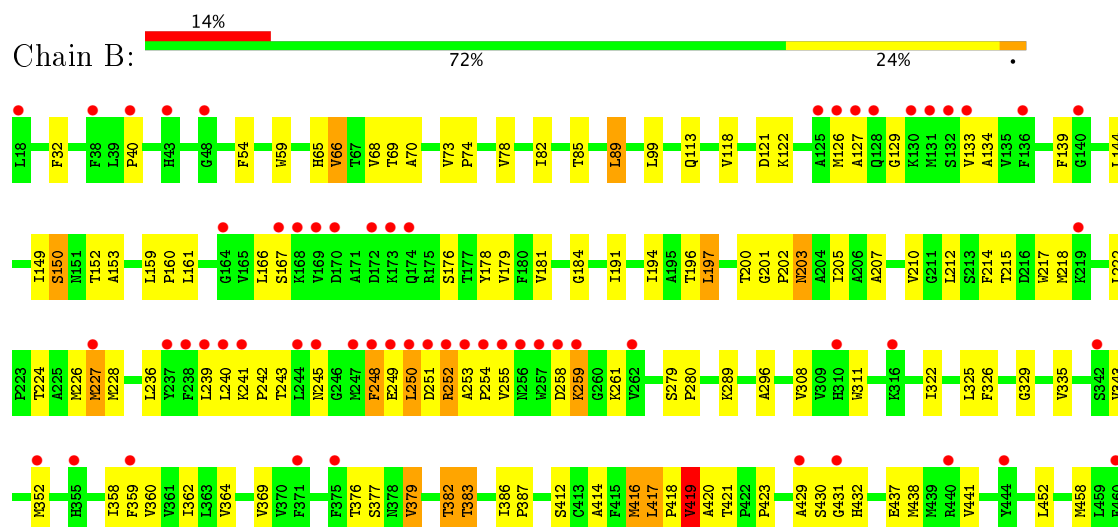
3 Residue-property plots

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: Transporter, NadC family

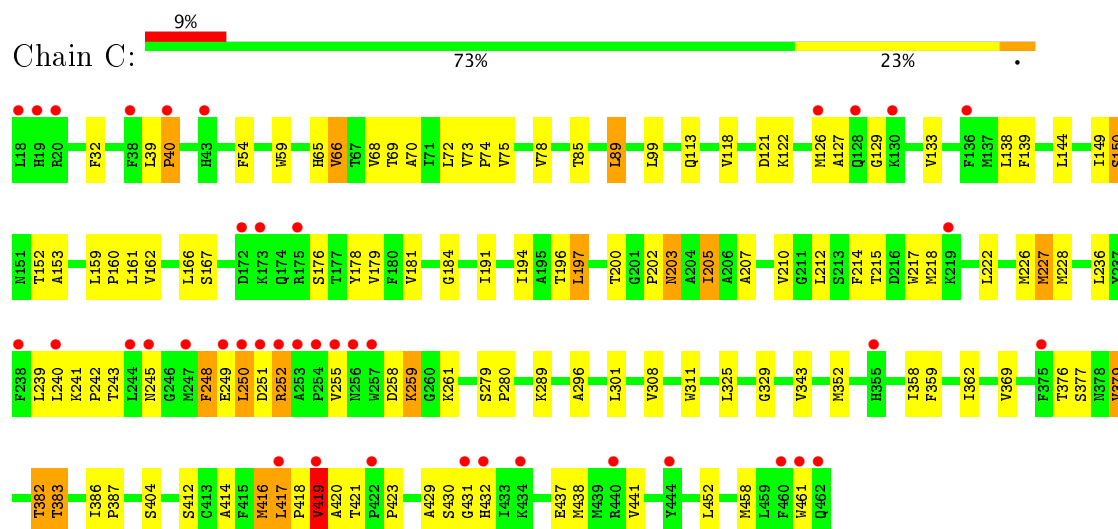


• Molecule 1: Transporter, NadC family

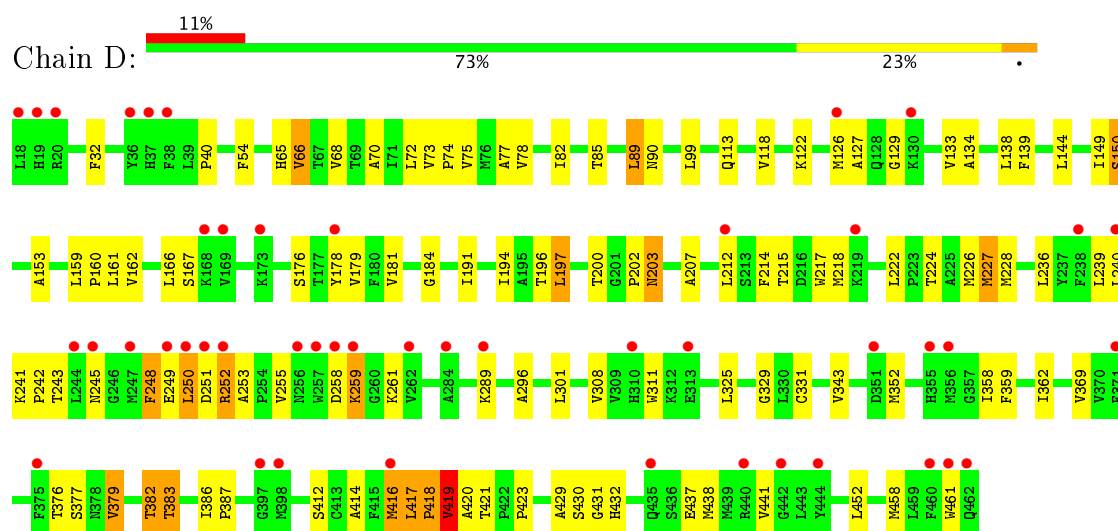




- Molecule 1: Transporter, NadC family



- Molecule 1: Transporter, NadC family



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	106.09Å 101.53Å 168.88Å 90.00° 99.73° 90.00°	Depositor
Resolution (Å)	15.00 – 2.78 15.00 – 2.78	Depositor EDS
% Data completeness (in resolution range)	88.9 (15.00-2.78) 89.0 (15.00-2.78)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.00 (at 2.77Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.252 , 0.268 0.272 , 0.278	Depositor DCC
R_{free} test set	3980 reflections (5.32%)	DCC
Wilson B-factor (Å ²)	74.3	Xtriage
Anisotropy	0.613	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13456	wwPDB-VP
Average B, all atoms (Å ²)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% 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: NA, CIT

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	0.34	0/3427	0.52	0/4673
1	B	0.33	0/3427	0.52	0/4673
1	C	0.36	0/3427	0.53	0/4673
1	D	0.36	0/3427	0.54	0/4673
All	All	0.34	0/13708	0.53	0/18692

There are no bond length outliers.

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	3349	0	3504	80	0
1	B	3349	0	3504	77	0
1	C	3349	0	3504	80	0
1	D	3349	0	3504	76	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	13	0	5	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	13	0	5	1	0
3	C	13	0	5	1	0
3	D	13	0	5	0	0
All	All	13456	0	14036	306	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 11.

All (306) 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:421:THR:CG2	1:A:423:PRO:HD2	1.89	1.01
1:C:421:THR:CG2	1:C:423:PRO:HD2	1.91	1.00
1:D:421:THR:CG2	1:D:423:PRO:HD2	1.91	1.00
1:B:421:THR:CG2	1:B:423:PRO:HD2	1.93	0.99
1:C:421:THR:HG22	1:C:423:PRO:HD2	0.99	0.99
1:B:421:THR:HG22	1:B:423:PRO:HD2	0.99	0.98
1:D:421:THR:HG22	1:D:423:PRO:HD2	0.99	0.98
1:A:421:THR:HG22	1:A:423:PRO:CD	1.93	0.98
1:C:421:THR:HG22	1:C:423:PRO:CD	1.95	0.96
1:A:421:THR:HG22	1:A:423:PRO:HD2	0.96	0.95
1:D:421:THR:HG22	1:D:423:PRO:CD	1.95	0.95
1:B:421:THR:HG22	1:B:423:PRO:CD	1.96	0.92
1:B:78:VAL:HG11	1:B:85:THR:HG22	1.54	0.89
1:A:78:VAL:HG11	1:A:85:THR:HG22	1.54	0.89
1:D:78:VAL:HG11	1:D:85:THR:HG22	1.55	0.88
1:C:416:MET:O	1:C:438:MET:HG2	1.74	0.88
1:A:416:MET:O	1:A:438:MET:HG2	1.73	0.88
1:C:78:VAL:HG11	1:C:85:THR:HG22	1.56	0.85
1:B:416:MET:O	1:B:438:MET:HG2	1.77	0.85
1:D:416:MET:O	1:D:438:MET:HG2	1.74	0.85
1:A:73:VAL:HB	1:A:74:PRO:HD3	1.62	0.81
1:C:73:VAL:HB	1:C:74:PRO:HD3	1.62	0.81
1:D:73:VAL:HB	1:D:74:PRO:HD3	1.63	0.81
1:A:200:THR:HG22	1:A:203:ASN:HD21	1.50	0.77
1:B:73:VAL:HB	1:B:74:PRO:HD3	1.66	0.76
1:D:200:THR:HG22	1:D:203:ASN:HD21	1.50	0.76
1:C:166:LEU:HD11	1:C:181:VAL:HB	1.67	0.76
1:D:166:LEU:HD11	1:D:181:VAL:HB	1.68	0.75
1:A:166:LEU:HD11	1:A:181:VAL:HB	1.69	0.75
1:C:200:THR:HG22	1:C:203:ASN:HD21	1.51	0.75

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:THR:HG22	1:B:203:ASN:HD21	1.53	0.74
1:B:166:LEU:HD11	1:B:181:VAL:HB	1.69	0.73
1:B:382:THR:HG22	1:B:386:ILE:HG13	1.74	0.69
1:C:222:LEU:O	1:C:226:MET:HG2	1.92	0.69
1:A:329:GLY:HA3	1:A:383:THR:HG22	1.76	0.68
1:A:227:MET:HG2	1:A:452:LEU:HD11	1.76	0.68
1:C:329:GLY:HA3	1:C:383:THR:HG22	1.75	0.68
1:A:167:SER:HB3	1:A:249:GLU:OE2	1.94	0.68
1:A:122:LYS:O	1:A:126:MET:HG2	1.94	0.67
1:A:382:THR:HG22	1:A:386:ILE:HG13	1.74	0.67
1:A:129:GLY:HA2	1:A:248:PHE:HB2	1.76	0.67
1:B:222:LEU:O	1:B:226:MET:HG2	1.95	0.66
1:D:129:GLY:HA2	1:D:248:PHE:HB2	1.77	0.66
1:C:129:GLY:HA2	1:C:248:PHE:HB2	1.77	0.66
1:B:227:MET:HG2	1:B:452:LEU:HD11	1.77	0.66
1:D:382:THR:HG22	1:D:386:ILE:HG13	1.76	0.66
1:B:122:LYS:O	1:B:126:MET:HG2	1.95	0.65
1:C:227:MET:HG2	1:C:452:LEU:HD11	1.76	0.65
1:D:167:SER:HB3	1:D:249:GLU:OE2	1.96	0.65
1:C:382:THR:HG22	1:C:386:ILE:HG13	1.78	0.65
1:B:129:GLY:HA2	1:B:248:PHE:HB2	1.77	0.65
1:D:227:MET:HG2	1:D:452:LEU:HD11	1.78	0.65
1:C:122:LYS:O	1:C:126:MET:HG2	1.96	0.65
1:D:122:LYS:O	1:D:126:MET:HG2	1.95	0.65
1:D:329:GLY:HA3	1:D:383:THR:HG22	1.79	0.65
1:D:197:LEU:HD12	1:D:214:PHE:HA	1.78	0.65
1:D:222:LEU:O	1:D:226:MET:HG2	1.98	0.64
1:B:329:GLY:HA3	1:B:383:THR:HG22	1.78	0.64
1:C:197:LEU:HD12	1:C:214:PHE:HA	1.80	0.64
1:C:167:SER:HB3	1:C:249:GLU:OE2	1.98	0.64
1:A:200:THR:HG22	1:A:203:ASN:ND2	2.13	0.63
1:B:167:SER:HB3	1:B:249:GLU:OE2	1.98	0.63
1:A:150:SER:HB3	1:A:153:ALA:HB3	1.81	0.63
1:A:78:VAL:CG1	1:A:85:THR:HG22	2.28	0.62
1:D:200:THR:HG22	1:D:203:ASN:ND2	2.14	0.62
1:D:150:SER:HB3	1:D:153:ALA:HB3	1.80	0.62
1:B:197:LEU:HD12	1:B:214:PHE:HA	1.81	0.62
1:C:200:THR:HG22	1:C:203:ASN:ND2	2.14	0.62
1:A:222:LEU:O	1:A:226:MET:HG2	1.99	0.62
1:B:113:GLN:HG3	1:B:261:LYS:HG2	1.81	0.62
1:A:197:LEU:HD12	1:A:214:PHE:HA	1.80	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:THR:HG22	1:B:203:ASN:ND2	2.15	0.61
1:C:78:VAL:CG1	1:C:85:THR:HG22	2.30	0.60
1:D:113:GLN:HG3	1:D:261:LYS:HG2	1.82	0.60
1:B:78:VAL:CG1	1:B:85:THR:HG22	2.29	0.60
1:C:113:GLN:HG3	1:C:261:LYS:HG2	1.82	0.59
1:D:418:PRO:C	1:D:420:ALA:H	2.06	0.59
1:A:113:GLN:HG3	1:A:261:LYS:HG2	1.84	0.59
1:A:418:PRO:C	1:A:420:ALA:H	2.06	0.58
1:D:362:ILE:HD11	1:D:458:MET:HE2	1.85	0.58
1:D:196:THR:HG22	1:D:218:MET:HG3	1.84	0.58
1:B:150:SER:HB3	1:B:153:ALA:HB3	1.85	0.57
1:B:418:PRO:C	1:B:420:ALA:H	2.07	0.57
1:A:196:THR:HG22	1:A:218:MET:HG3	1.86	0.57
1:C:418:PRO:C	1:C:420:ALA:H	2.08	0.57
1:D:417:LEU:HD23	1:D:417:LEU:H	1.68	0.57
1:D:78:VAL:CG1	1:D:85:THR:HG22	2.31	0.57
1:A:414:ALA:HB1	1:A:420:ALA:HB1	1.87	0.57
1:B:417:LEU:H	1:B:417:LEU:HD23	1.70	0.56
1:A:417:LEU:HD23	1:A:417:LEU:H	1.70	0.56
1:C:150:SER:HB3	1:C:153:ALA:HB3	1.85	0.56
1:C:417:LEU:H	1:C:417:LEU:HD23	1.70	0.56
1:C:159:LEU:HB3	1:C:160:PRO:HD3	1.88	0.56
1:C:196:THR:HG22	1:C:218:MET:HG3	1.88	0.56
1:C:65:HIS:HB3	1:C:68:VAL:HG23	1.88	0.56
1:D:414:ALA:HB1	1:D:420:ALA:HB1	1.89	0.55
1:D:73:VAL:HB	1:D:74:PRO:CD	2.35	0.55
1:B:196:THR:HG22	1:B:218:MET:HG3	1.89	0.55
1:C:414:ALA:HB1	1:C:420:ALA:HB1	1.88	0.55
1:D:194:ILE:O	1:D:194:ILE:HG22	2.06	0.55
1:A:362:ILE:HD11	1:A:458:MET:HE2	1.88	0.55
1:B:414:ALA:HB1	1:B:420:ALA:HB1	1.88	0.55
1:B:159:LEU:HB3	1:B:160:PRO:HD3	1.89	0.55
1:A:32:PHE:HB2	1:A:54:PHE:HD1	1.72	0.54
1:C:65:HIS:CD2	1:D:311:TRP:HB3	2.42	0.54
1:D:159:LEU:HB3	1:D:160:PRO:HD3	1.90	0.54
1:C:194:ILE:O	1:C:194:ILE:HG22	2.08	0.54
1:B:194:ILE:O	1:B:194:ILE:HG22	2.08	0.53
1:D:32:PHE:HB2	1:D:54:PHE:HD1	1.73	0.53
1:A:431:GLY:HA2	1:D:253:ALA:HB3	1.89	0.53
1:A:65:HIS:CD2	1:B:311:TRP:HB3	2.43	0.53
1:D:85:THR:O	1:D:89:LEU:HD22	2.08	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:32:PHE:HB2	1:B:54:PHE:HD1	1.71	0.53
1:C:362:ILE:HD11	1:C:458:MET:HE2	1.91	0.53
1:C:311:TRP:HB3	1:D:65:HIS:CD2	2.43	0.53
1:A:159:LEU:HB3	1:A:160:PRO:HD3	1.91	0.53
1:A:376:THR:HG22	1:A:377:SER:N	2.24	0.53
1:A:194:ILE:HG22	1:A:194:ILE:O	2.07	0.52
1:A:99:LEU:HD12	1:A:296:ALA:HB2	1.91	0.52
1:B:65:HIS:HB3	1:B:68:VAL:HG23	1.90	0.52
1:C:32:PHE:HB2	1:C:54:PHE:HD1	1.74	0.52
1:B:376:THR:HG22	1:B:377:SER:N	2.24	0.52
1:D:258:ASP:OD1	1:D:261:LYS:HG3	2.10	0.52
1:A:236:LEU:HD23	1:A:441:VAL:HG11	1.92	0.52
1:B:99:LEU:HD12	1:B:296:ALA:HB2	1.91	0.52
1:B:212:LEU:HD13	1:B:217:TRP:HD1	1.76	0.51
1:B:437:GLU:O	1:B:441:VAL:HG23	2.11	0.51
1:C:236:LEU:HD23	1:C:441:VAL:HG11	1.93	0.51
1:B:362:ILE:HD11	1:B:458:MET:HE2	1.93	0.51
1:D:437:GLU:O	1:D:441:VAL:HG23	2.10	0.51
1:C:376:THR:HG22	1:C:377:SER:N	2.26	0.51
1:D:65:HIS:HB3	1:D:68:VAL:HG23	1.92	0.51
1:B:359:PHE:CD1	1:B:458:MET:HE3	2.46	0.50
1:A:258:ASP:OD1	1:A:261:LYS:HG3	2.10	0.50
1:C:258:ASP:OD1	1:C:261:LYS:HG3	2.11	0.50
1:C:358:ILE:O	1:C:362:ILE:HG23	2.10	0.50
1:D:376:THR:HG22	1:D:377:SER:N	2.25	0.50
1:A:65:HIS:HB3	1:A:68:VAL:HG23	1.93	0.50
1:A:311:TRP:HB3	1:B:65:HIS:CD2	2.46	0.50
1:B:236:LEU:HD23	1:B:441:VAL:HG11	1.94	0.50
1:C:99:LEU:HD12	1:C:296:ALA:HB2	1.93	0.50
1:C:437:GLU:O	1:C:441:VAL:HG23	2.11	0.50
1:A:437:GLU:O	1:A:441:VAL:HG23	2.11	0.50
1:A:418:PRO:O	1:A:420:ALA:N	2.45	0.49
1:D:212:LEU:HD13	1:D:217:TRP:HD1	1.77	0.49
1:C:418:PRO:HD3	1:C:438:MET:HE3	1.94	0.49
1:B:258:ASP:OD1	1:B:261:LYS:HG3	2.12	0.49
1:C:212:LEU:HD13	1:C:217:TRP:HD1	1.77	0.49
1:D:149:ILE:O	1:D:150:SER:HB2	2.12	0.48
1:A:70:ALA:HB2	1:A:325:LEU:HD12	1.95	0.48
1:B:176:SER:HA	1:B:179:VAL:HG12	1.95	0.48
1:B:418:PRO:O	1:B:419:VAL:HG12	2.14	0.48
1:D:418:PRO:O	1:D:420:ALA:N	2.46	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:118:VAL:HG12	1:C:255:VAL:HB	1.95	0.48
1:B:70:ALA:HB2	1:B:325:LEU:HD12	1.96	0.48
1:A:212:LEU:HD13	1:A:217:TRP:HD1	1.78	0.48
1:C:418:PRO:O	1:C:419:VAL:HG12	2.14	0.48
1:C:429:ALA:C	1:C:431:GLY:H	2.17	0.48
1:D:99:LEU:HD12	1:D:296:ALA:HB2	1.95	0.48
1:D:118:VAL:HG12	1:D:255:VAL:HB	1.95	0.48
1:A:149:ILE:O	1:A:150:SER:HB2	2.14	0.48
1:B:191:ILE:HG12	1:B:228:MET:CE	2.42	0.48
1:C:176:SER:HA	1:C:179:VAL:HG12	1.96	0.47
1:A:118:VAL:HG12	1:A:255:VAL:HB	1.95	0.47
1:B:382:THR:HG22	1:B:386:ILE:CG1	2.43	0.47
1:B:205:ILE:HD12	1:B:382:THR:HB	1.96	0.47
1:C:251:ASP:O	1:C:252:ARG:HB3	2.15	0.47
1:C:329:GLY:HA3	1:C:383:THR:CG2	2.45	0.47
1:A:429:ALA:C	1:A:431:GLY:H	2.18	0.47
1:C:191:ILE:HG12	1:C:228:MET:CE	2.44	0.47
1:A:358:ILE:O	1:A:362:ILE:HG23	2.14	0.47
1:D:70:ALA:HB2	1:D:325:LEU:HD12	1.96	0.47
1:A:382:THR:HG22	1:A:386:ILE:CG1	2.45	0.47
1:C:75:VAL:HG11	1:D:301:LEU:HD11	1.96	0.47
1:D:386:ILE:HB	1:D:387:PRO:HD3	1.96	0.47
1:B:118:VAL:HG12	1:B:255:VAL:HB	1.97	0.47
1:B:149:ILE:O	1:B:150:SER:HB2	2.15	0.47
1:D:251:ASP:O	1:D:252:ARG:HB3	2.15	0.47
1:D:429:ALA:C	1:D:431:GLY:H	2.18	0.47
1:A:73:VAL:HB	1:A:74:PRO:CD	2.41	0.46
1:D:250:LEU:HD23	1:D:250:LEU:H	1.81	0.46
1:D:236:LEU:HD23	1:D:441:VAL:HG11	1.96	0.46
1:B:429:ALA:C	1:B:431:GLY:H	2.19	0.46
1:A:251:ASP:O	1:A:252:ARG:HB3	2.15	0.46
1:B:251:ASP:O	1:B:252:ARG:HB3	2.15	0.46
1:C:72:LEU:O	1:C:75:VAL:HG12	2.16	0.46
1:A:127:ALA:HB1	1:A:133:VAL:HG13	1.98	0.46
1:D:129:GLY:CA	1:D:248:PHE:HB2	2.44	0.46
1:B:207:ALA:HA	1:B:212:LEU:HD12	1.97	0.46
1:D:202:PRO:HD3	1:D:379:VAL:HG13	1.98	0.46
1:A:194:ILE:CG2	1:A:194:ILE:O	2.64	0.46
1:B:358:ILE:O	1:B:362:ILE:HG23	2.15	0.46
1:B:386:ILE:HB	1:B:387:PRO:HD3	1.98	0.46
1:C:70:ALA:HB2	1:C:325:LEU:HD12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:418:PRO:O	1:C:420:ALA:N	2.49	0.46
1:A:210:VAL:HG23	1:A:212:LEU:HG	1.98	0.45
1:D:138:LEU:HD13	1:D:162:VAL:HG22	1.98	0.45
1:A:191:ILE:HG12	1:A:228:MET:CE	2.46	0.45
1:B:191:ILE:HG12	1:B:228:MET:HE3	1.99	0.45
1:C:418:PRO:HD3	1:C:438:MET:CE	2.46	0.45
1:D:194:ILE:O	1:D:194:ILE:CG2	2.64	0.45
1:C:127:ALA:HB1	1:C:133:VAL:HG13	1.99	0.45
1:C:205:ILE:HD12	1:C:382:THR:HB	1.97	0.45
1:D:207:ALA:HA	1:D:212:LEU:HD12	1.97	0.45
1:C:210:VAL:HG23	1:C:212:LEU:HG	1.99	0.45
1:C:129:GLY:CA	1:C:248:PHE:HB2	2.45	0.45
1:C:250:LEU:HD23	1:C:250:LEU:H	1.82	0.45
1:D:418:PRO:HD3	1:D:438:MET:HE3	1.98	0.45
1:A:207:ALA:HA	1:A:212:LEU:HD12	1.98	0.45
1:A:205:ILE:HD12	1:A:382:THR:HB	1.98	0.45
1:C:139:PHE:CE2	1:C:184:GLY:HA3	2.52	0.45
1:C:73:VAL:HB	1:C:74:PRO:CD	2.40	0.45
1:A:129:GLY:CA	1:A:248:PHE:HB2	2.44	0.45
1:A:202:PRO:HD3	1:A:379:VAL:HG13	1.99	0.45
1:B:418:PRO:O	1:B:420:ALA:N	2.50	0.45
1:C:152:THR:OG1	3:C:503:CIT:O4	2.27	0.45
1:D:358:ILE:O	1:D:362:ILE:HG23	2.17	0.45
1:A:250:LEU:HD23	1:A:250:LEU:H	1.82	0.45
1:D:191:ILE:HG12	1:D:228:MET:CE	2.46	0.44
1:B:127:ALA:HB1	1:B:133:VAL:HG13	1.99	0.44
1:D:418:PRO:O	1:D:419:VAL:HG12	2.17	0.44
1:A:417:LEU:HB2	1:A:418:PRO:HD2	2.00	0.44
1:A:176:SER:HA	1:A:179:VAL:HG12	2.00	0.44
1:A:329:GLY:HA3	1:A:383:THR:CG2	2.46	0.44
1:C:301:LEU:HD11	1:D:75:VAL:HG11	2.00	0.44
1:D:127:ALA:HB1	1:D:133:VAL:HG13	1.99	0.44
1:D:224:THR:O	1:D:228:MET:HB2	2.17	0.44
1:C:194:ILE:CG2	1:C:194:ILE:O	2.65	0.44
1:D:176:SER:HA	1:D:179:VAL:HG12	2.00	0.44
1:B:250:LEU:HD23	1:B:250:LEU:H	1.82	0.44
1:C:191:ILE:HG12	1:C:228:MET:HE3	1.99	0.44
1:B:176:SER:HB2	1:B:240:LEU:O	2.18	0.43
1:B:129:GLY:CA	1:B:248:PHE:HB2	2.45	0.43
1:C:386:ILE:HB	1:C:387:PRO:HD3	2.00	0.43
1:D:176:SER:HB2	1:D:240:LEU:O	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:LEU:HD13	1:A:162:VAL:HG22	2.01	0.43
1:A:139:PHE:CE2	1:A:184:GLY:HA3	2.53	0.43
1:C:176:SER:HB2	1:C:240:LEU:O	2.18	0.43
1:D:418:PRO:HD3	1:D:438:MET:CE	2.48	0.43
1:A:118:VAL:HA	1:A:255:VAL:HG21	2.00	0.43
1:A:176:SER:HB2	1:A:240:LEU:O	2.17	0.43
1:B:194:ILE:CG2	1:B:194:ILE:O	2.66	0.43
1:C:118:VAL:HA	1:C:255:VAL:HG21	2.00	0.43
1:D:73:VAL:HG12	1:D:331:CYS:SG	2.58	0.43
1:D:382:THR:HG22	1:D:386:ILE:CG1	2.44	0.43
1:B:417:LEU:HB2	1:B:418:PRO:HD2	2.00	0.43
1:C:417:LEU:HB2	1:C:418:PRO:HD2	2.01	0.43
1:C:359:PHE:CD1	1:C:458:MET:HE3	2.53	0.43
1:D:118:VAL:HA	1:D:255:VAL:HG21	2.01	0.43
1:B:85:THR:O	1:B:89:LEU:HD22	2.19	0.43
1:C:200:THR:CG2	1:C:203:ASN:ND2	2.81	0.43
1:C:149:ILE:O	1:C:150:SER:HB2	2.19	0.43
1:D:139:PHE:CE2	1:D:184:GLY:HA3	2.54	0.43
1:A:418:PRO:HD3	1:A:438:MET:CE	2.49	0.42
1:A:279:SER:HB3	1:A:280:PRO:HD3	2.01	0.42
1:B:139:PHE:CE2	1:B:184:GLY:HA3	2.54	0.42
1:C:207:ALA:HA	1:C:212:LEU:HD12	2.01	0.42
1:C:359:PHE:HA	1:C:458:MET:HE1	2.01	0.42
1:D:243:THR:C	1:D:245:ASN:H	2.22	0.42
1:A:71:ILE:O	1:A:74:PRO:HD2	2.20	0.42
1:A:386:ILE:HB	1:A:387:PRO:HD3	2.01	0.42
1:A:418:PRO:O	1:A:419:VAL:HG12	2.19	0.42
1:B:59:TRP:NE1	1:B:69:THR:HB	2.35	0.42
1:D:77:ALA:HA	1:D:82:ILE:HD12	2.02	0.42
1:B:202:PRO:HD3	1:B:379:VAL:HG13	2.01	0.42
1:D:72:LEU:O	1:D:75:VAL:HG12	2.19	0.42
1:A:416:MET:O	1:A:438:MET:CG	2.58	0.42
1:D:418:PRO:C	1:D:420:ALA:N	2.72	0.42
1:D:417:LEU:HB2	1:D:418:PRO:HD2	2.02	0.42
1:A:418:PRO:HD3	1:A:438:MET:HE3	2.00	0.42
1:A:359:PHE:CD1	1:A:458:MET:HE3	2.55	0.42
1:B:418:PRO:HD3	1:B:438:MET:CE	2.50	0.42
1:A:418:PRO:C	1:A:420:ALA:N	2.72	0.41
1:B:224:THR:O	1:B:228:MET:HB2	2.20	0.41
1:D:200:THR:CG2	1:D:203:ASN:ND2	2.82	0.41
1:D:359:PHE:HA	1:D:458:MET:HE1	2.01	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:224:THR:O	1:A:228:MET:HB2	2.19	0.41
1:B:118:VAL:HA	1:B:255:VAL:HG21	2.01	0.41
1:B:82:ILE:HD13	1:B:335:VAL:HG13	2.01	0.41
1:C:59:TRP:NE1	1:C:69:THR:HB	2.36	0.41
1:B:152:THR:OG1	3:B:503:CIT:O3	2.26	0.41
1:C:85:THR:O	1:C:89:LEU:HD22	2.21	0.41
1:B:253:ALA:HA	1:B:254:PRO:HD3	1.97	0.41
1:A:243:THR:C	1:A:245:ASN:H	2.24	0.41
1:B:134:ALA:HB2	1:B:248:PHE:CE1	2.56	0.41
1:B:359:PHE:HA	1:B:458:MET:HE1	2.02	0.41
1:A:134:ALA:HB2	1:A:248:PHE:CE1	2.56	0.41
1:B:243:THR:C	1:B:245:ASN:H	2.23	0.41
1:C:243:THR:C	1:C:245:ASN:H	2.24	0.41
1:D:134:ALA:HB2	1:D:248:PHE:CE1	2.56	0.41
1:A:72:LEU:O	1:A:75:VAL:HG12	2.21	0.41
1:C:202:PRO:HD3	1:C:379:VAL:HG13	2.03	0.41
1:C:418:PRO:C	1:C:420:ALA:N	2.74	0.41
1:A:200:THR:CG2	1:A:203:ASN:ND2	2.82	0.40
1:A:214:PHE:CD2	1:A:275:TRP:HB3	2.56	0.40
1:A:104:PHE:CG	1:A:318:ALA:HA	2.57	0.40
1:B:210:VAL:HG23	1:B:212:LEU:HG	2.02	0.40
1:B:279:SER:HB3	1:B:280:PRO:HD3	2.02	0.40
1:B:360:VAL:O	1:B:364:VAL:HG23	2.22	0.40
1:C:138:LEU:HD13	1:C:162:VAL:HG22	2.03	0.40
1:B:322:ILE:HG22	1:B:326:PHE:CZ	2.56	0.40
1:C:386:ILE:HD13	1:C:404:SER:HA	2.04	0.40
1:C:39:LEU:HA	1:C:40:PRO:HD3	1.89	0.40
1:A:76:MET:O	1:A:77:ALA:C	2.60	0.40
1:B:201:GLY:HA3	1:B:379:VAL:CG1	2.51	0.40
1:C:279:SER:HB3	1:C:280:PRO:HD3	2.02	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	443/445 (100%)	400 (90%)	31 (7%)	12 (3%)	6	18
1	B	443/445 (100%)	401 (90%)	33 (7%)	9 (2%)	9	26
1	C	443/445 (100%)	399 (90%)	35 (8%)	9 (2%)	9	26
1	D	443/445 (100%)	400 (90%)	32 (7%)	11 (2%)	6	20
All	All	1772/1780 (100%)	1600 (90%)	131 (7%)	41 (2%)	7	22

All (41) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	242	PRO
1	A	419	VAL
1	B	242	PRO
1	B	419	VAL
1	C	242	PRO
1	C	419	VAL
1	D	242	PRO
1	D	419	VAL
1	A	150	SER
1	A	252	ARG
1	A	259	LYS
1	A	416	MET
1	B	150	SER
1	B	252	ARG
1	B	259	LYS
1	B	416	MET
1	C	150	SER
1	C	252	ARG
1	C	259	LYS
1	C	416	MET
1	D	150	SER
1	D	252	ARG
1	D	259	LYS
1	D	416	MET
1	C	66	VAL
1	D	90	ASN
1	A	430	SER
1	B	430	SER
1	C	430	SER
1	D	430	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	40	PRO
1	A	90	ASN
1	B	66	VAL
1	B	40	PRO
1	D	40	PRO
1	D	66	VAL
1	C	40	PRO
1	A	66	VAL
1	A	418	PRO
1	D	418	PRO
1	A	129	GLY

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	355/355 (100%)	327 (92%)	28 (8%)	14	36
1	B	355/355 (100%)	327 (92%)	28 (8%)	14	36
1	C	355/355 (100%)	326 (92%)	29 (8%)	13	34
1	D	355/355 (100%)	328 (92%)	27 (8%)	15	38
All	All	1420/1420 (100%)	1308 (92%)	112 (8%)	14	36

All (112) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	VAL
1	A	89	LEU
1	A	121	ASP
1	A	144	LEU
1	A	161	LEU
1	A	178	TYR
1	A	197	LEU
1	A	203	ASN
1	A	215	THR
1	A	227	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	239	LEU
1	A	241	LYS
1	A	248	PHE
1	A	250	LEU
1	A	259	LYS
1	A	289	LYS
1	A	308	VAL
1	A	343	VAL
1	A	352	MET
1	A	369	VAL
1	A	379	VAL
1	A	382	THR
1	A	383	THR
1	A	412	SER
1	A	417	LEU
1	A	419	VAL
1	A	432	HIS
1	A	461	TRP
1	B	66	VAL
1	B	89	LEU
1	B	121	ASP
1	B	144	LEU
1	B	161	LEU
1	B	178	TYR
1	B	197	LEU
1	B	203	ASN
1	B	215	THR
1	B	227	MET
1	B	239	LEU
1	B	241	LYS
1	B	248	PHE
1	B	250	LEU
1	B	259	LYS
1	B	289	LYS
1	B	308	VAL
1	B	343	VAL
1	B	352	MET
1	B	369	VAL
1	B	379	VAL
1	B	382	THR
1	B	383	THR
1	B	412	SER

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	417	LEU
1	B	419	VAL
1	B	432	HIS
1	B	461	TRP
1	C	66	VAL
1	C	89	LEU
1	C	121	ASP
1	C	144	LEU
1	C	161	LEU
1	C	178	TYR
1	C	197	LEU
1	C	203	ASN
1	C	205	ILE
1	C	215	THR
1	C	227	MET
1	C	239	LEU
1	C	241	LYS
1	C	248	PHE
1	C	250	LEU
1	C	259	LYS
1	C	289	LYS
1	C	308	VAL
1	C	343	VAL
1	C	352	MET
1	C	369	VAL
1	C	379	VAL
1	C	382	THR
1	C	383	THR
1	C	412	SER
1	C	417	LEU
1	C	419	VAL
1	C	432	HIS
1	C	461	TRP
1	D	66	VAL
1	D	89	LEU
1	D	144	LEU
1	D	161	LEU
1	D	178	TYR
1	D	197	LEU
1	D	203	ASN
1	D	215	THR
1	D	227	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	239	LEU
1	D	241	LYS
1	D	248	PHE
1	D	250	LEU
1	D	259	LYS
1	D	289	LYS
1	D	308	VAL
1	D	343	VAL
1	D	352	MET
1	D	369	VAL
1	D	379	VAL
1	D	382	THR
1	D	383	THR
1	D	412	SER
1	D	417	LEU
1	D	419	VAL
1	D	432	HIS
1	D	461	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	432	HIS
1	B	43	HIS
1	B	203	ASN
1	C	43	HIS
1	C	432	HIS
1	D	43	HIS
1	D	432	HIS

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

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	$\# Z > 2$
3	CIT	A	503	-	3,12,12	0.61	0	3,17,17	1.58	1 (33%)
3	CIT	B	503	-	3,12,12	0.66	0	3,17,17	1.98	1 (33%)
3	CIT	C	503	-	3,12,12	0.91	0	3,17,17	1.73	1 (33%)
3	CIT	D	503	-	3,12,12	0.75	0	3,17,17	1.66	1 (33%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	CIT	A	503	-	-	0/6/16/16	0/0/0/0
3	CIT	B	503	-	-	0/6/16/16	0/0/0/0
3	CIT	C	503	-	-	0/6/16/16	0/0/0/0
3	CIT	D	503	-	-	0/6/16/16	0/0/0/0

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	503	CIT	C3-C4-C5	-2.63	110.84	114.95
3	C	503	CIT	C3-C4-C5	-2.53	111.00	114.95
3	D	503	CIT	C3-C4-C5	-2.38	111.23	114.95
3	A	503	CIT	C3-C4-C5	-2.18	111.54	114.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	503	CIT	1	0
3	C	503	CIT	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	445/445 (100%)	0.48	56 (12%) 4 3	33, 77, 130, 173	0
1	B	445/445 (100%)	0.52	61 (13%) 3 2	45, 85, 142, 186	0
1	C	445/445 (100%)	0.36	41 (9%) 10 6	26, 70, 136, 190	0
1	D	445/445 (100%)	0.23	47 (10%) 7 4	6, 56, 101, 165	0
All	All	1780/1780 (100%)	0.40	205 (11%) 5 3	6, 73, 133, 190	0

All (205) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	462	GLN	14.7
1	C	250	LEU	10.5
1	A	130	LYS	8.9
1	C	254	PRO	8.2
1	C	462	GLN	8.2
1	B	462	GLN	8.0
1	C	355	HIS	7.6
1	B	247	MET	7.6
1	B	132	SER	6.9
1	B	133	VAL	6.9
1	A	240	LEU	6.8
1	B	240	LEU	6.2
1	B	258	ASP	6.2
1	A	247	MET	6.1
1	C	247	MET	6.0
1	B	259	LYS	6.0
1	A	128	GLN	6.0
1	B	128	GLN	5.9
1	C	128	GLN	5.8
1	B	245	ASN	5.7
1	C	253	ALA	5.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	245	ASN	5.5
1	A	249	GLU	5.4
1	A	252	ARG	5.4
1	D	130	LYS	5.4
1	B	173	LYS	5.4
1	A	462	GLN	5.3
1	C	251	ASP	5.3
1	A	19	HIS	5.2
1	A	168	LYS	5.2
1	D	168	LYS	5.2
1	C	461	TRP	5.2
1	A	245	ASN	5.2
1	A	255	VAL	5.1
1	A	251	ASP	5.1
1	B	257	TRP	5.1
1	A	173	LYS	5.0
1	B	255	VAL	5.0
1	A	18	LEU	4.9
1	C	130	LYS	4.9
1	D	245	ASN	4.9
1	B	238	PHE	4.9
1	B	355	HIS	4.9
1	A	355	HIS	4.8
1	C	256	ASN	4.8
1	B	168	LYS	4.7
1	A	461	TRP	4.7
1	B	18	LEU	4.6
1	B	126	MET	4.6
1	B	127	ALA	4.6
1	B	40	PRO	4.5
1	B	256	ASN	4.5
1	D	247	MET	4.5
1	C	172	ASP	4.4
1	C	38	PHE	4.4
1	C	18	LEU	4.4
1	A	257	TRP	4.3
1	D	440	ARG	4.3
1	A	354	SER	4.2
1	D	19	HIS	4.2
1	D	461	TRP	4.2
1	D	460	PHE	4.2
1	A	256	ASN	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	431	GLY	4.1
1	A	250	LEU	4.1
1	C	444	TYR	4.1
1	B	125	ALA	4.0
1	B	169	VAL	4.0
1	D	356	MET	4.0
1	D	256	ASN	4.0
1	C	19	HIS	4.0
1	D	398	MET	3.9
1	D	259	LYS	3.9
1	D	444	TYR	3.9
1	D	257	TRP	3.9
1	D	355	HIS	3.8
1	D	38	PHE	3.8
1	A	254	PRO	3.8
1	B	461	TRP	3.8
1	A	253	ALA	3.8
1	D	310	HIS	3.7
1	A	310	HIS	3.7
1	C	175	ARG	3.7
1	A	460	PHE	3.6
1	D	250	LEU	3.6
1	B	170	ASP	3.6
1	C	238	PHE	3.5
1	A	171	ALA	3.5
1	C	252	ARG	3.5
1	B	167	SER	3.4
1	B	172	ASP	3.4
1	B	444	TYR	3.4
1	D	126	MET	3.4
1	B	248	PHE	3.4
1	D	249	GLU	3.4
1	C	375	PHE	3.4
1	C	240	LEU	3.4
1	B	38	PHE	3.4
1	C	249	GLU	3.3
1	A	239	LEU	3.3
1	A	172	ASP	3.3
1	D	258	ASP	3.3
1	B	253	ALA	3.2
1	A	286	GLY	3.2
1	C	173	LYS	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	431	GLY	3.2
1	B	375	PHE	3.2
1	B	244	LEU	3.2
1	B	174	GLN	3.2
1	A	397	GLY	3.2
1	D	416	MET	3.1
1	B	460	PHE	3.1
1	D	238	PHE	3.1
1	D	18	LEU	3.1
1	A	277	PHE	3.1
1	A	417	LEU	3.1
1	B	219	LYS	3.1
1	B	131	MET	3.1
1	D	375	PHE	3.1
1	C	20	ARG	3.0
1	C	257	TRP	3.0
1	B	251	ASP	3.0
1	B	262	VAL	2.9
1	D	435	GLN	2.8
1	D	173	LYS	2.8
1	A	258	ASP	2.8
1	C	434	LYS	2.8
1	D	397	GLY	2.8
1	C	126	MET	2.8
1	A	246	GLY	2.8
1	B	130	LYS	2.8
1	B	239	LEU	2.7
1	D	240	LEU	2.7
1	B	252	ARG	2.7
1	C	440	ARG	2.7
1	B	164	GLY	2.7
1	C	244	LEU	2.7
1	A	217	TRP	2.7
1	A	347	ASN	2.6
1	A	416	MET	2.6
1	B	250	LEU	2.6
1	D	289	LYS	2.6
1	C	255	VAL	2.6
1	A	170	ASP	2.6
1	C	40	PRO	2.6
1	B	249	GLU	2.6
1	C	422	PRO	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	37	HIS	2.5
1	A	440	ARG	2.5
1	A	38	PHE	2.5
1	C	432	HIS	2.5
1	B	316	LYS	2.5
1	A	20	ARG	2.5
1	B	440	ARG	2.5
1	A	459	LEU	2.5
1	A	287	GLY	2.5
1	C	136	PHE	2.5
1	D	219	LYS	2.4
1	B	48	GLY	2.4
1	A	444	TYR	2.4
1	A	316	LYS	2.4
1	A	131	MET	2.4
1	B	429	ALA	2.4
1	D	284	ALA	2.4
1	C	219	LYS	2.4
1	B	254	PRO	2.3
1	C	43	HIS	2.3
1	D	36	TYR	2.3
1	D	351	ASP	2.3
1	D	262	VAL	2.3
1	D	442	GLY	2.3
1	B	310	HIS	2.3
1	D	313	GLU	2.3
1	A	351	ASP	2.3
1	B	352	MET	2.2
1	A	242	PRO	2.2
1	B	342	SER	2.2
1	A	350	SER	2.2
1	A	262	VAL	2.2
1	D	252	ARG	2.2
1	C	417	LEU	2.2
1	D	244	LEU	2.2
1	B	140	GLY	2.2
1	D	251	ASP	2.2
1	A	238	PHE	2.2
1	A	36	TYR	2.2
1	D	169	VAL	2.2
1	B	43	HIS	2.2
1	A	447	ILE	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	419	VAL	2.1
1	B	227	MET	2.1
1	D	371	PHE	2.1
1	A	169	VAL	2.1
1	D	20	ARG	2.1
1	A	313	GLU	2.1
1	B	371	PHE	2.1
1	B	237	TYR	2.1
1	D	37	HIS	2.1
1	A	178	TYR	2.1
1	B	359	PHE	2.1
1	D	212	LEU	2.1
1	D	178	TYR	2.1
1	B	136	PHE	2.1
1	B	241	LYS	2.0
1	C	460	PHE	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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	NA	D	501	1/1	0.96	0.45	7.92	72,72,72,72	0
3	CIT	B	503	13/13	0.84	0.32	4.04	53,77,87,89	0
3	CIT	C	503	13/13	0.84	0.35	2.89	50,67,73,83	0
2	NA	A	502	1/1	0.80	0.28	2.32	70,70,70,70	0
2	NA	D	502	1/1	0.73	0.21	1.83	57,57,57,57	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	CIT	D	503	13/13	0.87	0.20	1.61	58,78,86,91	0
3	CIT	A	503	13/13	0.88	0.21	1.09	49,68,72,73	0
2	NA	B	502	1/1	0.94	0.24	0.88	104,104,104,104	0
2	NA	C	502	1/1	0.92	0.21	0.36	69,69,69,69	0
2	NA	B	501	1/1	0.93	0.19	0.18	95,95,95,95	0
2	NA	A	501	1/1	0.98	0.17	-0.19	63,63,63,63	0
2	NA	C	501	1/1	0.95	0.14	-0.90	72,72,72,72	0

6.5 Other polymers [i](#)

There are no such residues in this entry.