



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 03:27 am BST

PDB ID : 3Q17
Title : Structure of a slow CLC Cl⁻/H⁺ antiporter from a cyanobacterium in Bromide
Authors : Jayaram, H.; Robertson, J.L.; Fang, W.; Williams, C.; Miller, C.
Deposited on : 2010-12-16
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	:	2.11
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

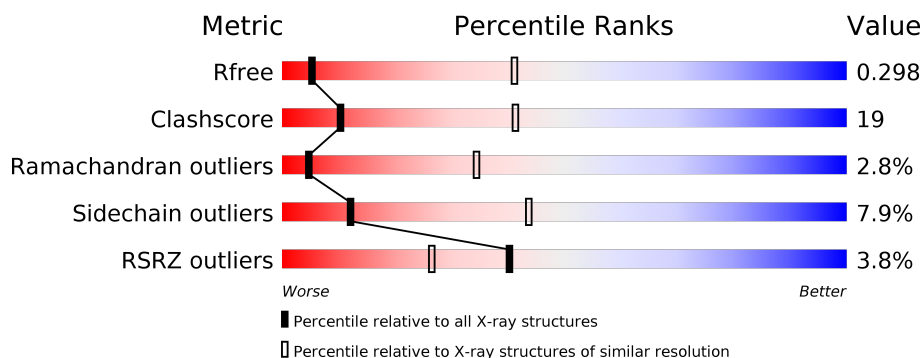
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.60 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 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	466	<div> <div>2%</div> <div> <div></div> <div>52%</div> <div>33%</div> <div>6%</div> <div>9%</div> </div> </div>
1	B	466	<div> <div>5%</div> <div> <div></div> <div>58%</div> <div>29%</div> <div>•</div> <div>9%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6400 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 Sll0855 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	425	Total	C	N	O	S	0	0	0
			3199	2110	533	536	20			
1	B	425	Total	C	N	O	S	0	0	0
			3199	2110	533	536	20			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	451	GLY	-	EXPRESSION TAG	UNP P73745
A	452	SER	-	EXPRESSION TAG	UNP P73745
A	453	LEU	-	EXPRESSION TAG	UNP P73745
A	454	VAL	-	EXPRESSION TAG	UNP P73745
A	455	PRO	-	EXPRESSION TAG	UNP P73745
A	456	ARG	-	EXPRESSION TAG	UNP P73745
A	457	GLY	-	EXPRESSION TAG	UNP P73745
A	458	SER	-	EXPRESSION TAG	UNP P73745
A	459	GLY	-	EXPRESSION TAG	UNP P73745
A	460	GLY	-	EXPRESSION TAG	UNP P73745
A	461	HIS	-	EXPRESSION TAG	UNP P73745
A	462	HIS	-	EXPRESSION TAG	UNP P73745
A	463	HIS	-	EXPRESSION TAG	UNP P73745
A	464	HIS	-	EXPRESSION TAG	UNP P73745
A	465	HIS	-	EXPRESSION TAG	UNP P73745
A	466	HIS	-	EXPRESSION TAG	UNP P73745
B	451	GLY	-	EXPRESSION TAG	UNP P73745
B	452	SER	-	EXPRESSION TAG	UNP P73745
B	453	LEU	-	EXPRESSION TAG	UNP P73745
B	454	VAL	-	EXPRESSION TAG	UNP P73745
B	455	PRO	-	EXPRESSION TAG	UNP P73745
B	456	ARG	-	EXPRESSION TAG	UNP P73745
B	457	GLY	-	EXPRESSION TAG	UNP P73745
B	458	SER	-	EXPRESSION TAG	UNP P73745
B	459	GLY	-	EXPRESSION TAG	UNP P73745

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Chain	Residue	Modelled	Actual	Comment	Reference
B	460	GLY	-	EXPRESSION TAG	UNP P73745
B	461	HIS	-	EXPRESSION TAG	UNP P73745
B	462	HIS	-	EXPRESSION TAG	UNP P73745
B	463	HIS	-	EXPRESSION TAG	UNP P73745
B	464	HIS	-	EXPRESSION TAG	UNP P73745
B	465	HIS	-	EXPRESSION TAG	UNP P73745
B	466	HIS	-	EXPRESSION TAG	UNP P73745

- Molecule 2 is BROMIDE ION (three-letter code: BR) (formula: Br).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Br	0	0
			1	1		
2	A	1	Total	Br	0	0
			1	1		

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 ($\text{RSRZ} > 2$). 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.

[illegible]

Chain B:

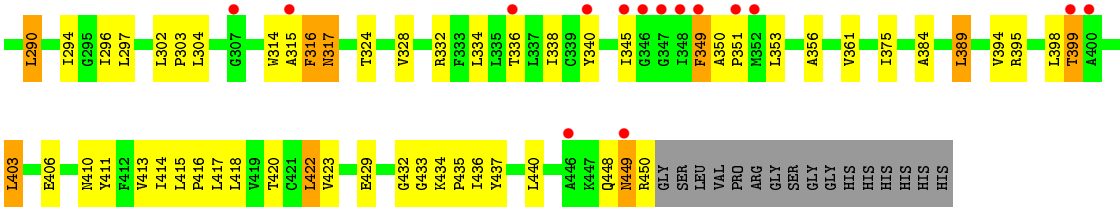
58% 29% 9%

5%

MET
ALA
ALA
ALA
ASP
PHE
GLU
THR
SER
ASN
ARG
ARG
TRP
LEU
ASP
ASP
LYS
PRO
ARG
ASN
LEU
THR
ASP
SER
SER
ALA
ARG

Q84
Q85
L88
S89
F90
Q93
Q94
Q95
Q96
Q97
F98
S103
G104
I105
P106
Q107
I108
L112
K115
L116
L117
L118
Q121
L124
P125
L140
L141
G142
F143
E144
G145
P146
Q149
I154
G160
K163
Q166
Q169
Y175
T183
F185
K186

A187
P188
V192
A193
L194
E197
S204
S205
Q206
Q207
L208
A209
Y210
L213
L214
F215
V218
T221
R225
R228
G229
Q230
I234
P243
S246
F250
I251
I252
L253
G254
I255
L256
F257
G258
V259
M260
L268
D273
R277
L278
D279



4 Data and refinement statistics

Property	Value	Source
Space group	P 3 2 1	Depositor
Cell constants a, b, c, α , β , γ	207.21Å 207.21Å 105.98Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	68.48 – 3.60 68.48 – 3.60	Depositor EDS
% Data completeness (in resolution range)	97.3 (68.48-3.60) 97.4 (68.48-3.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.26	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 3.58Å)	Xtriage
Refinement program	PHENIX 1.6.1_357, REFMAC 5.5.0109	Depositor
R, R_{free}	0.281 , 0.310 0.267 , 0.298	Depositor DCC
R_{free} test set	1495 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	95.0	Xtriage
Anisotropy	0.697	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.059 for -h,-k,l	Xtriage
F_o, F_c correlation	0.80	EDS
Total number of atoms	6400	wwPDB-VP
Average B, all atoms (Å ²)	121.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.06% 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: BR

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	0.23	0/3276	0.42	0/4457
1	B	0.23	0/3276	0.41	0/4457
All	All	0.23	0/6552	0.42	0/8914

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

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	3199	0	3360	146	0
1	B	3199	0	3360	114	0
2	A	1	0	0	1	0
2	B	1	0	0	0	0
All	All	6400	0	6720	245	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 19.

All (245) 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:225:ARG:HD3	1:A:230:GLN:HG3	1.27	1.10
1:B:225:ARG:HD3	1:B:230:GLN:HG3	1.35	1.09
1:B:71:PRO:HB2	1:B:72:PRO:HD2	1.34	1.08
1:A:278:LEU:HB3	1:A:279:PRO:HA	1.38	1.01
1:B:278:LEU:HB3	1:B:279:PRO:HA	1.41	1.00
1:A:36:ILE:HD11	1:A:215:PHE:HD1	1.28	0.98
1:B:71:PRO:HB2	1:B:72:PRO:CD	1.96	0.95
1:A:71:PRO:HB2	1:A:72:PRO:HD2	1.47	0.94
1:A:278:LEU:HB3	1:A:279:PRO:CA	2.01	0.90
1:A:71:PRO:HB2	1:A:72:PRO:CD	2.04	0.88
1:B:278:LEU:HB3	1:B:279:PRO:CA	2.04	0.87
1:A:36:ILE:HD11	1:A:215:PHE:CD1	2.13	0.83
1:B:144:GLU:HG3	1:B:349:PHE:HB2	1.60	0.82
1:A:218:VAL:HG22	1:B:418:LEU:HD13	1.64	0.80
1:A:418:LEU:HD13	1:B:218:VAL:HG22	1.64	0.78
1:A:188:PRO:HG3	1:A:221:THR:HG21	1.64	0.77
1:A:144:GLU:HG3	1:A:349:PHE:HB2	1.65	0.77
1:B:71:PRO:HD2	1:B:73:LEU:HB2	1.67	0.76
1:A:436:ILE:O	1:A:440:LEU:HB2	1.86	0.76
1:B:116:LEU:HD23	1:B:117:PRO:HD2	1.69	0.75
1:B:243:PRO:HG2	1:B:246:SER:HB3	1.71	0.72
1:B:68:ALA:N	1:B:69:PRO:HD2	2.05	0.71
1:B:411:TYR:CE1	1:B:414:ILE:HD12	2.27	0.70
1:A:71:PRO:HD2	1:A:73:LEU:HB2	1.73	0.69
1:B:268:LEU:HD12	1:B:436:ILE:HD11	1.73	0.69
1:A:37:VAL:O	1:A:41:ILE:HG12	1.92	0.69
1:A:251:ILE:O	1:A:255:ILE:HG12	1.94	0.68
1:B:356:ALA:HB2	1:B:389:LEU:HB2	1.75	0.68
1:A:395:ARG:O	1:A:395:ARG:HG2	1.93	0.68
1:A:225:ARG:HA	1:A:229:GLY:HA3	1.75	0.67
1:A:303:PRO:HG3	1:A:314:TRP:CG	2.30	0.67
1:A:68:ALA:N	1:A:69:PRO:HD2	2.10	0.67
1:B:251:ILE:O	1:B:255:ILE:HG12	1.95	0.67
1:B:192:VAL:HG21	1:B:214:LEU:HD23	1.78	0.65
1:A:268:LEU:HD12	1:A:436:ILE:HD11	1.80	0.64
1:A:95:ARG:HH22	1:A:450:ARG:HH22	1.44	0.64
1:B:28:HIS:CE1	1:B:30:ARG:HB2	2.33	0.64
1:B:395:ARG:O	1:B:395:ARG:HG2	1.97	0.63
1:B:41:ILE:HG22	1:B:154:ILE:HD13	1.81	0.63
1:B:303:PRO:HG3	1:B:314:TRP:CG	2.34	0.62
1:B:175:VAL:HA	1:B:213:LEU:HD23	1.80	0.62
1:A:135:LEU:HG	1:A:141:ALA:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:TYR:CE1	1:A:414:ILE:HD12	2.35	0.62
1:B:225:ARG:HA	1:B:229:GLY:HA3	1.81	0.62
1:A:422:LEU:HD11	1:B:215:PHE:CZ	2.35	0.61
1:B:315:ALA:HB1	1:B:361:VAL:HG21	1.82	0.61
1:A:112:LEU:HD11	1:A:174:ALA:HB2	1.82	0.61
1:A:396:ALA:HB1	1:A:399:THR:CG2	2.32	0.60
1:A:384:ALA:HB1	1:A:420:THR:HG21	1.84	0.59
1:A:94:LYS:HB3	1:A:98:PRO:HG3	1.84	0.59
1:A:315:ALA:HB1	1:A:361:VAL:HG21	1.84	0.59
1:B:395:ARG:HD3	1:B:435:PRO:HG3	1.84	0.59
1:A:215:PHE:CZ	1:B:422:LEU:HD13	2.38	0.59
1:A:234:ILE:HD12	1:A:313:LEU:HD23	1.85	0.59
1:B:394:VAL:O	1:B:395:ARG:HB3	2.03	0.59
1:A:116:LEU:HD23	1:A:117:PRO:HD2	1.84	0.58
1:A:340:TYR:OH	1:A:440:LEU:HD21	2.03	0.58
1:B:94:LYS:HB3	1:B:98:PRO:HG3	1.86	0.58
1:A:394:VAL:O	1:A:395:ARG:HB3	2.03	0.58
1:A:38:VAL:O	1:A:42:THR:HG22	2.03	0.58
1:A:243:PRO:HG2	1:A:246:SER:HB3	1.86	0.57
1:A:306:ASP:HB2	1:A:310:ASN:HD21	1.69	0.57
1:A:304:LEU:HD23	1:A:304:LEU:H	1.69	0.57
1:B:436:ILE:O	1:B:440:LEU:HB2	2.05	0.57
1:B:188:PRO:HG3	1:B:221:THR:HG21	1.86	0.57
1:A:175:VAL:HA	1:A:213:LEU:HD23	1.86	0.56
1:B:207:THR:HG23	1:B:208:LEU:HD22	1.87	0.56
1:B:37:VAL:O	1:B:41:ILE:HG12	2.05	0.56
1:A:187:ALA:HB1	1:A:406:GLU:OE1	2.06	0.56
1:A:257:PHE:HA	1:A:260:MET:HB2	1.88	0.56
1:A:413:VAL:O	1:A:413:VAL:HG12	2.06	0.56
1:A:308:GLY:O	1:A:312:VAL:HG23	2.06	0.55
1:A:416:PRO:O	1:A:420:THR:HG22	2.05	0.55
1:B:26:SER:HB2	1:B:208:LEU:HD23	1.88	0.55
1:B:422:LEU:HD12	1:B:423:VAL:N	2.21	0.55
1:A:192:VAL:HG21	1:A:214:LEU:HD23	1.88	0.55
1:B:384:ALA:HB1	1:B:420:THR:HG21	1.88	0.55
1:A:278:LEU:CB	1:A:279:PRO:HA	2.26	0.55
1:A:71:PRO:CB	1:A:72:PRO:CD	2.83	0.55
1:B:413:VAL:O	1:B:413:VAL:HG12	2.07	0.54
1:A:41:ILE:HB	1:A:154:ILE:HG21	1.90	0.54
1:B:414:ILE:HG23	1:B:415:LEU:N	2.23	0.54
1:A:197:GLU:HG3	1:B:210:TYR:HD2	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:PHE:CD2	1:A:403:LEU:HD21	2.43	0.53
1:B:141:ALA:HB1	1:B:142:GLY:HA3	1.90	0.53
1:B:410:ASN:OD1	1:B:413:VAL:HG23	2.09	0.53
1:A:225:ARG:HA	1:A:229:GLY:CA	2.37	0.53
1:A:398:LEU:HD23	1:B:214:LEU:HD21	1.90	0.53
1:A:215:PHE:CE2	1:B:422:LEU:HD13	2.43	0.53
1:A:267:GLY:O	1:A:271:VAL:HG23	2.08	0.53
1:A:414:ILE:HG23	1:A:415:LEU:N	2.24	0.53
1:A:210:TYR:HD2	1:B:197:GLU:HG3	1.74	0.53
1:A:356:ALA:HB2	1:A:389:LEU:HB2	1.91	0.53
1:B:350:ALA:HB3	1:B:351:PRO:HD3	1.90	0.52
1:A:201:PRO:HG2	1:A:203:PHE:CE1	2.44	0.52
1:B:375:ILE:HG22	1:B:375:ILE:O	2.09	0.52
1:A:214:LEU:HD21	1:B:398:LEU:HD23	1.91	0.52
1:B:62:GLN:O	1:B:66:ILE:HG13	2.09	0.52
1:A:234:ILE:HG23	1:A:234:ILE:O	2.10	0.52
1:A:395:ARG:HD3	1:A:435:PRO:HG3	1.91	0.52
1:B:185:PHE:CD2	1:B:403:LEU:HD21	2.45	0.52
1:A:375:ILE:HG22	1:A:375:ILE:O	2.10	0.52
1:A:124:LEU:HB3	1:A:125:PRO:HD3	1.92	0.51
1:A:28:HIS:CE1	1:A:30:ARG:HB2	2.45	0.51
1:B:72:PRO:O	1:B:75:TRP:HB2	2.11	0.51
1:A:197:GLU:HA	1:B:210:TYR:HE2	1.75	0.51
1:B:187:ALA:HB1	1:B:406:GLU:OE1	2.10	0.51
1:B:268:LEU:HD21	1:B:340:TYR:HD2	1.76	0.51
1:A:197:GLU:OE1	1:A:399:THR:HG22	2.11	0.51
1:B:278:LEU:CB	1:B:279:PRO:HA	2.28	0.50
1:A:71:PRO:CB	1:A:72:PRO:HD2	2.31	0.50
1:B:250:PHE:HB3	1:B:420:THR:HB	1.93	0.50
1:B:225:ARG:HA	1:B:229:GLY:CA	2.41	0.50
1:A:189:LEU:HB3	1:A:402:LEU:HD13	1.94	0.50
1:A:36:ILE:CD1	1:A:215:PHE:HD1	2.14	0.50
1:A:222:ILE:HG12	1:B:415:LEU:HD13	1.92	0.50
1:B:46:GLY:HA3	1:B:183:THR:HG21	1.93	0.49
1:A:199:MET:O	1:A:199:MET:HG2	2.12	0.49
1:B:90:PHE:HA	1:B:93:MET:HE3	1.95	0.49
1:A:104:GLY:CA	1:A:149:GLN:HG3	2.43	0.48
1:A:97:ALA:C	1:A:99:ASP:H	2.17	0.48
1:A:141:ALA:HB1	1:A:142:GLY:HA3	1.94	0.48
1:A:194:LEU:O	1:A:198:GLU:O	2.31	0.48
1:A:144:GLU:HG3	1:A:349:PHE:CB	2.41	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:PHE:HA	1:B:260:MET:HB2	1.94	0.48
1:A:104:GLY:HA2	1:A:149:GLN:HG3	1.96	0.48
1:B:144:GLU:CG	1:B:349:PHE:HB2	2.40	0.48
1:A:26:SER:HB2	1:A:208:LEU:HD23	1.95	0.47
1:A:207:THR:HG23	1:A:208:LEU:HD22	1.96	0.47
1:B:68:ALA:N	1:B:69:PRO:CD	2.76	0.47
1:A:198:GLU:HG3	1:A:394:VAL:HG12	1.97	0.47
1:A:214:LEU:O	1:A:218:VAL:HG23	2.15	0.47
1:B:34:ALA:O	1:B:38:VAL:HG23	2.15	0.47
1:A:111:HIS:O	1:A:170:ARG:NH2	2.48	0.47
1:A:304:LEU:CD2	1:A:304:LEU:H	2.28	0.47
1:A:72:PRO:O	1:A:75:TRP:HB2	2.14	0.47
1:A:410:ASN:OD1	1:A:413:VAL:HG23	2.15	0.47
1:B:124:LEU:HB3	1:B:125:PRO:HD3	1.97	0.47
1:A:127:LYS:HD2	1:A:146:PRO:HA	1.97	0.46
1:A:278:LEU:CB	1:A:279:PRO:CA	2.84	0.46
1:A:350:ALA:HB3	1:A:351:PRO:HD3	1.97	0.46
1:B:394:VAL:HG12	1:B:394:VAL:O	2.15	0.46
1:B:394:VAL:HG13	1:B:437:TYR:HD2	1.79	0.46
1:A:233:ILE:HB	1:A:407:MET:HB2	1.97	0.46
1:B:81:ILE:O	1:B:85:MET:HG3	2.15	0.46
1:A:353:LEU:HA	1:A:353:LEU:HD12	1.75	0.46
1:B:108:ILE:O	1:B:112:LEU:HB2	2.16	0.46
1:B:278:LEU:CB	1:B:279:PRO:CA	2.85	0.46
1:A:71:PRO:HD2	1:A:73:LEU:CB	2.43	0.46
1:B:41:ILE:HB	1:B:154:ILE:HG21	1.98	0.46
1:B:429:GLU:OE1	1:B:435:PRO:HD3	2.16	0.46
1:A:280:PRO:O	1:A:284:LYS:HG2	2.16	0.46
1:A:250:PHE:CZ	1:A:416:PRO:HB3	2.51	0.46
1:A:438:THR:O	1:A:442:GLU:HG3	2.16	0.46
1:A:314:TRP:CZ3	1:A:325:LEU:HD23	2.51	0.45
1:B:71:PRO:CD	1:B:73:LEU:HB2	2.42	0.45
1:A:95:ARG:HH22	1:A:450:ARG:NH2	2.14	0.45
1:B:198:GLU:O	1:B:199:MET:HB3	2.16	0.45
1:A:175:VAL:HG22	1:A:213:LEU:HA	1.98	0.45
1:A:303:PRO:HG3	1:A:314:TRP:CD2	2.52	0.45
1:B:73:LEU:O	1:B:73:LEU:HD23	2.16	0.45
1:B:221:THR:O	1:B:225:ARG:HG3	2.17	0.45
1:B:234:ILE:HG23	1:B:234:ILE:O	2.17	0.45
1:A:103:SER:OG	1:A:104:GLY:N	2.50	0.45
1:A:273:ASP:O	1:A:277:ARG:HD3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:VAL:O	1:A:417:LEU:HB2	2.17	0.45
1:B:332:ARG:O	1:B:336:THR:HG23	2.17	0.45
1:B:416:PRO:O	1:B:420:THR:HG22	2.17	0.45
1:A:103:SER:OG	2:A:1:BR:BR	2.84	0.45
1:B:229:GLY:HA3	1:B:230:GLN:HA	1.77	0.45
1:B:273:ASP:O	1:B:277:ARG:HD3	2.16	0.45
1:B:422:LEU:HD12	1:B:423:VAL:HG23	1.98	0.44
1:B:315:ALA:HB1	1:B:361:VAL:CG2	2.45	0.44
1:A:297:LEU:O	1:A:304:LEU:HD21	2.18	0.44
1:B:449:ASN:O	1:B:450:ARG:C	2.54	0.44
1:A:419:VAL:O	1:A:423:VAL:HB	2.17	0.44
1:A:433:GLY:O	1:A:434:LYS:HB2	2.18	0.44
1:A:404:THR:OG1	1:A:417:LEU:HD11	2.18	0.44
1:B:290:LEU:HD21	1:B:338:ILE:CG2	2.47	0.44
1:A:354:GLY:O	1:A:358:ILE:HG13	2.18	0.44
1:B:294:ILE:HD13	1:B:297:LEU:HD12	1.99	0.44
1:A:197:GLU:HG3	1:B:210:TYR:CD2	2.52	0.43
1:B:84:GLY:O	1:B:88:LEU:HB2	2.17	0.43
1:A:105:ILE:HD12	1:A:105:ILE:N	2.33	0.43
1:B:250:PHE:HA	1:B:253:LEU:HB3	1.99	0.43
1:A:401:ILE:HD13	1:A:418:LEU:HD23	2.00	0.43
1:A:94:LYS:HA	1:A:95:ARG:HA	1.64	0.43
1:B:197:GLU:OE1	1:B:399:THR:HG23	2.18	0.43
1:A:411:TYR:CE1	1:B:406:GLU:HG2	2.53	0.43
1:A:221:THR:O	1:A:225:ARG:HG3	2.18	0.43
1:B:334:LEU:O	1:B:338:ILE:HD13	2.19	0.43
1:A:100:THR:HG21	1:A:126:ILE:HG22	2.00	0.43
1:B:70:ILE:HA	1:B:71:PRO:HA	1.78	0.43
1:A:255:ILE:HD13	1:A:427:VAL:HG21	2.01	0.43
1:A:68:ALA:N	1:A:69:PRO:CD	2.80	0.43
1:B:105:ILE:N	1:B:106:PRO:CD	2.82	0.43
1:A:294:ILE:HD11	1:A:335:LEU:HD22	2.00	0.42
1:A:144:GLU:CG	1:A:349:PHE:HB2	2.42	0.42
1:A:204:ARG:HA	1:A:205:SER:HA	1.47	0.42
1:A:379:ALA:O	1:A:383:ILE:HG13	2.18	0.42
1:A:62:GLN:O	1:A:66:ILE:HG13	2.19	0.42
1:A:225:ARG:CA	1:A:229:GLY:HA3	2.47	0.42
1:A:95:ARG:NH2	1:A:450:ARG:HH12	2.18	0.42
1:A:183:THR:O	1:A:183:THR:HG22	2.19	0.42
1:B:199:MET:HG2	1:B:199:MET:O	2.18	0.42
1:B:324:THR:O	1:B:328:VAL:HG23	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:256:LEU:O	1:B:259:VAL:HG22	2.20	0.42
1:A:348:ILE:HG23	1:A:352:MET:HE1	2.02	0.42
1:A:34:ALA:O	1:A:38:VAL:HG23	2.19	0.42
1:A:315:ALA:HB1	1:A:361:VAL:CG2	2.49	0.42
1:A:392:ALA:HA	1:A:425:SER:HA	2.02	0.42
1:B:200:HIS:HA	1:B:201:PRO:HD3	1.81	0.42
1:B:302:LEU:HD12	1:B:302:LEU:HA	1.94	0.42
1:B:316:PHE:HA	1:B:317:ASN:HA	1.67	0.42
1:A:447:LYS:C	1:A:449:ASN:H	2.23	0.42
1:B:140:LEU:HD12	1:B:336:THR:HG22	2.02	0.42
1:A:374:GLN:C	1:A:376:PRO:HD3	2.40	0.41
1:B:194:LEU:O	1:B:198:GLU:O	2.38	0.41
1:A:47:ALA:HB3	1:A:227:ILE:HD12	2.01	0.41
1:A:105:ILE:HD11	1:A:148:ILE:HD12	2.02	0.41
1:A:250:PHE:HB3	1:A:420:THR:HB	2.02	0.41
1:A:64:ALA:O	1:A:68:ALA:HB2	2.19	0.41
1:B:144:GLU:H	1:B:144:GLU:CD	2.24	0.41
1:B:79:ALA:HB2	1:B:296:ILE:CD1	2.50	0.41
1:B:433:GLY:O	1:B:434:LYS:HB2	2.20	0.41
1:B:143:PHE:O	1:B:146:PRO:HD2	2.21	0.41
1:A:234:ILE:HG12	1:A:236:LEU:CD1	2.50	0.41
1:A:415:LEU:HD11	1:B:225:ARG:HD2	2.02	0.41
1:A:150:MET:O	1:A:154:ILE:HG13	2.21	0.41
1:A:81:ILE:O	1:A:85:MET:HG3	2.21	0.41
1:A:223:ILE:O	1:A:227:ILE:HG13	2.20	0.41
1:B:105:ILE:HD12	1:B:105:ILE:N	2.36	0.41
1:B:204:ARG:HA	1:B:205:SER:HA	1.48	0.41
1:A:422:LEU:HD11	1:B:215:PHE:CE1	2.55	0.41
1:B:340:TYR:OH	1:B:440:LEU:HD21	2.21	0.41
1:B:70:ILE:HG23	1:B:70:ILE:O	2.20	0.41
1:A:316:PHE:HA	1:A:317:ASN:HA	1.76	0.41
1:B:50:LYS:HG2	1:B:143:PHE:CD1	2.56	0.41
1:B:440:LEU:HA	1:B:440:LEU:HD12	1.86	0.41
1:A:115:LYS:HD2	1:A:115:LYS:H	1.86	0.41
1:A:369:LEU:HD13	1:A:369:LEU:C	2.42	0.41
1:A:364:ALA:HB1	1:A:378:PRO:O	2.21	0.40
1:A:70:ILE:O	1:A:70:ILE:HG23	2.21	0.40
1:B:160:GLY:O	1:B:163:LYS:HD2	2.21	0.40
1:A:249:MET:HG2	1:A:367:PHE:CE1	2.56	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	423/466 (91%)	367 (87%)	43 (10%)	13 (3%)	4	32
1	B	423/466 (91%)	374 (88%)	38 (9%)	11 (3%)	5	35
All	All	846/932 (91%)	741 (88%)	81 (10%)	24 (3%)	5	34

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	71	PRO
1	B	71	PRO
1	A	142	GLY
1	A	278	LEU
1	A	449	ASN
1	B	103	SER
1	B	278	LEU
1	A	96	PHE
1	A	103	SER
1	B	104	GLY
1	B	142	GLY
1	A	116	LEU
1	A	318	SER
1	B	96	PHE
1	B	116	LEU
1	B	345	ILE
1	A	434	LYS
1	B	449	ASN
1	A	234	ILE
1	A	345	ILE
1	B	38	VAL
1	A	104	GLY
1	A	98	PRO
1	B	432	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	334/368 (91%)	307 (92%)	27 (8%)	11	43
1	B	334/368 (91%)	308 (92%)	26 (8%)	12	44
All	All	668/736 (91%)	615 (92%)	53 (8%)	12	44

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	LEU
1	A	42	THR
1	A	63	LEU
1	A	88	LEU
1	A	95	ARG
1	A	96	PHE
1	A	112	LEU
1	A	115	LYS
1	A	116	LEU
1	A	120	TRP
1	A	121	GLN
1	A	126	ILE
1	A	166	GLN
1	A	228	ARG
1	A	236	LEU
1	A	260	MET
1	A	268	LEU
1	A	316	PHE
1	A	317	ASN
1	A	349	PHE
1	A	353	LEU
1	A	389	LEU
1	A	399	THR
1	A	403	LEU
1	A	417	LEU
1	A	422	LEU
1	A	447	LYS

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Mol	Chain	Res	Type
1	B	27	LEU
1	B	30	ARG
1	B	42	THR
1	B	63	LEU
1	B	88	LEU
1	B	95	ARG
1	B	115	LYS
1	B	116	LEU
1	B	121	GLN
1	B	166	GLN
1	B	169	GLN
1	B	215	PHE
1	B	228	ARG
1	B	268	LEU
1	B	290	LEU
1	B	304	LEU
1	B	316	PHE
1	B	317	ASN
1	B	349	PHE
1	B	353	LEU
1	B	389	LEU
1	B	399	THR
1	B	403	LEU
1	B	417	LEU
1	B	422	LEU
1	B	448	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	206	GLN
1	A	230	GLN
1	A	448	GLN
1	A	449	ASN
1	B	206	GLN
1	B	230	GLN

5.3.3 RNA ⓘ

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 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 [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	425/466 (91%)	-0.01	9 (2%) 63 48	68, 106, 159, 262	0
1	B	425/466 (91%)	0.23	23 (5%) 25 16	66, 126, 186, 252	0
All	All	850/932 (91%)	0.11	32 (3%) 40 26	66, 114, 180, 262	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	346	GLY	5.1
1	A	141	ALA	4.9
1	B	348	ILE	4.9
1	B	141	ALA	4.3
1	A	55	ASN	4.1
1	B	347	GLY	4.0
1	B	449	ASN	3.5
1	A	140	LEU	3.4
1	B	349	PHE	3.4
1	B	345	ILE	3.3
1	B	399	THR	3.3
1	A	204	ARG	3.2
1	B	140	LEU	3.0
1	B	70	ILE	3.0
1	B	204	ARG	2.9
1	B	400	ALA	2.8
1	B	340	TYR	2.8
1	B	69	PRO	2.7
1	B	351	PRO	2.7
1	B	352	MET	2.6
1	B	118	LEU	2.5
1	B	142	GLY	2.4
1	B	315	ALA	2.4
1	B	307	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	54	ASN	2.3
1	A	70	ILE	2.2
1	A	307	GLY	2.2
1	A	345	ILE	2.2
1	A	348	ILE	2.2
1	B	336	THR	2.1
1	B	149	GLN	2.1
1	B	446	ALA	2.1

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. 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(\AA^2)	Q<0.9
2	BR	A	1	1/1	0.91	0.35	147,147,147,147	0
2	BR	B	1	1/1	0.95	0.74	176,176,176,176	0

6.5 Other polymers [i](#)

There are no such residues in this entry.