



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:06 PM GMT

PDB ID : 4KKC
Title : Structure of the E148A mutant of CLC-ec1 deltaNC construct in 20mM Bromide
Authors : Lim, H.-H.; Miller, C.
Deposited on : 2013-05-05
Resolution : 3.18 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 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
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) : trunk26865

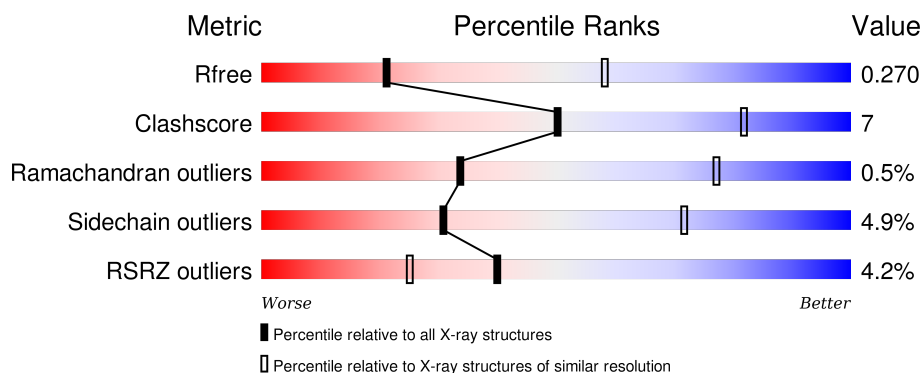
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.18 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	1115 (3.22-3.14)
Clashscore	102246	1125 (3.20-3.16)
Ramachandran outliers	100387	1105 (3.20-3.16)
Sidechain outliers	100360	1104 (3.20-3.16)
RSRZ outliers	91569	1120 (3.22-3.14)

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	446	<div> <div>3%</div> <div>77%</div> <div>20%</div> <div>.</div> </div>
1	B	446	<div> <div>5%</div> <div>74%</div> <div>24%</div> <div>..</div> </div>
2	C	222	<div> <div>3%</div> <div>85%</div> <div>13%</div> <div>.</div> </div>
2	E	222	<div> <div>3%</div> <div>83%</div> <div>14%</div> <div>.</div> </div>
3	D	211	<div> <div>7%</div> <div>81%</div> <div>17%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	211	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a small red segment at the beginning labeled '4%', a large green segment in the middle labeled '82%', and a small yellow segment at the end labeled '16%'. A small black dot is located at the far right end of the bar.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13215 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 H(+)/Cl(-) exchange transporter ClcA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	444	Total	C	N	O	S	0	0	0
			3329	2188	560	561	20			
1	B	441	Total	C	N	O	S	0	0	0
			3300	2172	553	555	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	EXPRESSION TAG	UNP P37019
A	148	ALA	GLU	ENGINEERED MUTATION	UNP P37019
A	461	LYS	-	EXPRESSION TAG	UNP P37019
B	16	MET	-	EXPRESSION TAG	UNP P37019
B	148	ALA	GLU	ENGINEERED MUTATION	UNP P37019
B	461	LYS	-	EXPRESSION TAG	UNP P37019

- Molecule 2 is a protein called Fab, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			
2	E	221	Total	C	N	O	S	0	0	0
			1672	1077	274	315	6			

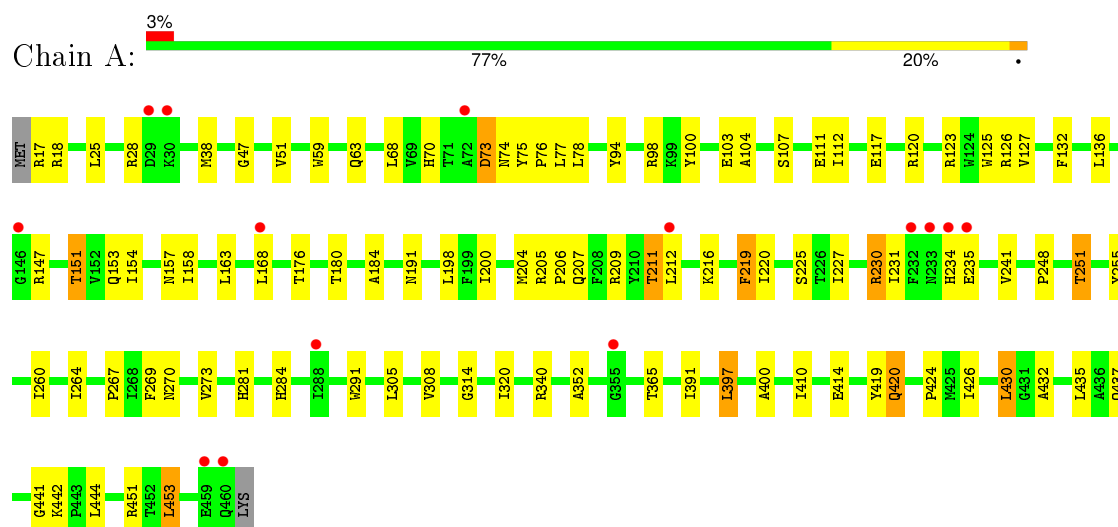
- Molecule 3 is a protein called Fab, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			
3	F	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			

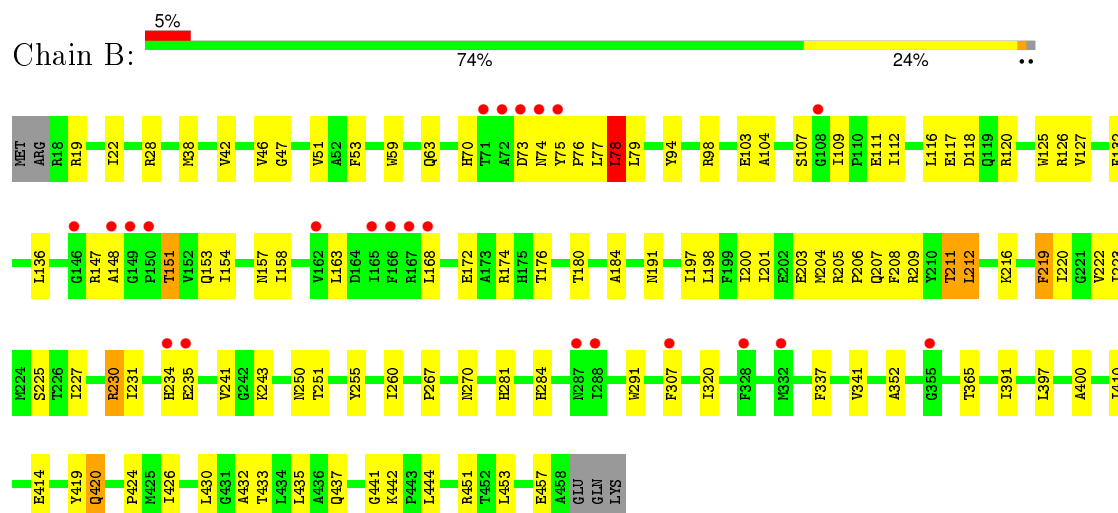
3 Residue-property plots [i](#)

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.

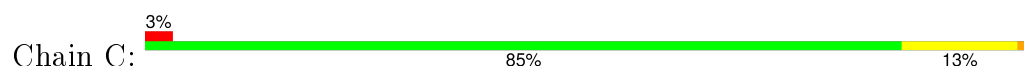
- Molecule 1: H(+)/Cl(-) exchange transporter ClcA

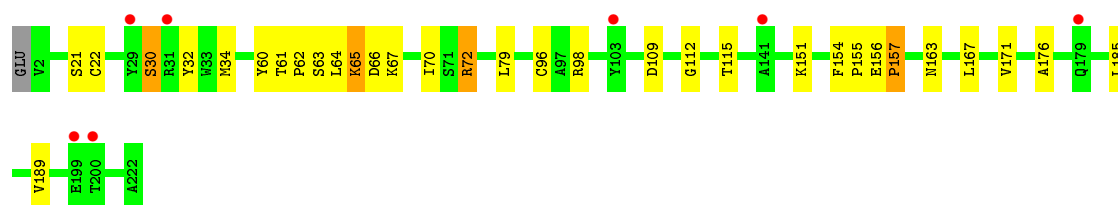


- Molecule 1: H(+)/Cl(-) exchange transporter ClcA

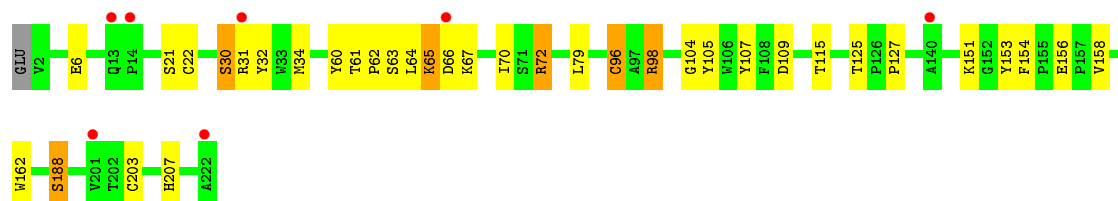
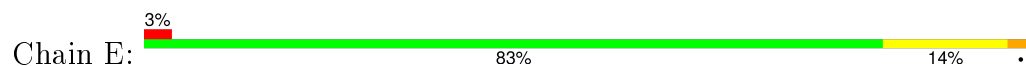


- Molecule 2: Fab, heavy chain

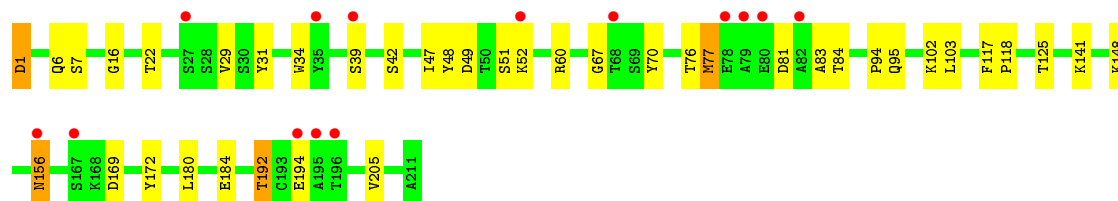
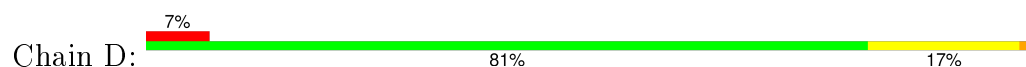




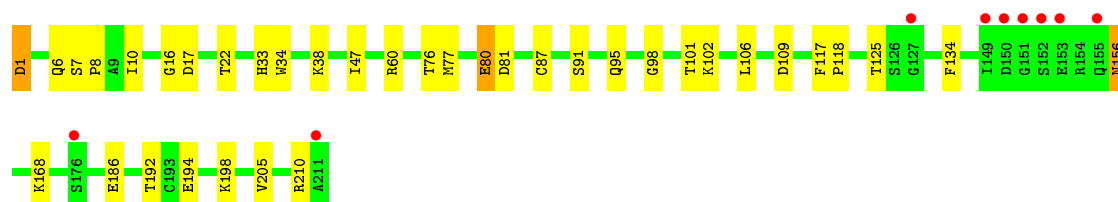
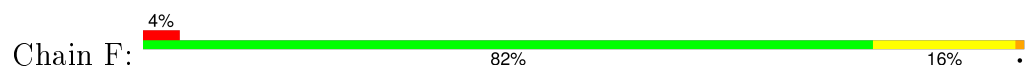
• Molecule 2: Fab, heavy chain



• Molecule 3: Fab, light chain



• Molecule 3: Fab, light chain



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	231.21Å 99.24Å 170.51Å 90.00° 132.00° 90.00°	Depositor
Resolution (Å)	29.53 – 3.18 29.66 – 3.18	Depositor EDS
% Data completeness (in resolution range)	98.3 (29.53-3.18) 98.5 (29.66-3.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 3.18Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.231 , 0.264 0.241 , 0.270	Depositor DCC
R_{free} test set	2426 reflections (5.34%)	DCC
Wilson B-factor (Å ²)	95.1	Xtriage
Anisotropy	0.505	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 20.0	EDS
Estimated twinning fraction	0.004 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 47864 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	13215	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.47% 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	0.30	0/3401	0.42	0/4616
1	B	0.30	0/3372	0.43	1/4578 (0.0%)
2	C	0.34	0/1721	0.46	0/2355
2	E	0.34	0/1721	0.47	0/2355
3	D	0.29	0/1660	0.47	0/2257
3	F	0.33	0/1660	0.47	0/2257
All	All	0.31	0/13535	0.45	1/18418 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	78	LEU	CA-CB-CG	6.16	129.47	115.30

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	3329	0	3483	64	0
1	B	3300	0	3456	70	0
2	C	1672	0	1654	15	0
2	E	1672	0	1654	21	0
3	D	1621	0	1546	21	0
3	F	1621	0	1546	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	13215	0	13339	187	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 7.

All (187) 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:18:ARG:HH11	1:B:457:GLU:HB3	1.46	0.79
1:B:147:ARG:O	1:B:151:THR:OG1	2.04	0.76
1:A:200:ILE:HD12	1:A:204:MET:HG3	1.69	0.74
3:D:1:ASP:N	3:D:1:ASP:OD2	2.21	0.73
1:A:241:VAL:HG11	1:A:391:ILE:HD11	1.70	0.72
2:E:98:ARG:NH1	2:E:109:ASP:OD2	2.23	0.71
1:A:216:LYS:NZ	1:B:437:GLN:OE1	2.23	0.71
1:A:147:ARG:O	1:A:151:THR:OG1	2.06	0.71
3:F:1:ASP:OD2	3:F:1:ASP:N	2.23	0.70
1:B:241:VAL:HG11	1:B:391:ILE:HD11	1.74	0.69
1:A:200:ILE:HA	1:A:204:MET:HB2	1.74	0.68
1:B:200:ILE:HD12	1:B:204:MET:HG3	1.74	0.68
1:B:200:ILE:HA	1:B:204:MET:HB2	1.76	0.68
3:F:60:ARG:NH2	3:F:81:ASP:OD2	2.27	0.67
1:A:437:GLN:OE1	1:B:216:LYS:NZ	2.27	0.66
3:D:95:GLN:N	3:D:95:GLN:OE1	2.27	0.65
1:B:75:TYR:HA	1:B:78:LEU:HD12	1.77	0.65
3:F:95:GLN:N	3:F:95:GLN:OE1	2.29	0.64
1:B:117:GLU:OE1	1:B:209:ARG:NH1	2.31	0.63
3:D:194:GLU:HG2	3:D:205:VAL:HG12	1.80	0.61
2:C:22:CYS:HB3	2:C:79:LEU:HB3	1.82	0.61
1:B:206:PRO:HG2	1:B:211:THR:HG21	1.81	0.61
2:C:32:TYR:O	2:C:72:ARG:NH2	2.34	0.61
2:C:98:ARG:NH1	2:C:109:ASP:OD2	2.34	0.59
2:E:61:THR:O	2:E:63:SER:N	2.35	0.59
1:A:111:GLU:OE2	1:A:120:ARG:NE	2.36	0.58
1:A:73:ASP:OD1	1:A:73:ASP:N	2.36	0.58
1:B:38:MET:HG3	1:B:168:LEU:HD11	1.85	0.58
1:B:111:GLU:OE2	1:B:120:ARG:NE	2.36	0.58
2:E:64:LEU:HB2	2:E:67:LYS:HB2	1.86	0.58
1:A:260:ILE:HG23	1:A:435:LEU:HG	1.86	0.57
2:C:64:LEU:HB2	2:C:67:LYS:HB2	1.87	0.57
1:A:270:ASN:ND2	1:A:442:LYS:O	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:163:ASN:HD22	2:C:167:LEU:HD13	1.69	0.56
1:B:163:LEU:HD12	1:B:168:LEU:HB2	1.88	0.56
3:F:38:LYS:NZ	3:F:80:GLU:O	2.36	0.55
1:B:94:TYR:CZ	1:B:352:ALA:HB2	2.42	0.55
3:D:60:ARG:NH2	3:D:81:ASP:OD2	2.39	0.55
2:C:61:THR:O	2:C:63:SER:N	2.40	0.54
1:A:117:GLU:OE1	1:A:209:ARG:NH1	2.40	0.54
3:F:16:GLY:HA2	3:F:76:THR:HG23	1.90	0.54
1:B:198:LEU:HG	1:B:410:ILE:HD12	1.89	0.54
1:A:28:ARG:HE	1:B:207:GLN:HG2	1.73	0.53
1:B:74:ASN:HB3	1:B:77:LEU:HB3	1.91	0.53
1:A:112:ILE:HG13	1:A:153:GLN:HA	1.91	0.52
1:B:125:TRP:CD1	1:B:126:ARG:HG3	2.44	0.52
2:E:34:MET:HB3	2:E:79:LEU:HD22	1.92	0.52
1:B:98:ARG:HD2	1:B:291:TRP:CE3	2.45	0.52
1:A:38:MET:HG3	1:A:168:LEU:HD11	1.91	0.52
1:B:281:HIS:HA	1:B:284:HIS:CE1	2.45	0.52
1:A:206:PRO:HG2	1:A:211:THR:HG21	1.91	0.51
3:F:194:GLU:HG2	3:F:205:VAL:HG12	1.92	0.51
1:A:104:ALA:HB2	1:A:127:VAL:HG13	1.91	0.51
1:A:198:LEU:HG	1:A:410:ILE:HD12	1.92	0.51
1:A:414:GLU:OE1	1:B:419:TYR:OH	2.24	0.51
2:C:34:MET:HB3	2:C:79:LEU:HD22	1.91	0.51
1:A:28:ARG:NH2	1:B:203:GLU:OE1	2.30	0.51
1:A:184:ALA:HB1	1:A:225:SER:HB2	1.92	0.51
1:B:270:ASN:ND2	1:B:442:LYS:O	2.44	0.50
1:B:112:ILE:HG13	1:B:153:GLN:HA	1.94	0.49
3:D:31:TYR:HB3	3:D:49:ASP:HA	1.94	0.49
1:A:227:ILE:O	1:A:231:ILE:HG12	2.13	0.49
1:B:227:ILE:O	1:B:231:ILE:HG12	2.13	0.49
2:E:22:CYS:HB3	2:E:79:LEU:HB3	1.93	0.49
1:A:98:ARG:HD2	1:A:291:TRP:CE3	2.47	0.49
1:B:104:ALA:HB2	1:B:127:VAL:HG13	1.93	0.49
1:A:419:TYR:OH	1:B:414:GLU:OE1	2.26	0.48
3:D:156:ASN:N	3:D:156:ASN:OD1	2.46	0.48
2:E:32:TYR:O	2:E:72:ARG:NH2	2.46	0.48
1:A:430:LEU:HD11	1:B:219:PHE:HB3	1.94	0.48
2:E:125:THR:N	2:E:154:PHE:O	2.39	0.48
3:F:156:ASN:OD1	3:F:156:ASN:N	2.45	0.48
1:A:267:PRO:HG3	1:A:441:GLY:HA3	1.94	0.48
1:A:314:GLY:O	1:A:340:ARG:NH2	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:ASN:OD1	1:A:230:ARG:NH1	2.47	0.48
1:A:132:PHE:O	1:A:136:LEU:HB2	2.14	0.48
1:A:176:THR:O	1:A:180:THR:HG23	2.14	0.48
1:A:248:PRO:O	1:A:251:THR:HG22	2.13	0.48
2:C:65:LYS:H	2:C:65:LYS:HG3	1.38	0.47
1:A:281:HIS:HA	1:A:284:HIS:CE1	2.49	0.47
1:B:234:HIS:CD2	1:B:235:GLU:HG2	2.50	0.47
1:B:184:ALA:HB1	1:B:225:SER:HB2	1.95	0.47
1:A:94:TYR:CZ	1:A:352:ALA:HB2	2.50	0.47
1:B:176:THR:O	1:B:180:THR:HG23	2.15	0.47
3:D:29:VAL:O	3:D:70:TYR:OH	2.25	0.47
1:A:400:ALA:HB2	1:A:432:ALA:HB1	1.97	0.46
1:B:127:VAL:HB	1:B:157:ASN:ND2	2.30	0.46
1:B:73:ASP:OD1	1:B:73:ASP:N	2.48	0.46
2:E:127:PRO:HB3	2:E:153:TYR:HB3	1.98	0.46
1:A:216:LYS:O	1:A:220:ILE:HG13	2.16	0.46
1:B:42:VAL:O	1:B:46:VAL:HG23	2.16	0.46
3:D:84:THR:HA	3:D:102:LYS:HA	1.97	0.46
3:D:1:ASP:HB3	3:D:94:PRO:HD2	1.99	0.45
2:E:65:LYS:HG3	2:E:65:LYS:H	1.40	0.45
1:B:400:ALA:HB2	1:B:432:ALA:HB1	1.97	0.45
2:C:60:TYR:HE2	2:C:70:ILE:HG13	1.81	0.45
3:F:34:TRP:HB2	3:F:47:ILE:HB	1.97	0.45
1:B:53:PHE:HE2	1:B:147:ARG:HG2	1.82	0.45
1:B:216:LYS:O	1:B:220:ILE:HG13	2.16	0.45
3:F:109:ASP:OD2	3:F:198:LYS:NZ	2.49	0.45
1:A:68:LEU:HB3	1:A:78:LEU:HD11	1.99	0.45
3:F:7:SER:HB3	3:F:8:PRO:HD3	1.98	0.45
2:E:6:GLU:HA	2:E:22:CYS:HA	1.97	0.45
1:B:191:ASN:OD1	1:B:230:ARG:NH1	2.47	0.45
1:A:184:ALA:HB1	1:A:225:SER:CB	2.47	0.45
2:E:6:GLU:OE2	2:E:96:CYS:N	2.46	0.45
1:B:59:TRP:O	1:B:63:GLN:HG2	2.18	0.44
3:D:141:LYS:HB3	3:D:172:TYR:CZ	2.52	0.44
1:A:25:LEU:HD23	1:B:208:PHE:HE1	1.81	0.44
2:E:158:VAL:HG12	2:E:207:HIS:HB2	2.00	0.44
2:C:156:GLU:HA	2:C:157:PRO:HA	1.79	0.44
1:B:267:PRO:HG3	1:B:441:GLY:HA3	1.99	0.44
1:A:125:TRP:CD1	1:A:126:ARG:HG3	2.53	0.44
1:B:132:PHE:O	1:B:136:LEU:HB2	2.17	0.44
1:A:28:ARG:NE	1:B:207:GLN:HG2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:260:ILE:HG23	1:B:435:LEU:HG	1.99	0.43
2:C:30:SER:C	2:C:32:TYR:H	2.21	0.43
1:B:420:GLN:HG3	1:B:420:GLN:H	1.51	0.43
1:A:397:LEU:HD23	1:A:397:LEU:HA	1.75	0.43
3:D:117:PHE:HA	3:D:118:PRO:HD3	1.78	0.43
2:E:162:TRP:CZ3	2:E:203:CYS:HB3	2.54	0.43
2:C:171:VAL:HG22	2:C:189:VAL:HG23	2.00	0.43
2:E:30:SER:C	2:E:32:TYR:H	2.22	0.43
3:D:6:GLN:HA	3:D:22:THR:O	2.19	0.43
1:B:250:ASN:OD1	2:E:104:GLY:HA3	2.19	0.43
1:B:197:ILE:HG12	1:B:222:VAL:HG21	2.01	0.43
1:A:59:TRP:O	1:A:63:GLN:HG2	2.18	0.43
3:F:117:PHE:HA	3:F:118:PRO:HD3	1.75	0.43
3:D:34:TRP:HB2	3:D:47:ILE:HB	2.01	0.43
1:B:78:LEU:HD11	1:B:307:PHE:CE2	2.53	0.43
1:A:163:LEU:HD12	1:A:168:LEU:HB2	2.01	0.43
3:D:7:SER:HB3	3:D:22:THR:HB	2.00	0.43
3:F:10:ILE:HG12	3:F:102:LYS:HB3	2.01	0.43
2:C:154:PHE:HA	2:C:155:PRO:HA	1.85	0.43
3:D:48:TYR:CE1	3:D:52:LYS:HD2	2.54	0.42
2:C:176:ALA:HB2	2:C:185:LEU:HD23	2.00	0.42
3:D:180:LEU:HD22	3:D:184:GLU:HG2	2.00	0.42
1:B:154:ILE:O	1:B:158:ILE:HG12	2.20	0.42
3:F:6:GLN:HA	3:F:22:THR:O	2.19	0.42
1:A:127:VAL:HB	1:A:157:ASN:ND2	2.34	0.42
1:A:74:ASN:HB3	1:A:77:LEU:HB3	2.01	0.42
1:B:320:ILE:HG23	1:B:365:THR:HG21	2.01	0.42
1:A:255:TYR:CD2	1:A:424:PRO:HB3	2.55	0.42
1:B:118:ASP:CG	1:B:174:ARG:HH21	2.22	0.42
1:B:78:LEU:HD13	1:B:79:LEU:HD23	2.01	0.42
1:A:426:ILE:HG22	1:B:223:ILE:HD11	2.02	0.42
1:A:430:LEU:HD22	1:B:223:ILE:CD1	2.50	0.42
1:A:410:ILE:O	1:A:414:GLU:HG3	2.20	0.41
3:F:186:GLU:HG2	3:F:210:ARG:NH1	2.34	0.41
1:A:154:ILE:O	1:A:158:ILE:HG12	2.20	0.41
1:A:219:PHE:CE2	1:B:426:ILE:HG23	2.55	0.41
2:E:107:TYR:HB3	3:F:33:HIS:CD2	2.55	0.41
1:B:116:LEU:HB3	1:B:206:PRO:HD3	2.01	0.41
1:A:47:GLY:O	1:A:51:VAL:HG23	2.19	0.41
1:A:420:GLN:HG3	1:A:420:GLN:H	1.57	0.41
1:A:234:HIS:CD2	1:A:235:GLU:HG2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:87:CYS:O	3:F:98:GLY:N	2.52	0.41
1:B:47:GLY:O	1:B:51:VAL:HG23	2.19	0.41
2:E:60:TYR:HE2	2:E:70:ILE:HG13	1.86	0.41
1:A:216:LYS:HE2	1:B:433:THR:HG22	2.03	0.41
3:D:148:LYS:HB2	3:D:192:THR:OG1	2.20	0.41
1:B:243:LYS:HB3	2:E:31:ARG:HH21	1.85	0.41
1:A:430:LEU:HD22	1:B:223:ILE:HD12	2.02	0.41
1:A:305:LEU:HA	1:A:308:VAL:HG22	2.02	0.41
2:E:188:SER:HB2	3:F:134:PHE:CD2	2.56	0.41
2:C:112:GLY:O	3:D:42:SER:OG	2.33	0.41
1:B:337:PHE:O	1:B:341:VAL:HG23	2.20	0.41
3:F:8:PRO:O	3:F:101:THR:HG23	2.21	0.41
1:A:100:TYR:O	1:A:126:ARG:NH1	2.52	0.41
1:A:207:GLN:HG2	1:B:28:ARG:HE	1.86	0.41
1:B:75:TYR:HB3	1:B:76:PRO:HD3	2.03	0.41
3:D:49:ASP:O	3:D:51:SER:N	2.46	0.41
1:B:19:ARG:HD2	1:B:19:ARG:HA	1.94	0.41
1:A:320:ILE:HG23	1:A:365:THR:HG21	2.02	0.41
2:E:105:TYR:CD2	3:F:91:SER:HA	2.56	0.41
1:A:75:TYR:HB3	1:A:76:PRO:HD3	2.02	0.41
3:D:16:GLY:N	3:D:77:MET:O	2.50	0.41
1:B:109:ILE:HG23	1:B:204:MET:SD	2.61	0.41
1:B:198:LEU:HD13	1:B:201:ILE:HD11	2.03	0.41
1:B:410:ILE:O	1:B:414:GLU:HG3	2.21	0.41
1:B:172:GLU:HG3	1:B:212:LEU:O	2.21	0.40
1:A:269:PHE:O	1:A:273:VAL:HG12	2.21	0.40
1:A:123:ARG:HE	1:A:126:ARG:HD2	1.87	0.40
2:E:162:TRP:CH2	2:E:203:CYS:HB3	2.56	0.40
3:D:83:ALA:O	3:D:103:LEU:N	2.52	0.40
1:B:255:TYR:CE2	1:B:424:PRO:HB3	2.57	0.40
1:A:453:LEU:HB3	1:B:22:ILE:HG12	2.03	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	442/446 (99%)	423 (96%)	18 (4%)	1 (0%)	52	88
1	B	439/446 (98%)	419 (95%)	18 (4%)	2 (0%)	34	77
2	C	219/222 (99%)	200 (91%)	17 (8%)	2 (1%)	21	66
2	E	219/222 (99%)	203 (93%)	15 (7%)	1 (0%)	34	77
3	D	209/211 (99%)	190 (91%)	16 (8%)	3 (1%)	14	56
3	F	209/211 (99%)	192 (92%)	17 (8%)	0	100	100
All	All	1737/1758 (99%)	1627 (94%)	101 (6%)	9 (0%)	34	77

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	62	PRO
2	C	62	PRO
3	D	76	THR
1	A	107	SER
1	B	107	SER
1	B	148	ALA
3	D	169	ASP
3	D	67	GLY
2	C	157	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	334/336 (99%)	316 (95%)	18 (5%)	27	67
1	B	331/336 (98%)	315 (95%)	16 (5%)	31	72
2	C	181/182 (100%)	173 (96%)	8 (4%)	35	74
2	E	181/182 (100%)	170 (94%)	11 (6%)	23	63
3	D	185/185 (100%)	179 (97%)	6 (3%)	46	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	F	185/185 (100%)	176 (95%)	9 (5%)	31	72
All	All	1397/1406 (99%)	1329 (95%)	68 (5%)	31	72

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	70	HIS
1	A	73	ASP
1	A	103	GLU
1	A	151	THR
1	A	205	ARG
1	A	211	THR
1	A	212	LEU
1	A	219	PHE
1	A	230	ARG
1	A	251	THR
1	A	264	ILE
1	A	397	LEU
1	A	420	GLN
1	A	430	LEU
1	A	444	LEU
1	A	451	ARG
1	A	453	LEU
1	B	70	HIS
1	B	78	LEU
1	B	103	GLU
1	B	151	THR
1	B	205	ARG
1	B	211	THR
1	B	212	LEU
1	B	219	PHE
1	B	230	ARG
1	B	251	THR
1	B	397	LEU
1	B	420	GLN
1	B	430	LEU
1	B	444	LEU
1	B	451	ARG
1	B	453	LEU
2	C	21	SER
2	C	30	SER

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Mol	Chain	Res	Type
2	C	65	LYS
2	C	66	ASP
2	C	72	ARG
2	C	96	CYS
2	C	115	THR
2	C	151	LYS
3	D	1	ASP
3	D	39	SER
3	D	77	MET
3	D	125	THR
3	D	156	ASN
3	D	192	THR
2	E	21	SER
2	E	30	SER
2	E	65	LYS
2	E	66	ASP
2	E	72	ARG
2	E	96	CYS
2	E	98	ARG
2	E	115	THR
2	E	151	LYS
2	E	156	GLU
2	E	188	SER
3	F	1	ASP
3	F	17	ASP
3	F	77	MET
3	F	80	GLU
3	F	106	LEU
3	F	125	THR
3	F	156	ASN
3	F	168	LYS
3	F	192	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	HIS
1	B	284	HIS
2	C	163	ASN
3	F	37	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	444/446 (99%)	-0.07	14 (3%)	51	36	37, 57, 85, 128	0
1	B	441/446 (98%)	0.10	23 (5%)	31	17	37, 61, 96, 128	0
2	C	221/222 (99%)	-0.06	7 (3%)	51	36	29, 56, 95, 126	0
2	E	221/222 (99%)	-0.06	7 (3%)	51	36	29, 54, 89, 133	0
3	D	211/211 (100%)	0.19	14 (6%)	22	12	37, 66, 97, 120	0
3	F	211/211 (100%)	0.11	9 (4%)	39	24	31, 50, 99, 120	0
All	All	1749/1758 (99%)	0.03	74 (4%)	40	25	29, 58, 95, 133	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	460	GLN	9.6
3	D	79	ALA	9.5
1	A	72	ALA	6.3
3	D	167	SER	5.6
1	B	235	GLU	5.3
1	B	72	ALA	5.2
2	E	222	ALA	5.1
1	B	73	ASP	4.8
3	D	80	GLU	4.8
1	A	235	GLU	4.8
1	B	307	PHE	4.1
1	B	74	ASN	3.9
1	B	166	PHE	3.7
1	B	168	LEU	3.7
3	D	27	SER	3.7
1	B	234	HIS	3.5
3	D	156	ASN	3.5
2	E	14	PRO	3.4
1	B	75	TYR	3.3

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Mol	Chain	Res	Type	RSRZ
2	C	199	GLU	3.3
1	A	459	GLU	3.2
1	B	165	ILE	3.2
1	B	288	ILE	3.1
2	C	179	GLN	3.0
1	B	71	THR	3.0
1	A	234	HIS	3.0
2	E	140	ALA	2.9
2	C	141	ALA	2.9
3	F	211	ALA	2.9
3	F	153	GLU	2.8
3	F	150	ASP	2.8
1	A	288	ILE	2.8
3	F	151	GLY	2.7
3	F	127	GLY	2.6
1	B	332	MET	2.6
1	B	146	GLY	2.6
2	E	13	GLN	2.6
3	D	78	GLU	2.6
1	B	150	PRO	2.5
3	F	152	SER	2.5
3	F	155	GLN	2.5
1	A	212	LEU	2.5
2	C	31	ARG	2.4
2	C	200	THR	2.4
3	D	68	THR	2.3
3	D	195	ALA	2.3
1	A	233	ASN	2.3
3	D	194	GLU	2.3
1	B	162	VAL	2.3
1	A	29	ASP	2.3
3	D	39	SER	2.3
1	B	167	ARG	2.3
2	E	66	ASP	2.3
1	A	146	GLY	2.3
1	B	287	ASN	2.2
1	A	30	LYS	2.2
1	B	108	GLY	2.2
1	B	328	PHE	2.2
1	B	148	ALA	2.2
1	A	168	LEU	2.2
1	A	232	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
2	E	31	ARG	2.1
3	F	149	ILE	2.1
3	D	82	ALA	2.1
1	B	355	GLY	2.1
3	D	196	THR	2.1
1	B	149	GLY	2.1
1	A	355	GLY	2.1
2	C	103	TYR	2.1
3	D	35	TYR	2.1
2	E	201	VAL	2.1
3	F	176	SER	2.0
3	D	52	LYS	2.0
2	C	29	TYR	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.