Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:29 PM GMT

PDB ID	:	4LOU
Title	:	Structure of the E148Q mutant of CLC-ec1 deltaNC construct in the absence of halide
Authors	:	Lim, H.-H.; Miller, C.
Deposited on	:	2013-07-13
Resolution	:	2.98 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:

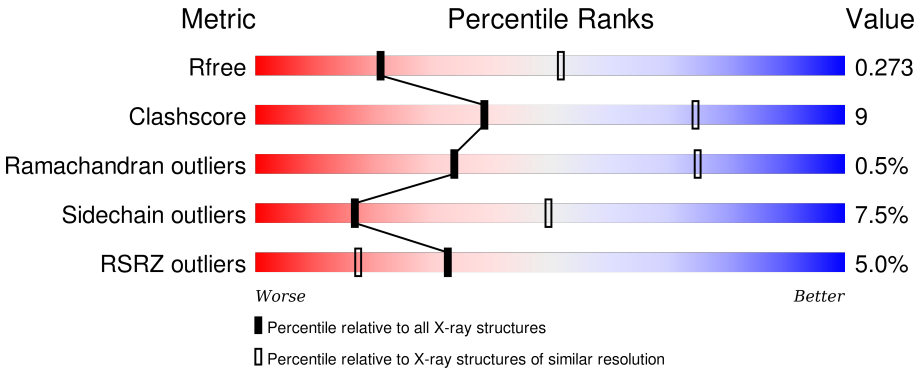
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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	1992 (3.00-2.96)
Clashscore	102246	2349 (3.00-2.96)
Ramachandran outliers	100387	2274 (3.00-2.96)
Sidechain outliers	100360	2277 (3.00-2.96)
RSRZ outliers	91569	2007 (3.00-2.96)

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 <=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	6% 76% 20%
1	B	446	5% 69% 27%
2	C	222	7% 80% 19%
2	E	222	2% 74% 23%
3	D	211	3% 79% 19%

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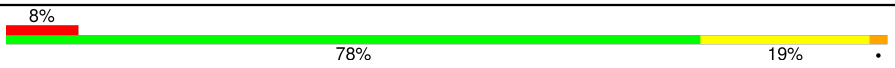
Mol	Chain	Length	Quality of chain
3	F	211	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13243 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
			3333	2190	561	562	20			
1	B	442	Total	C	N	O	S	0	0	0
			3315	2180	558	557	20			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	MET	-	INITIATING METHIONINE	UNP P37019
A	148	GLN	GLU	ENGINEERED MUTATION	UNP P37019
A	461	LYS	-	EXPRESSION TAG	UNP P37019
B	16	MET	-	INITIATING METHIONINE	UNP P37019
B	148	GLN	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	222	Total	C	N	O	S	0	0	0
			1681	1082	275	318	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.

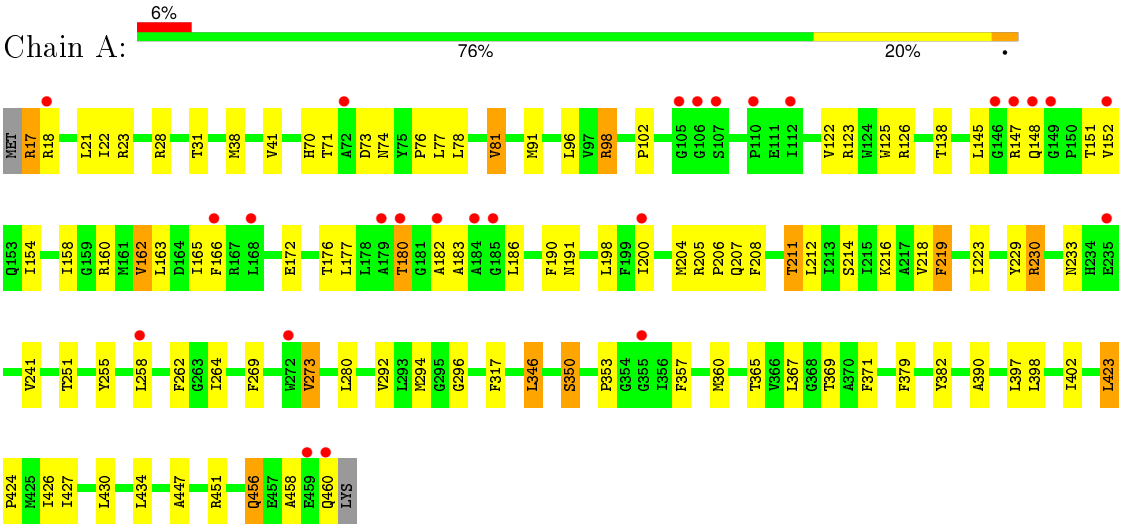
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			
3	F	211	Total	C	N	O	S	0	0	0
			1621	1008	271	334	8			

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.

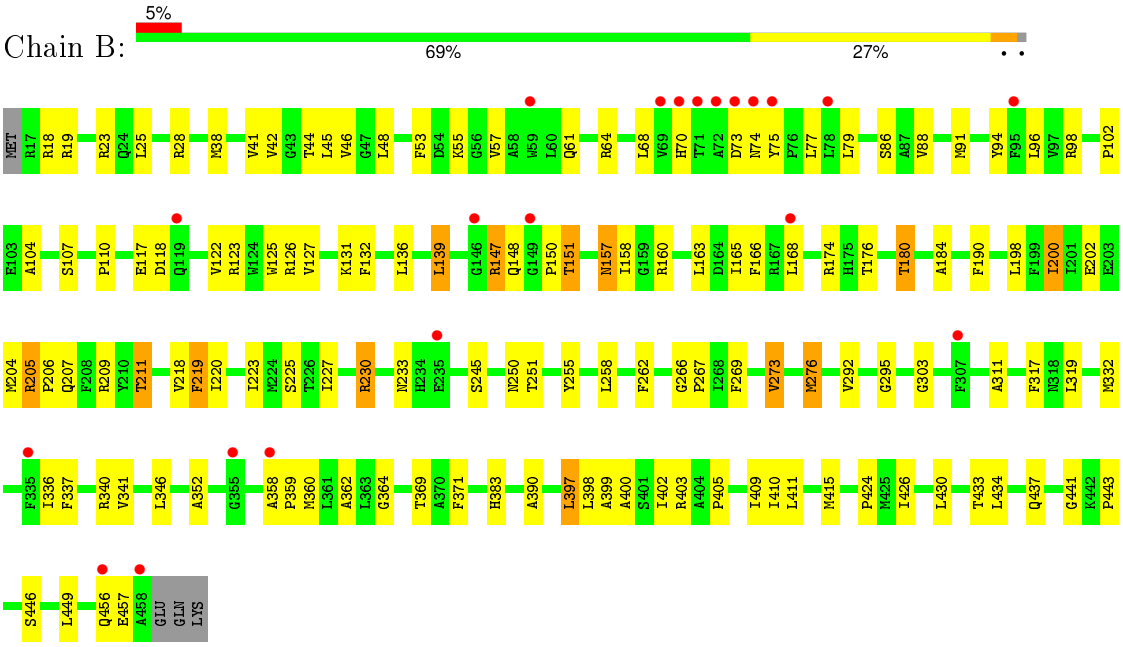
- Molecule 1: H(+)/Cl(-) exchange transporter ClcA

Chain A:



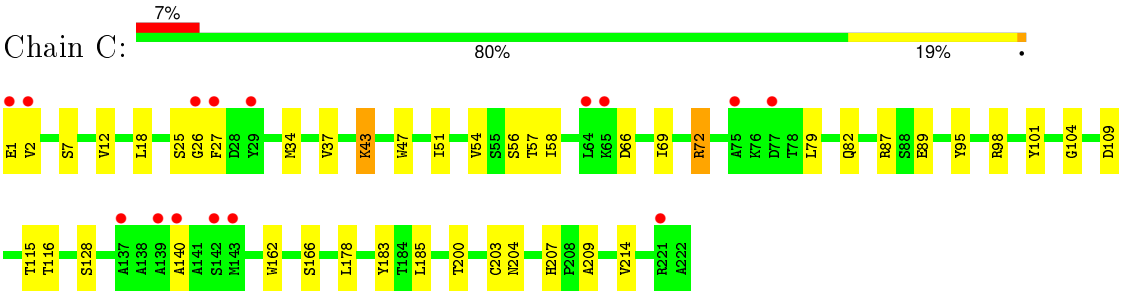
- Molecule 1: H(+)/Cl(-) exchange transporter ClcA

Chain B:



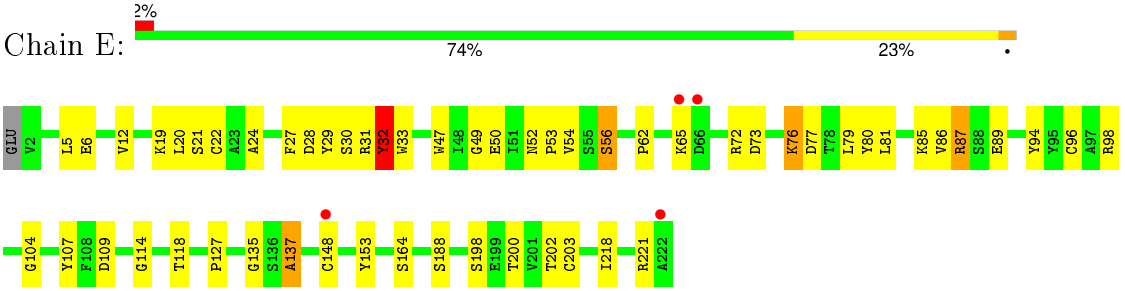
- Molecule 2: Fab heavy chain

Chain C:



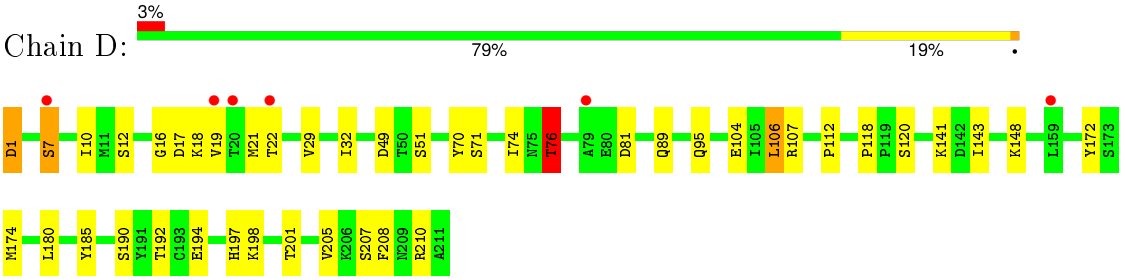
• Molecule 2: Fab heavy chain

Chain E:



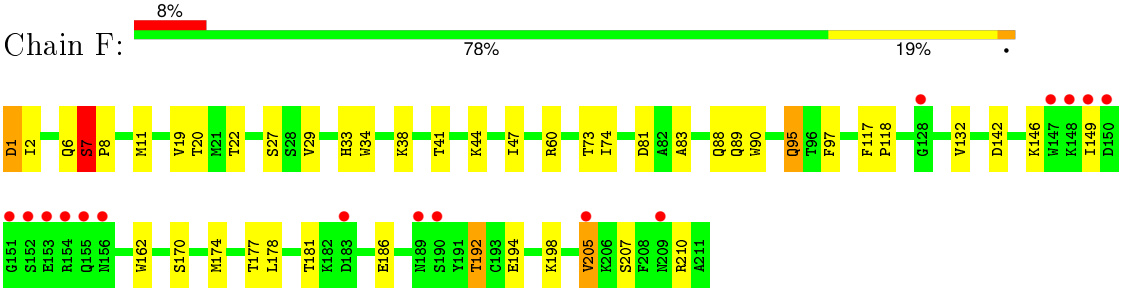
• Molecule 3: Fab light chain

Chain D:



• Molecule 3: Fab light chain

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	231.62Å 100.32Å 170.96Å 90.00° 131.71° 90.00°	Depositor
Resolution (Å)	39.72 – 2.98 39.72 – 2.98	Depositor EDS
% Data completeness (in resolution range)	98.3 (39.72-2.98) 98.3 (39.72-2.98)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.81 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.210 , 0.253 0.222 , 0.273	Depositor DCC
R_{free} test set	2981 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	81.8	Xtriage
Anisotropy	0.538	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 36.8	EDS
Estimated twinning fraction	0.010 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 58878 reflections	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	13243	wwPDB-VP
Average B, all atoms (Å^2)	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.43	0/3405	0.57	0/4621
1	B	0.42	0/3387	0.57	0/4597
2	C	0.51	0/1730	0.65	0/2367
2	E	0.46	0/1721	0.65	1/2355 (0.0%)
3	D	0.47	0/1660	0.63	0/2257
3	F	0.47	0/1660	0.64	1/2257 (0.0%)
All	All	0.45	0/13563	0.61	2/18454 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	F	6	GLN	CB-CA-C	11.25	132.90	110.40
2	E	32	TYR	N-CA-C	-5.13	97.15	111.00

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	3333	0	3486	72	0
1	B	3315	0	3472	94	0
2	C	1681	0	1663	18	0
2	E	1672	0	1656	32	0
3	D	1621	0	1546	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	F	1621	0	1546	27	0
All	All	13243	0	13369	239	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 9.

All (239) 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)
3:F:7:SER:HB2	3:F:8:PRO:CD	1.55	1.27
2:E:148:CYS:SG	2:E:218:ILE:HD11	1.86	1.15
3:F:7:SER:HB2	3:F:8:PRO:HD2	1.14	1.10
2:E:30:SER:O	2:E:31:ARG:HB2	1.72	0.89
1:A:207:GLN:HG2	1:B:28:ARG:HD2	1.56	0.88
1:A:219:PHE:HB3	1:B:430:LEU:HD21	1.58	0.86
3:F:7:SER:CB	3:F:8:PRO:CD	2.43	0.86
2:E:148:CYS:SG	2:E:218:ILE:CD1	2.64	0.85
3:D:95:GLN:N	3:D:95:GLN:OE1	2.08	0.85
1:A:180:THR:HB	1:A:218:VAL:HA	1.59	0.82
3:F:7:SER:HB2	3:F:8:PRO:HD3	1.60	0.80
1:B:206:PRO:HG2	1:B:211:THR:HG21	1.64	0.79
1:B:117:GLU:OE1	1:B:209:ARG:NH1	2.20	0.75
3:D:194:GLU:HG2	3:D:205:VAL:HG12	1.69	0.74
1:B:38:MET:HG3	1:B:168:LEU:HD11	1.68	0.74
3:F:192:THR:HB	3:F:207:SER:HB3	1.70	0.73
3:F:186:GLU:O	3:F:210:ARG:NH2	2.21	0.73
2:C:34:MET:HB3	2:C:79:LEU:HD22	1.71	0.72
2:E:32:TYR:H	2:E:53:PRO:HG3	1.55	0.71
3:D:1:ASP:N	3:D:1:ASP:OD2	2.19	0.70
3:D:29:VAL:O	3:D:70:TYR:OH	2.06	0.70
2:E:98:ARG:NH1	2:E:109:ASP:OD2	2.25	0.69
2:E:107:TYR:HB3	3:F:33:HIS:CD2	2.28	0.69
1:A:28:ARG:HH11	1:B:207:GLN:HG2	1.56	0.69
3:F:60:ARG:NH2	3:F:81:ASP:OD2	2.25	0.69
3:F:1:ASP:OD1	3:F:1:ASP:N	2.26	0.68
1:A:122:VAL:HB	1:A:160:ARG:HG2	1.75	0.68
3:F:95:GLN:H	3:F:95:GLN:CD	1.98	0.67
1:A:430:LEU:HD21	1:B:219:PHE:HB3	1.76	0.66
1:A:360:MET:HE3	1:A:398:LEU:HD23	1.78	0.65
1:B:122:VAL:HB	1:B:160:ARG:HG2	1.79	0.64
1:A:198:LEU:HD11	1:B:198:LEU:HD11	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ARG:HD2	1:B:207:GLN:HG2	1.80	0.62
1:B:147:ARG:O	1:B:151:THR:OG1	2.16	0.62
2:C:98:ARG:NH1	2:C:109:ASP:OD2	2.32	0.62
1:A:125:TRP:CD1	1:A:126:ARG:HG3	2.35	0.61
3:D:29:VAL:HG12	3:D:32:ILE:HD11	1.83	0.60
1:A:205:ARG:HH12	1:B:205:ARG:HH12	1.47	0.60
1:A:18:ARG:HH11	1:B:457:GLU:HB3	1.66	0.60
1:B:38:MET:O	1:B:42:VAL:HG23	2.01	0.60
1:B:61:GLN:HG2	1:B:64:ARG:HH21	1.66	0.60
1:B:200:ILE:HA	1:B:204:MET:HB2	1.84	0.60
2:E:54:VAL:HG23	2:E:56:SER:HB3	1.83	0.60
1:A:17:ARG:HH22	1:A:21:LEU:HD13	1.67	0.59
3:D:192:THR:HG22	3:D:207:SER:HB3	1.84	0.58
1:B:123:ARG:HE	1:B:126:ARG:HD2	1.68	0.58
3:F:95:GLN:CD	3:F:95:GLN:N	2.56	0.58
2:E:127:PRO:HB3	2:E:153:TYR:HB3	1.86	0.58
1:B:157:ASN:N	1:B:157:ASN:HD22	2.02	0.58
1:B:360:MET:HE3	1:B:398:LEU:HD23	1.85	0.56
1:A:183:ALA:HB2	1:A:200:ILE:HG12	1.87	0.56
1:B:44:THR:O	1:B:48:LEU:HG	2.06	0.56
2:C:51:ILE:HD13	2:C:72:ARG:HG2	1.87	0.56
3:F:149:ILE:HD11	3:F:178:LEU:HD21	1.88	0.56
3:F:132:VAL:HG22	3:F:177:THR:HG23	1.87	0.55
1:A:77:LEU:O	1:A:81:VAL:HG13	2.07	0.55
1:B:88:VAL:HA	1:B:91:MET:HE2	1.87	0.55
2:E:30:SER:O	2:E:31:ARG:CB	2.44	0.54
3:D:197:HIS:CG	3:D:198:LYS:H	2.25	0.54
1:B:443:PRO:HB2	1:B:446:SER:HB2	1.90	0.54
1:B:269:PHE:O	1:B:273:VAL:HG12	2.09	0.53
1:A:138:THR:HG21	1:A:353:PRO:HD2	1.90	0.53
3:F:38:LYS:HG2	3:F:83:ALA:HB2	1.90	0.53
3:D:17:ASP:OD1	3:D:18:LYS:N	2.37	0.53
1:B:176:THR:O	1:B:180:THR:HG23	2.09	0.53
3:D:74:ILE:HG21	3:D:81:ASP:OD2	2.09	0.53
1:A:38:MET:HB3	1:A:177:LEU:HD11	1.91	0.53
1:B:319:LEU:HD11	1:B:362:ALA:HB1	1.90	0.53
3:D:192:THR:HG22	3:D:207:SER:CB	2.39	0.52
1:A:91:MET:HG3	1:A:296:GLY:HA3	1.90	0.52
1:A:191:ASN:OD1	1:A:230:ARG:NH1	2.42	0.52
3:D:29:VAL:CG1	3:D:32:ILE:HD11	2.38	0.52
3:F:7:SER:CB	3:F:8:PRO:HD3	2.29	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:360:MET:HG2	1:B:397:LEU:HD13	1.91	0.52
1:B:255:TYR:CD1	1:B:424:PRO:HB3	2.44	0.52
2:E:135:GLY:HA2	2:E:221:ARG:HD2	1.90	0.51
1:A:28:ARG:HH21	1:B:443:PRO:HB3	1.75	0.51
1:A:172:GLU:HG3	1:A:212:LEU:HB3	1.92	0.51
3:D:16:GLY:HA2	3:D:76:THR:OG1	2.11	0.51
2:C:207:HIS:CE1	2:C:209:ALA:HB3	2.46	0.51
1:B:332:MET:O	1:B:336:ILE:HG13	2.10	0.51
1:B:200:ILE:HD12	1:B:204:MET:HG3	1.93	0.51
1:A:200:ILE:HD13	1:A:204:MET:HG3	1.93	0.51
1:B:125:TRP:CD1	1:B:126:ARG:HG3	2.46	0.50
1:B:262:PHE:HZ	1:B:364:GLY:HA2	1.76	0.50
2:E:22:CYS:HB3	2:E:79:LEU:HB3	1.93	0.50
1:B:383:HIS:NE2	2:E:50:GLU:OE1	2.45	0.50
1:B:94:TYR:OH	1:B:352:ALA:HB2	2.12	0.50
3:D:141:LYS:HD3	3:D:172:TYR:CZ	2.48	0.49
1:A:200:ILE:HA	1:A:204:MET:HB2	1.94	0.49
3:F:90:TRP:CG	3:F:95:GLN:HB3	2.47	0.49
1:B:64:ARG:O	1:B:68:LEU:HG	2.13	0.49
3:D:89:GLN:O	3:D:95:GLN:HB2	2.13	0.48
1:B:41:VAL:O	1:B:45:LEU:HG	2.13	0.48
1:A:207:GLN:HG2	1:B:28:ARG:HH11	1.77	0.48
2:C:87:ARG:HH21	2:C:89:GLU:CD	2.15	0.48
2:E:31:ARG:H	2:E:53:PRO:HB3	1.78	0.48
1:A:430:LEU:HD11	1:B:219:PHE:CG	2.48	0.48
1:B:19:ARG:NH1	1:B:19:ARG:HA	2.28	0.48
1:A:430:LEU:HD23	1:B:220:ILE:HG12	1.94	0.48
2:C:7:SER:HA	2:C:115:THR:HG21	1.94	0.48
1:A:91:MET:HG2	1:A:292:VAL:O	2.14	0.48
2:E:33:TRP:CZ2	2:E:52:ASN:HB3	2.48	0.48
2:E:31:ARG:HH11	2:E:31:ARG:HG3	1.78	0.48
3:F:194:GLU:HG2	3:F:205:VAL:HB	1.94	0.47
1:A:18:ARG:NH1	1:B:457:GLU:HB3	2.29	0.47
1:A:183:ALA:HB2	1:A:200:ILE:CG1	2.44	0.47
2:E:20:LEU:HD12	2:E:81:LEU:HD23	1.96	0.47
1:B:190:PHE:HE2	1:B:317:PHE:HZ	1.61	0.47
1:A:430:LEU:HD22	1:B:223:ILE:HD11	1.96	0.47
1:B:157:ASN:H	1:B:157:ASN:HD22	1.61	0.47
1:B:74:ASN:HB3	1:B:77:LEU:HB3	1.97	0.47
2:C:101:TYR:HB2	2:C:104:GLY:HA2	1.96	0.47
1:B:267:PRO:HG3	1:B:441:GLY:HA3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:409:ILE:HD13	1:B:426:ILE:HG12	1.96	0.47
3:F:117:PHE:HA	3:F:118:PRO:HD3	1.74	0.47
1:B:165:ILE:HG22	1:B:166:PHE:CD2	2.50	0.47
3:F:186:GLU:HG2	3:F:210:ARG:NH1	2.30	0.46
1:A:365:THR:HG23	1:A:390:ALA:HB1	1.97	0.46
1:A:346:LEU:O	1:A:350:SER:HB3	2.16	0.46
3:D:118:PRO:HB3	3:D:208:PHE:CE1	2.50	0.46
1:B:337:PHE:O	1:B:341:VAL:HG23	2.14	0.46
1:B:118:ASP:OD1	1:B:174:ARG:NH2	2.28	0.46
1:A:426:ILE:HG22	1:B:223:ILE:HD11	1.97	0.46
1:A:430:LEU:HD22	1:B:223:ILE:CD1	2.45	0.46
1:B:180:THR:HB	1:B:218:VAL:HA	1.97	0.46
1:A:258:LEU:HD13	1:A:371:PHE:CG	2.50	0.46
1:A:229:TYR:O	1:A:233:ASN:HB2	2.15	0.46
3:D:106:LEU:HD23	3:D:107:ARG:N	2.31	0.46
3:F:34:TRP:HB2	3:F:47:ILE:HB	1.97	0.46
1:A:216:LYS:HD3	1:B:434:LEU:HD23	1.97	0.46
2:E:32:TYR:N	2:E:53:PRO:HG3	2.28	0.46
1:B:42:VAL:O	1:B:46:VAL:HG23	2.16	0.46
3:D:112:PRO:HG3	3:D:143:ILE:HD11	1.97	0.46
1:A:262:PHE:CE2	1:A:367:LEU:HD23	2.51	0.46
1:B:411:LEU:O	1:B:415:MET:HG3	2.16	0.45
1:A:262:PHE:CZ	1:A:367:LEU:HD23	2.52	0.45
3:F:88:GLN:HB2	3:F:97:PHE:CD1	2.52	0.45
2:E:53:PRO:HA	2:E:72:ARG:CZ	2.47	0.45
1:B:198:LEU:HG	1:B:410:ILE:HD12	1.98	0.45
3:D:12:SER:HA	3:D:104:GLU:O	2.16	0.45
1:A:123:ARG:HH21	1:A:126:ARG:HD3	1.81	0.45
1:B:202:GLU:OE2	1:B:405:PRO:HD2	2.16	0.45
1:A:165:ILE:HG22	1:A:166:PHE:CD2	2.52	0.45
1:A:223:ILE:HD11	1:B:426:ILE:HG22	1.97	0.45
1:A:31:THR:O	1:B:437:GLN:NE2	2.48	0.45
1:A:434:LEU:HD11	1:B:220:ILE:HD11	1.98	0.45
1:B:75:TYR:CZ	1:B:79:LEU:HD21	2.52	0.45
1:A:456:GLN:OE1	1:B:18:ARG:NH2	2.50	0.45
1:A:205:ARG:HH12	1:B:205:ARG:NH1	2.10	0.45
2:C:47:TRP:CE2	3:D:95:GLN:NE2	2.85	0.45
1:A:427:ILE:HD11	1:B:227:ILE:HD11	1.99	0.45
1:B:369:THR:OG1	1:B:390:ALA:HB2	2.17	0.44
1:A:255:TYR:CD1	1:A:424:PRO:HB3	2.52	0.44
2:C:51:ILE:HG13	2:C:58:ILE:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:250:ASN:OD1	2:E:104:GLY:HA3	2.17	0.44
1:A:369:THR:OG1	1:A:390:ALA:HB2	2.18	0.44
2:E:24:ALA:HB1	2:E:27:PHE:CZ	2.52	0.44
3:D:49:ASP:O	3:D:51:SER:N	2.44	0.44
3:F:11:MET:HE1	3:F:19:VAL:HG13	1.99	0.44
1:A:152:VAL:HG13	1:A:182:ALA:HB1	2.00	0.44
1:B:430:LEU:HA	1:B:433:THR:HG22	1.99	0.44
1:A:190:PHE:HE2	1:A:317:PHE:HZ	1.65	0.44
1:B:311:ALA:O	1:B:340:ARG:HD2	2.18	0.44
1:B:53:PHE:O	1:B:57:VAL:HG23	2.18	0.44
1:B:104:ALA:HB2	1:B:127:VAL:HG13	1.99	0.44
3:F:20:THR:HG23	3:F:73:THR:OG1	2.18	0.44
1:B:91:MET:HG2	1:B:292:VAL:O	2.17	0.43
2:E:29:TYR:CD2	2:E:77:ASP:HA	2.52	0.43
1:B:399:ALA:O	1:B:403:ARG:HA	2.18	0.43
1:B:160:ARG:HA	1:B:160:ARG:HD2	1.79	0.43
1:B:397:LEU:HA	1:B:397:LEU:HD23	1.75	0.43
1:A:147:ARG:HG3	1:A:147:ARG:HH11	1.84	0.43
1:A:98:ARG:NH2	1:A:102:PRO:HB3	2.34	0.43
2:E:87:ARG:NE	2:E:89:GLU:OE1	2.51	0.43
1:B:86:SER:OG	1:B:303:GLY:HA3	2.18	0.43
2:E:47:TRP:CZ2	2:E:49:GLY:HA2	2.53	0.43
1:B:131:LYS:HE2	1:B:150:PRO:HA	1.99	0.43
1:A:176:THR:O	1:A:180:THR:HG22	2.18	0.43
1:B:46:VAL:HG22	1:B:158:ILE:HD12	2.00	0.43
2:C:162:TRP:CZ3	2:C:203:CYS:HB3	2.53	0.43
2:E:19:LYS:HE2	2:E:80:TYR:CD2	2.54	0.43
2:C:178:LEU:HB2	2:C:183:TYR:CE2	2.54	0.43
2:E:148:CYS:SG	2:E:203:CYS:CB	3.07	0.43
1:B:136:LEU:HA	1:B:136:LEU:HD23	1.85	0.43
1:A:269:PHE:O	1:A:273:VAL:HG12	2.18	0.43
2:E:135:GLY:O	2:E:137:ALA:N	2.51	0.43
1:A:214:SER:O	1:A:218:VAL:HG23	2.18	0.42
3:D:148:LYS:HB2	3:D:192:THR:OG1	2.18	0.42
1:A:458:ALA:C	1:A:460:GLN:H	2.22	0.42
1:A:186:LEU:HD12	1:A:186:LEU:HA	1.83	0.42
2:E:85:LYS:HD3	2:E:85:LYS:HA	1.67	0.42
1:B:132:PHE:O	1:B:136:LEU:HG	2.19	0.42
1:A:208:PHE:HE1	1:B:25:LEU:HD23	1.84	0.42
1:B:276:MET:HB2	1:B:276:MET:HE3	1.96	0.42
1:B:98:ARG:NH2	1:B:102:PRO:HB3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:60:ARG:HH21	3:F:81:ASP:CG	2.23	0.42
1:A:379:PHE:HB3	1:A:382:TYR:CD1	2.55	0.42
3:D:7:SER:HB3	3:D:22:THR:HB	2.01	0.42
1:B:198:LEU:HA	1:B:198:LEU:HD13	1.85	0.42
2:C:1:GLU:O	2:C:26:GLY:HA3	2.20	0.42
3:D:21:MET:H	3:D:21:MET:HG2	1.67	0.42
1:B:55:LYS:HA	1:B:55:LYS:HD3	1.82	0.42
1:A:423:LEU:HD13	1:B:230:ARG:NH2	2.35	0.42
1:B:358:ALA:HB3	1:B:359:PRO:HD3	2.02	0.41
1:A:74:ASN:OD1	1:A:76:PRO:HD2	2.19	0.41
3:F:7:SER:CB	3:F:8:PRO:HD2	2.10	0.41
1:A:71:THR:O	1:A:78:LEU:HD23	2.19	0.41
2:E:94:TYR:O	2:E:114:GLY:HA2	2.21	0.41
3:D:106:LEU:HD23	3:D:107:ARG:H	1.85	0.41
2:C:2:VAL:HG13	2:C:27:PHE:CD1	2.55	0.41
2:C:12:VAL:HG21	2:C:18:LEU:HD23	2.03	0.41
2:C:69:ILE:HB	2:C:82:GLN:HB2	2.01	0.41
1:A:160:ARG:HD2	1:A:160:ARG:HA	1.84	0.41
2:C:54:VAL:HG23	2:C:56:SER:HB3	2.02	0.41
1:B:163:LEU:HD12	1:B:168:LEU:HB2	2.02	0.41
1:B:110:PRO:O	1:B:449:LEU:HD13	2.20	0.41
1:A:447:ALA:O	1:A:451:ARG:HG3	2.21	0.41
1:B:139:LEU:HD12	1:B:147:ARG:HG3	2.02	0.41
1:B:266:GLY:HA3	1:B:400:ALA:HB1	2.02	0.41
2:E:31:ARG:NH1	2:E:31:ARG:HG3	2.36	0.41
1:A:18:ARG:O	1:A:22:ILE:HG13	2.20	0.41
2:E:6:GLU:CD	2:E:114:GLY:H	2.25	0.41
1:A:280:LEU:HD22	1:A:294:MET:SD	2.60	0.41
1:A:280:LEU:HD23	1:A:280:LEU:HA	1.81	0.41
1:B:94:TYR:CD1	1:B:295:GLY:HA3	2.56	0.40
3:F:162:TRP:CE2	3:F:174:MET:HG3	2.56	0.40
1:A:158:ILE:O	1:A:162:VAL:HG13	2.22	0.40
1:A:160:ARG:NE	1:A:163:LEU:HD23	2.37	0.40
3:F:89:GLN:O	3:F:95:GLN:HB2	2.21	0.40
1:B:258:LEU:HD13	1:B:371:PHE:CG	2.57	0.40
2:E:73:ASP:OD1	2:E:76:LYS:HB2	2.22	0.40
2:C:37:VAL:O	2:C:95:TYR:HB2	2.21	0.40
2:E:28:ASP:O	2:E:30:SER:O	2.38	0.40
1:A:154:ILE:O	1:A:158:ILE:HG13	2.21	0.40
2:C:43:LYS:HB3	2:C:43:LYS:HE2	1.74	0.40
3:D:185:TYR:CZ	3:D:210:ARG:HD3	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:PRO:HG2	1:A:211:THR:HG21	2.03	0.40
1:B:184:ALA:HB1	1:B:225:SER:HB2	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	442/446 (99%)	410 (93%)	32 (7%)	0	100	100
1	B	440/446 (99%)	408 (93%)	31 (7%)	1 (0%)	52	87
2	C	220/222 (99%)	200 (91%)	18 (8%)	2 (1%)	21	63
2	E	219/222 (99%)	193 (88%)	23 (10%)	3 (1%)	14	50
3	D	209/211 (99%)	184 (88%)	23 (11%)	2 (1%)	19	60
3	F	209/211 (99%)	196 (94%)	12 (6%)	1 (0%)	34	75
All	All	1739/1758 (99%)	1591 (92%)	139 (8%)	9 (0%)	34	75

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	65	LYS
2	E	137	ALA
3	F	7	SER
2	C	140	ALA
1	B	233	ASN
3	D	7	SER
3	D	76	THR
2	E	62	PRO
2	C	25	SER

5.3.2 Protein sidechains (i)

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	335/337 (99%)	308 (92%)	27 (8%)	15	45
1	B	333/337 (99%)	309 (93%)	24 (7%)	18	52
2	C	182/182 (100%)	171 (94%)	11 (6%)	24	61
2	E	181/182 (100%)	166 (92%)	15 (8%)	14	44
3	D	185/185 (100%)	174 (94%)	11 (6%)	24	61
3	F	185/185 (100%)	168 (91%)	17 (9%)	11	38
All	All	1401/1408 (100%)	1296 (92%)	105 (8%)	17	50

All (105) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ARG
1	A	23	ARG
1	A	41	VAL
1	A	70	HIS
1	A	73	ASP
1	A	81	VAL
1	A	96	LEU
1	A	98	ARG
1	A	145	LEU
1	A	148	GLN
1	A	151	THR
1	A	162	VAL
1	A	180	THR
1	A	211	THR
1	A	219	PHE
1	A	230	ARG
1	A	241	VAL
1	A	251	THR
1	A	264	ILE
1	A	273	VAL
1	A	346	LEU
1	A	350	SER

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Mol	Chain	Res	Type
1	A	357	PHE
1	A	397	LEU
1	A	402	ILE
1	A	423	LEU
1	A	456	GLN
1	B	23	ARG
1	B	70	HIS
1	B	73	ASP
1	B	96	LEU
1	B	107	SER
1	B	139	LEU
1	B	147	ARG
1	B	148	GLN
1	B	151	THR
1	B	157	ASN
1	B	180	THR
1	B	200	ILE
1	B	205	ARG
1	B	211	THR
1	B	219	PHE
1	B	230	ARG
1	B	245	SER
1	B	251	THR
1	B	273	VAL
1	B	276	MET
1	B	346	LEU
1	B	397	LEU
1	B	402	ILE
1	B	456	GLN
2	C	43	LYS
2	C	57	THR
2	C	66	ASP
2	C	72	ARG
2	C	116	THR
2	C	128	SER
2	C	166	SER
2	C	185	LEU
2	C	200	THR
2	C	204	ASN
2	C	214	VAL
3	D	1	ASP
3	D	10	ILE

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Mol	Chain	Res	Type
3	D	19	VAL
3	D	71	SER
3	D	76	THR
3	D	106	LEU
3	D	120	SER
3	D	174	MET
3	D	180	LEU
3	D	190	SER
3	D	201	THR
2	E	5	LEU
2	E	12	VAL
2	E	21	SER
2	E	32	TYR
2	E	56	SER
2	E	76	LYS
2	E	86	VAL
2	E	87	ARG
2	E	96	CYS
2	E	118	THR
2	E	164	SER
2	E	188	SER
2	E	198	SER
2	E	200	THR
2	E	202	THR
3	F	1	ASP
3	F	2	ILE
3	F	7	SER
3	F	22	THR
3	F	27	SER
3	F	29	VAL
3	F	41	THR
3	F	44	LYS
3	F	74	ILE
3	F	95	GLN
3	F	142	ASP
3	F	146	LYS
3	F	170	SER
3	F	181	THR
3	F	192	THR
3	F	198	LYS
3	F	205	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	157	ASN
3	F	95	GLN
3	F	123	GLN

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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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%)	0.15	26 (5%) 26 13	25, 44, 69, 114	0
1	B	442/446 (99%)	0.09	21 (4%) 34 19	26, 45, 83, 115	0
2	C	222/222 (100%)	-0.05	15 (6%) 20 10	11, 36, 71, 102	0
2	E	221/222 (99%)	-0.33	4 (1%) 71 49	16, 38, 70, 111	0
3	D	211/211 (100%)	-0.08	6 (2%) 56 34	23, 43, 62, 77	0
3	F	211/211 (100%)	0.07	16 (7%) 17 8	17, 31, 76, 90	0
All	All	1751/1758 (99%)	0.01	88 (5%) 32 17	11, 41, 73, 115	0

All (88) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	72	ALA	8.1
2	E	222	ALA	7.4
1	B	73	ASP	5.6
1	A	460	GLN	5.5
1	A	235	GLU	5.4
1	B	74	ASN	4.7
1	B	307	PHE	4.3
1	A	168	LEU	4.1
1	A	459	GLU	3.8
2	C	2	VAL	3.7
3	D	20	THR	3.7
1	B	75	TYR	3.7
3	F	151	GLY	3.6
2	C	65	LYS	3.6
1	A	72	ALA	3.6
3	F	156	ASN	3.6
1	B	146	GLY	3.5
1	B	71	THR	3.4
1	A	146	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
2	E	65	LYS	3.2
1	B	70	HIS	3.1
3	F	152	SER	3.1
2	C	142	SER	3.1
3	D	7	SER	3.0
3	F	155	GLN	3.0
1	A	182	ALA	2.9
1	B	119	GLN	2.9
1	A	106	GLY	2.9
3	D	79	ALA	2.9
2	C	27	PHE	2.9
2	C	1	GLU	2.8
1	B	458	ALA	2.8
1	B	168	LEU	2.8
1	A	110	PRO	2.8
3	F	149	ILE	2.8
1	A	148	GLN	2.7
1	A	149	GLY	2.7
2	C	29	TYR	2.7
1	B	456	GLN	2.7
2	C	75	ALA	2.7
1	B	69	VAL	2.6
1	B	78	LEU	2.6
2	C	143	MET	2.6
1	A	166	PHE	2.6
1	B	149	GLY	2.5
1	A	107	SER	2.5
2	C	77	ASP	2.5
1	A	152	VAL	2.5
3	F	150	ASP	2.4
3	D	159	LEU	2.4
1	B	95	PHE	2.4
3	F	183	ASP	2.4
1	A	184	ALA	2.4
1	A	200	ILE	2.4
2	C	139	ALA	2.4
1	B	335	PHE	2.3
3	F	205	VAL	2.3
2	C	64	LEU	2.3
1	A	180	THR	2.3
2	E	148	CYS	2.3
3	F	190	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	355	GLY	2.3
1	B	358	ALA	2.3
3	F	154	ARG	2.3
2	E	66	ASP	2.3
3	D	19	VAL	2.3
1	A	179	ALA	2.2
1	A	18	ARG	2.2
2	C	26	GLY	2.2
3	F	209	ASN	2.2
1	A	185	GLY	2.2
2	C	221	ARG	2.2
1	B	59	TRP	2.2
2	C	140	ALA	2.2
1	B	355	GLY	2.2
3	F	128	GLY	2.2
1	A	147	ARG	2.2
1	A	272	TRP	2.1
1	A	112	ILE	2.1
3	F	148	LYS	2.1
3	D	22	THR	2.1
2	C	137	ALA	2.1
1	B	235	GLU	2.1
3	F	189	ASN	2.1
1	A	258	LEU	2.1
3	F	147	TRP	2.0
1	A	105	GLY	2.0
3	F	153	GLU	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.