Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:05 PM GMT

PDB ID	:	4NQQ
Title	:	Crystal structure of mouse P-cadherin extracellular domains EC1-EC2
Authors	:	Brasch, J.; Shapiro, L.
Deposited on	:	2013-11-25
Resolution	:	3.20 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

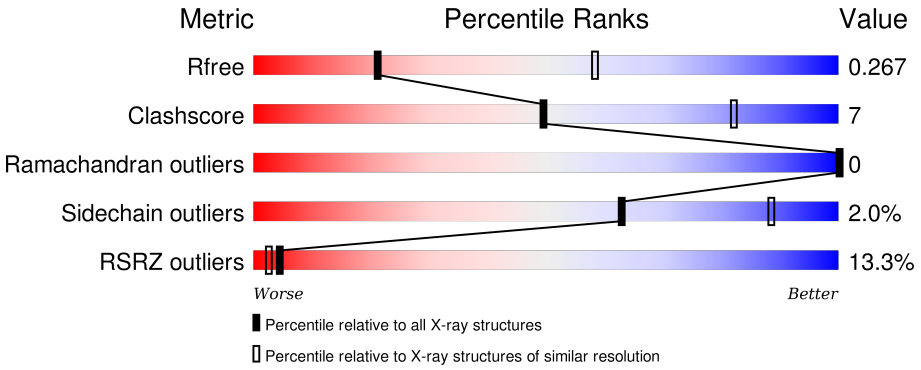
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	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 3.20 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	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	213	4% 90% 10%
1	B	213	11% 87% 13%
1	C	213	2% 87% 11%
1	D	213	36% 79% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12762 atoms, of which 6111 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 Cadherin-3.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	213	Total	C	H	N	O	S	0	0	0
			3229	1035	1581	272	334	7			
1	B	213	Total	C	H	N	O	S	0	1	0
			3207	1039	1554	272	334	8			
1	C	210	Total	C	H	N	O	S	0	0	0
			3132	1014	1513	268	330	7			
1	D	211	Total	C	H	N	O	S	0	0	0
			3095	1025	1463	270	330	7			

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	3	Total	Ca	0	0
			3	3		
2	A	4	Total	Ca	0	0
			4	4		
2	D	4	Total	Ca	0	0
			4	4		
2	C	3	Total	Ca	0	0
			3	3		

- Molecule 3 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Cu	0	0
			2	2		
3	A	2	Total	Cu	0	0
			2	2		
3	D	2	Total	Cu	0	0
			2	2		
3	C	3	Total	Cu	0	0
			3	3		

- Molecule 4 is water.

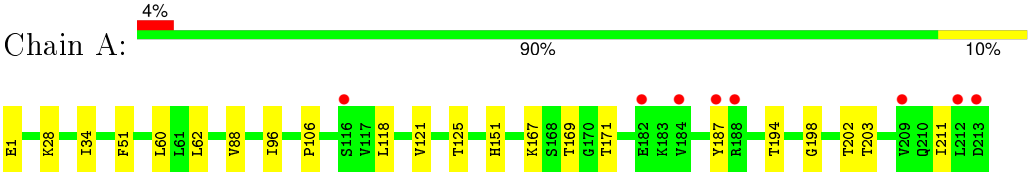
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	28	Total O 28 28	0	0
4	B	32	Total O 32 32	0	0
4	C	14	Total O 14 14	0	0
4	D	2	Total O 2 2	0	0

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.

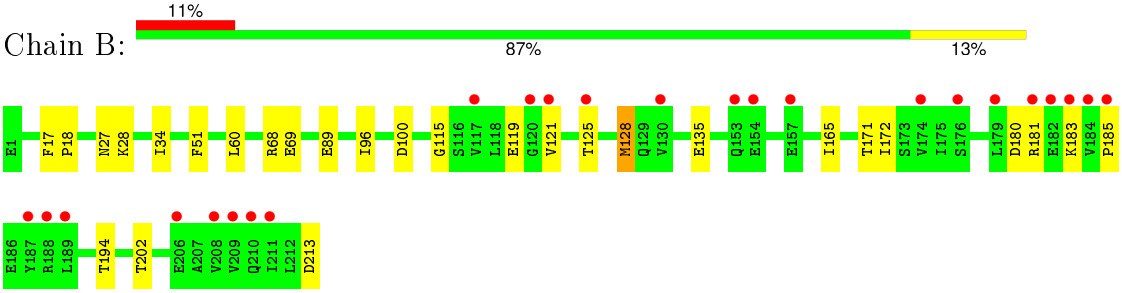
- Molecule 1: Cadherin-3

Chain A:



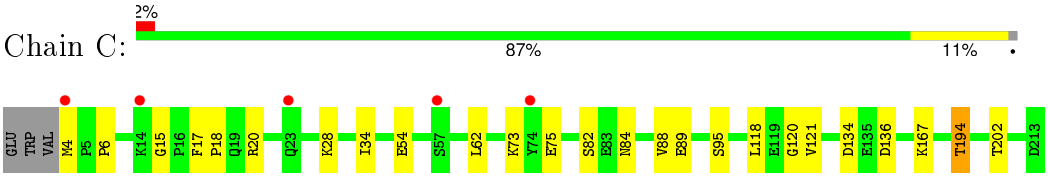
- Molecule 1: Cadherin-3

Chain B:



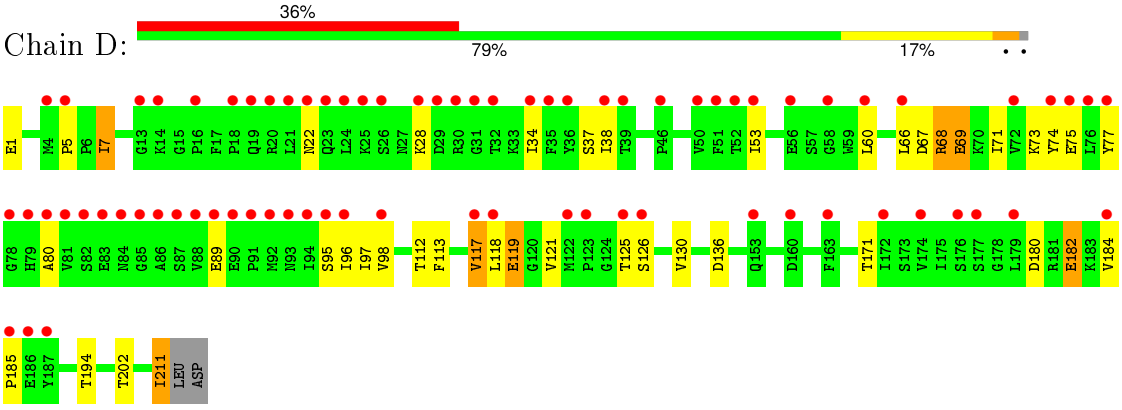
- Molecule 1: Cadherin-3

Chain C:



- Molecule 1: Cadherin-3

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	123.08Å 188.70Å 53.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 3.20 39.34 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (20.00-3.20) 94.9 (39.34-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.77 (at 3.18Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: DEV_1186)	Depositor
R, R_{free}	0.228 , 0.269 0.228 , 0.267	Depositor DCC
R_{free} test set	1010 reflections (5.02%)	DCC
Wilson B-factor (Å^2)	72.2	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 47.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 21058 reflections	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	12762	wwPDB-VP
Average B, all atoms (Å^2)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.58% 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

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

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	0.25	0/1684	0.45	0/2290
1	B	0.25	0/1692	0.45	0/2301
1	C	0.24	0/1653	0.47	1/2245 (0.0%)
1	D	0.24	0/1668	0.52	2/2268 (0.1%)
All	All	0.24	0/6697	0.47	3/9104 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	120	GLY	C-N-CA	6.89	138.93	121.70
1	D	119	GLU	CB-CA-C	-6.64	97.12	110.40
1	D	117	VAL	CB-CA-C	-5.18	101.55	111.40

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	1648	1581	1606	18	0
1	B	1653	1554	1615	22	0
1	C	1619	1513	1578	17	0
1	D	1632	1463	1590	40	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	4	0	0	0	0
2	B	3	0	0	0	0
2	C	3	0	0	0	0
2	D	4	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
4	A	28	0	0	0	2
4	B	32	0	0	0	2
4	C	14	0	0	0	2
4	D	2	0	0	0	0
All	All	6651	6111	6389	92	4

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 (92) 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:D:73:LYS:HD3	1:D:97:ILE:HG12	1.19	1.15
1:C:194:THR:CG2	1:C:202:THR:HG22	1.88	1.03
1:D:66:LEU:HD11	1:D:74:TYR:CE1	2.02	0.94
1:D:73:LYS:HD3	1:D:97:ILE:CG1	2.00	0.92
1:D:73:LYS:NZ	1:D:75:GLU:OE2	2.02	0.90
1:C:194:THR:HG23	1:C:202:THR:HG22	1.52	0.90
1:D:68:ARG:NH2	1:D:69:GLU:HG3	1.98	0.78
1:C:89:GLU:OE2	1:D:1:GLU:N	2.19	0.75
1:B:119:GLU:HB2	1:B:213:ASP:OD1	1.85	0.75
1:D:66:LEU:HD11	1:D:74:TYR:CZ	2.28	0.68
1:D:66:LEU:HD11	1:D:74:TYR:HE1	1.55	0.68
1:C:28:LYS:HD3	1:C:88:VAL:HB	1.76	0.66
1:C:28:LYS:HB3	1:C:34:ILE:HD11	1.79	0.65
1:D:73:LYS:CD	1:D:97:ILE:HG12	2.13	0.63
1:D:68:ARG:HG3	1:D:98:VAL:O	1.99	0.61
1:D:117:VAL:HG13	1:D:117:VAL:O	1.99	0.60
1:D:73:LYS:HD2	1:D:95:SER:HB2	1.83	0.60
1:B:194:THR:HG22	1:B:202:THR:HB	1.83	0.60
1:C:194:THR:HG21	1:C:202:THR:HG22	1.83	0.59
1:C:82:SER:OG	1:C:84:ASN:OD1	2.19	0.59
1:C:194:THR:HG23	1:C:202:THR:CG2	2.31	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:THR:HG22	1:B:202:THR:CB	2.36	0.56
1:A:194:THR:HB	1:A:202:THR:HG22	1.88	0.56
1:C:6:PRO:HA	1:C:95:SER:O	2.07	0.55
1:C:118:LEU:O	1:C:121:VAL:HG23	2.07	0.54
1:C:4:MET:HE2	1:D:5:PRO:HG3	1.89	0.54
1:A:28:LYS:HB2	1:A:34:ILE:HD11	1.90	0.54
1:B:28:LYS:HB2	1:B:34:ILE:HD11	1.90	0.53
1:D:118:LEU:HB2	1:D:121:VAL:HG23	1.90	0.52
1:A:194:THR:CB	1:A:202:THR:HG22	2.40	0.52
1:D:7:ILE:CD1	1:D:96:ILE:HA	2.40	0.52
1:B:180:ASP:OD2	1:B:183:LYS:HG3	2.11	0.51
1:D:66:LEU:HD11	1:D:74:TYR:OH	2.11	0.51
1:A:121:VAL:CG1	1:A:125:THR:OG1	2.58	0.51
1:A:1:GLU:HB3	1:B:27:ASN:ND2	2.25	0.51
1:D:7:ILE:CD1	1:D:96:ILE:HG12	2.41	0.50
1:B:194:THR:CG2	1:B:202:THR:HG22	2.41	0.50
1:A:28:LYS:HD2	1:A:88:VAL:HB	1.93	0.50
1:A:121:VAL:HG11	1:A:125:THR:OG1	2.12	0.49
1:D:184:VAL:O	1:D:211:ILE:CD1	2.61	0.49
1:D:118:LEU:HB2	1:D:121:VAL:CG2	2.43	0.48
1:A:51:PHE:CE1	1:A:96:ILE:HD13	2.49	0.48
1:D:7:ILE:HD13	1:D:96:ILE:HG12	1.96	0.48
1:A:194:THR:HG23	1:A:198:GLY:HA2	1.96	0.48
1:B:180:ASP:OD1	1:B:180:ASP:N	2.45	0.47
1:D:38:ILE:HA	1:D:77:TYR:O	2.15	0.47
1:A:194:THR:OG1	1:A:202:THR:HG22	2.15	0.47
1:D:117:VAL:CG1	1:D:117:VAL:O	2.62	0.46
1:D:80:ALA:HB3	1:D:89:GLU:HG2	1.97	0.46
1:D:119:GLU:HG2	1:D:119:GLU:O	2.14	0.46
1:D:68:ARG:HH22	1:D:136:ASP:HA	1.80	0.46
1:A:51:PHE:CE1	1:A:62:LEU:HD13	2.50	0.46
1:B:51:PHE:CE1	1:B:96:ILE:HD13	2.52	0.46
1:D:125:THR:HG22	1:D:126:SER:N	2.32	0.45
1:B:165:ILE:HG12	1:B:172:ILE:HG12	1.99	0.45
1:A:151:HIS:O	1:C:167:LYS:NZ	2.50	0.45
1:C:73:LYS:HE3	1:C:75:GLU:OE2	2.16	0.45
1:D:68:ARG:CG	1:D:98:VAL:O	2.65	0.44
1:A:118:LEU:HB2	1:A:121:VAL:HG23	1.99	0.44
1:A:34:ILE:HD13	1:A:88:VAL:HG21	1.99	0.44
1:D:184:VAL:O	1:D:211:ILE:HD13	2.18	0.44
1:D:194:THR:CG2	1:D:202:THR:HG22	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:17:PHE:HA	1:B:18:PRO:C	2.37	0.44
1:B:121:VAL:HG13	1:B:125:THR:HG21	1.99	0.44
1:B:69:GLU:HG3	1:B:135:GLU:O	2.18	0.44
1:D:71:ILE:HG13	1:D:74:TYR:CE2	2.53	0.44
1:B:181:ARG:NH1	1:B:185:PRO:HB3	2.33	0.43
1:B:121:VAL:CG1	1:B:125:THR:OG1	2.66	0.43
1:A:1:GLU:N	1:B:89:GLU:OE2	2.36	0.43
1:B:115:GLY:N	1:B:128:MET:CE	2.82	0.43
1:B:115:GLY:N	1:B:128:MET:HE3	2.34	0.43
1:D:113:PHE:CG	1:D:130:VAL:HG12	2.54	0.43
1:B:194:THR:HG22	1:B:202:THR:HG22	2.00	0.43
1:D:194:THR:HG22	1:D:202:THR:HG22	2.01	0.43
1:C:20:ARG:NH2	1:C:54:GLU:OE2	2.51	0.43
1:A:169:THR:OG1	1:A:171:THR:HG22	2.19	0.43
1:D:7:ILE:HG23	1:D:22:ASN:ND2	2.34	0.42
1:C:15:GLY:HA2	1:C:17:PHE:CD2	2.54	0.42
1:D:28:LYS:HB2	1:D:34:ILE:HD11	2.01	0.42
1:C:134:ASP:OD1	1:C:136:ASP:HB2	2.19	0.42
1:D:37:SER:HA	1:D:53:ILE:CG2	2.49	0.42
1:B:194:THR:HG22	1:B:202:THR:CG2	2.49	0.42
1:D:71:ILE:HG21	1:D:74:TYR:CG	2.55	0.41
1:C:18:PRO:HA	1:C:62:LEU:O	2.20	0.41
1:D:180:ASP:OD1	1:D:182:GLU:HG2	2.20	0.41
1:D:68:ARG:HB2	1:D:98:VAL:HG12	2.03	0.41
1:B:121:VAL:HG12	1:B:125:THR:OG1	2.20	0.41
1:D:194:THR:HG22	1:D:202:THR:CB	2.51	0.41
1:A:106:PRO:O	1:A:203:THR:HG21	2.20	0.41
1:D:185:PRO:O	1:D:211:ILE:HD12	2.21	0.40
1:A:187:TYR:CE1	1:A:211:ILE:HD11	2.56	0.40
1:B:68:ARG:HD3	1:B:100:ASP:HB2	2.04	0.40

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:73:LYS:O	1:D:77:TYR:OH[2_555]	1.93	0.27
4:B:405:HOH:O	4:C:404:HOH:O[4_557]	2.02	0.18
4:A:424:HOH:O	4:B:430:HOH:O[1_556]	2.10	0.10
4:A:410:HOH:O	4:C:410:HOH:O[4_557]	2.18	0.02

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	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
1	B	212/213 (100%)	205 (97%)	7 (3%)	0	100	100
1	C	208/213 (98%)	200 (96%)	8 (4%)	0	100	100
1	D	209/213 (98%)	201 (96%)	8 (4%)	0	100	100
All	All	840/852 (99%)	810 (96%)	30 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	187/187 (100%)	185 (99%)	2 (1%)	80	94
1	B	188/187 (100%)	185 (98%)	3 (2%)	70	91
1	C	184/187 (98%)	183 (100%)	1 (0%)	92	97
1	D	185/187 (99%)	176 (95%)	9 (5%)	31	72
All	All	744/748 (100%)	729 (98%)	15 (2%)	63	88

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	60	LEU
1	A	167	LYS

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Mol	Chain	Res	Type
1	B	60	LEU
1	B	128	MET
1	B	171	THR
1	C	194	THR
1	D	7	ILE
1	D	60	LEU
1	D	67	ASP
1	D	68	ARG
1	D	69	GLU
1	D	112	THR
1	D	171	THR
1	D	182	GLU
1	D	211	ILE

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

Mol	Chain	Res	Type
1	A	151	HIS
1	B	166	HIS
1	D	166	HIS

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)

Of 23 ligands modelled in this entry, 23 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	213/213 (100%)	0.23	8 (3%) 44 29	15, 35, 82, 113	0
1	B	213/213 (100%)	0.54	24 (11%) 7 4	11, 47, 134, 156	0
1	C	210/213 (98%)	0.37	5 (2%) 62 47	17, 51, 85, 113	0
1	D	211/213 (99%)	2.18	76 (36%) 0 0	65, 131, 205, 223	0
All	All	847/852 (99%)	0.83	113 (13%) 4 2	11, 59, 175, 223	0

All (113) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	86	ALA	16.8
1	D	91	PRO	16.2
1	D	30	ARG	13.2
1	D	84	ASN	12.8
1	D	87	SER	11.3
1	D	31	GLY	11.3
1	D	32	THR	10.5
1	D	22	ASN	10.2
1	D	93	ASN	9.4
1	D	90	GLU	8.2
1	D	52	THR	7.9
1	D	21	LEU	7.6
1	D	85	GLY	7.5
1	D	29	ASP	7.3
1	D	80	ALA	7.0
1	D	81	VAL	6.4
1	D	60	LEU	6.3
1	D	26	SER	6.2
1	D	24	LEU	6.2
1	D	82	SER	6.1
1	D	35	PHE	5.5

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Mol	Chain	Res	Type	RSRZ
1	D	76	LEU	5.3
1	D	123	PRO	5.1
1	D	36	TYR	5.1
1	D	53	ILE	5.1
1	D	78	GLY	4.9
1	D	75	GLU	4.9
1	D	58	GLY	4.8
1	D	92	MET	4.7
1	D	122	MET	4.6
1	B	179	LEU	4.2
1	D	77	TYR	4.2
1	D	88	VAL	4.2
1	D	125	THR	4.1
1	D	95	SER	4.1
1	D	34	ILE	4.1
1	B	154	GLU	4.1
1	B	184	VAL	4.0
1	D	187	TYR	3.9
1	B	120	GLY	3.9
1	A	213	ASP	3.9
1	D	66	LEU	3.8
1	B	185	PRO	3.8
1	D	25	LYS	3.8
1	D	126	SER	3.7
1	B	183	LYS	3.7
1	D	23	GLN	3.7
1	D	13	GLY	3.6
1	D	94	ILE	3.5
1	D	176	SER	3.5
1	D	177	SER	3.5
1	D	51	PHE	3.4
1	B	176	SER	3.4
1	D	186	GLU	3.4
1	D	38	ILE	3.4
1	D	28	LYS	3.2
1	B	210	GLN	3.2
1	B	181	ARG	3.2
1	D	4	MET	3.2
1	B	187	TYR	3.1
1	A	187	TYR	3.1
1	D	18	PRO	3.1
1	D	79	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	184	VAL	3.0
1	D	56	GLU	2.9
1	D	16	PRO	2.9
1	B	121	VAL	2.9
1	B	208	VAL	2.9
1	D	74	TYR	2.9
1	D	160	ASP	2.8
1	B	157	GLU	2.8
1	B	130	VAL	2.8
1	D	174	VAL	2.7
1	D	14	LYS	2.7
1	D	46	PRO	2.7
1	D	19	GLN	2.6
1	D	98	VAL	2.6
1	B	182	GLU	2.6
1	B	189	LEU	2.6
1	D	89	GLU	2.6
1	D	185	PRO	2.6
1	B	153	GLN	2.5
1	D	163	PHE	2.5
1	D	83	GLU	2.5
1	C	14	LYS	2.5
1	B	211	ILE	2.5
1	A	182	GLU	2.5
1	D	39	THR	2.4
1	D	96	ILE	2.4
1	B	188	ARG	2.4
1	B	209	VAL	2.4
1	D	179	LEU	2.3
1	D	184	VAL	2.3
1	D	20	ARG	2.3
1	A	212	LEU	2.3
1	D	117	VAL	2.3
1	D	5	PRO	2.3
1	B	117	VAL	2.2
1	C	23	GLN	2.2
1	D	172	ILE	2.2
1	D	50	VAL	2.2
1	C	74	TYR	2.2
1	A	116	SER	2.2
1	B	174	VAL	2.2
1	B	206	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	72	VAL	2.1
1	C	4	MET	2.1
1	D	118	LEU	2.1
1	D	153	GLN	2.1
1	B	125	THR	2.1
1	A	188	ARG	2.0
1	A	209	VAL	2.0
1	C	57	SER	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, 95^{th} 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(Å^2)	Q<0.9
2	CA	B	301	1/1	0.97	0.24	1.33	32,32,32,32	0
2	CA	A	302	1/1	0.98	0.22	1.19	23,23,23,23	0
2	CA	B	302	1/1	0.98	0.19	0.34	33,33,33,33	0
2	CA	A	301	1/1	0.93	0.20	0.25	24,24,24,24	0
2	CA	C	303	1/1	0.99	0.18	-0.56	25,25,25,25	0
2	CA	C	302	1/1	0.97	0.15	-0.77	32,32,32,32	0
2	CA	A	303	1/1	0.97	0.17	-0.80	20,20,20,20	0
2	CA	C	301	1/1	0.92	0.13	-0.82	34,34,34,34	0
2	CA	B	303	1/1	0.93	0.13	-1.36	43,43,43,43	0
2	CA	D	302	1/1	0.86	0.10	-1.40	92,92,92,92	0
2	CA	D	301	1/1	0.81	0.11	-1.50	85,85,85,85	0
2	CA	D	303	1/1	0.92	0.15	-1.56	102,102,102,102	0
2	CA	A	304	1/1	0.93	0.11	-1.71	75,75,75,75	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	CU	A	305	1/1	0.79	0.20	-	72,72,72,72	0
3	CU	A	306	1/1	0.98	0.26	-	52,52,52,52	0
2	CA	D	304	1/1	0.68	0.08	-	122,122,122,122	0
3	CU	C	305	1/1	0.93	0.32	-	70,70,70,70	0
3	CU	D	305	1/1	0.94	0.33	-	74,74,74,74	0
3	CU	D	306	1/1	0.43	0.17	-	131,131,131,131	0
3	CU	B	305	1/1	0.92	0.23	-	77,77,77,77	0
3	CU	C	306	1/1	0.97	0.18	-	86,86,86,86	0
3	CU	B	304	1/1	0.82	0.21	-	102,102,102,102	0
3	CU	C	304	1/1	0.97	0.25	-	51,51,51,51	0

6.5 Other polymers (i)

There are no such residues in this entry.