Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 04:54 am BST

PDB ID	:	4GAO
Title	:	DCNL complex with N-terminally acetylated NEDD8 E2 peptide
Authors	:	Monda, J.K.; Scott, D.C.; Miller, D.J.; Harper, J.W.; Bennett, E.J.; Schulman, B.A.
Deposited on	:	2012-07-25
Resolution	:	3.28 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:

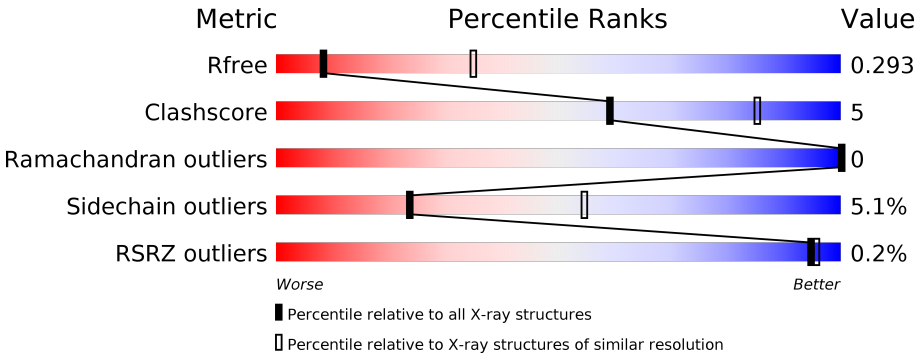
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 3.28 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	1177 (3.32-3.24)
Clashscore	141614	1044 (3.30-3.26)
Ramachandran outliers	138981	1026 (3.30-3.26)
Sidechain outliers	138945	1025 (3.30-3.26)
RSRZ outliers	127900	1141 (3.32-3.24)

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 <=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	200	80% 16%
1	B	200	% 84% 11%
1	D	200	% 81% 12% 6%
1	G	200	82% 14%
2	C	12	83% 17%
2	E	12	83% 17%

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Mol	Chain	Length	Quality of chain
2	F	12	92% 8%
2	H	12	83% 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6299 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 DCN1-like protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	193	Total	C	N	O	S	0	0	0
			1511	978	240	284	9			
1	B	192	Total	C	N	O	S	0	0	0
			1501	972	236	284	9			
1	D	188	Total	C	N	O	S	0	0	0
			1504	974	238	283	9			
1	G	193	Total	C	N	O	S	0	0	0
			1511	974	241	287	9			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	60	GLY	-	EXPRESSION TAG	UNP Q6PH85
A	61	SER	-	EXPRESSION TAG	UNP Q6PH85
B	60	GLY	-	EXPRESSION TAG	UNP Q6PH85
B	61	SER	-	EXPRESSION TAG	UNP Q6PH85
D	60	GLY	-	EXPRESSION TAG	UNP Q6PH85
D	61	SER	-	EXPRESSION TAG	UNP Q6PH85
G	60	GLY	-	EXPRESSION TAG	UNP Q6PH85
G	61	SER	-	EXPRESSION TAG	UNP Q6PH85

- Molecule 2 is a protein called NEDD8-conjugating enzyme Ubc12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	10	Total	C	N	O	S	0	0	0
			66	43	11	11	1			
2	E	10	Total	C	N	O	S	0	0	0
			69	46	10	12	1			
2	F	11	Total	C	N	O	S	0	0	0
			67	43	11	12	1			
2	H	10	Total	C	N	O	S	0	0	0
			68	46	10	11	1			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	1	AME	MET	ACETYLATION	UNP P61081
E	1	AME	MET	ACETYLATION	UNP P61081
F	1	AME	MET	ACETYLATION	UNP P61081
H	1	AME	MET	ACETYLATION	UNP P61081

- Molecule 3 is BROMIDE ION (three-letter code: BR) (formula: Br).

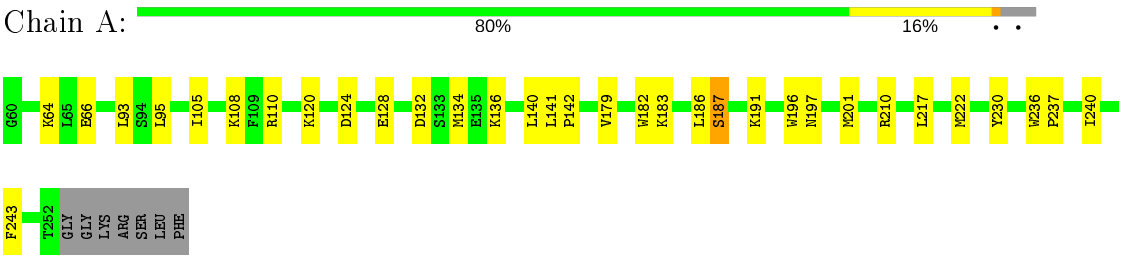
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Br 1 1	0	0
3	A	1	Total Br 1 1	0	0

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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

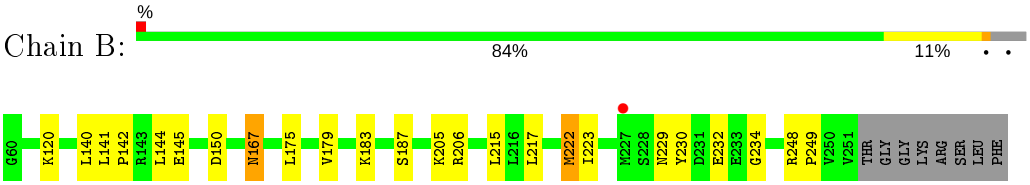
- Molecule 1: DCN1-like protein 2

Chain A:



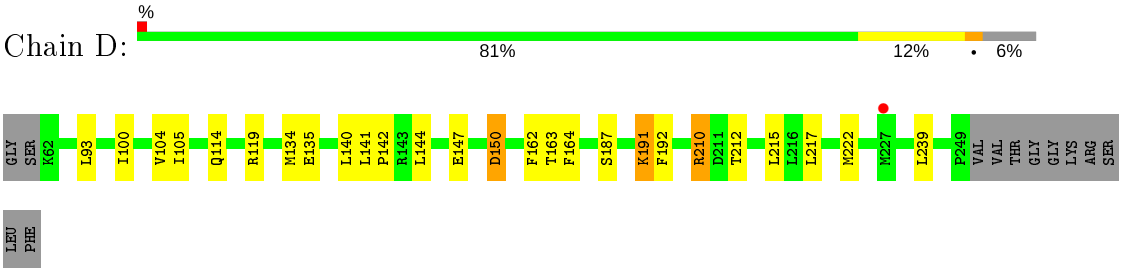
- Molecule 1: DCN1-like protein 2

Chain B:



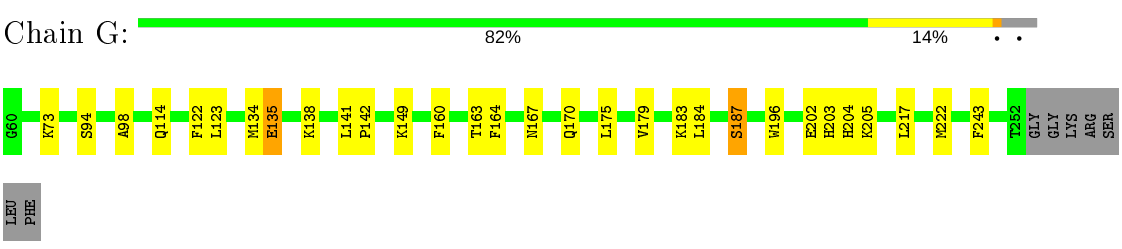
- Molecule 1: DCN1-like protein 2

Chain D:



- Molecule 1: DCN1-like protein 2

Chain G:



- Molecule 2: NEDD8-conjugating enzyme Ubc12

Chain C:

- Molecule 2: NEDD8-conjugating enzyme Ubc12

Chain E:

- Molecule 2: NEDD8-conjugating enzyme Ubc12

Chain F:

- Molecule 2: NEDD8-conjugating enzyme Ubc12

Chain H:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	48.57Å 190.15Å 49.07Å 90.00° 101.75° 90.00°	Depositor
Resolution (Å)	40.00 – 3.28 38.29 – 3.28	Depositor EDS
% Data completeness (in resolution range)	98.1 (40.00-3.28) 98.1 (38.29-3.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.20 (at 3.25Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.252 , 0.296 0.246 , 0.293	Depositor DCC
R_{free} test set	643 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	55.3	Xtriage
Anisotropy	0.095	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 8.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	0.070 for l,-k,h	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	6299	wwPDB-VP
Average B, all atoms (Å^2)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.85% 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, 0.333 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: AME, 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	0.47	0/1549	0.52	0/2102
1	B	0.45	0/1538	0.49	0/2088
1	D	0.48	0/1542	0.52	0/2088
1	G	0.50	0/1548	0.51	0/2099
2	C	0.45	0/54	0.42	0/72
2	E	0.52	0/58	0.41	0/78
2	F	0.40	0/55	0.39	0/75
2	H	0.50	0/57	0.41	0/77
All	All	0.47	0/6401	0.51	0/8679

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	1511	0	1407	17	0
1	B	1501	0	1401	15	0
1	D	1504	0	1422	12	0
1	G	1511	0	1406	14	0
2	C	66	0	59	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	69	0	58	0	0
2	F	67	0	50	0	0
2	H	68	0	55	0	0
3	A	1	0	0	1	0
3	B	1	0	0	0	0
All	All	6299	0	5858	57	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 5.

All (57) 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:B:175:LEU:HD22	1:B:205:LYS:HA	1.50	0.91
1:G:175:LEU:HD22	1:G:205:LYS:HA	1.55	0.89
1:D:212:THR:HG21	1:D:239:LEU:HD23	1.69	0.75
1:D:141:LEU:HB2	1:D:142:PRO:HD3	1.71	0.71
1:B:183:LYS:O	1:B:187:SER:HB2	1.94	0.68
1:A:141:LEU:HB2	1:A:142:PRO:HD3	1.76	0.68
1:B:175:LEU:CD2	1:B:205:LYS:HA	2.24	0.67
1:D:162:PHE:CE2	1:D:210:ARG:HG2	2.29	0.67
1:D:140:LEU:O	1:D:144:LEU:HG	1.95	0.67
1:A:183:LYS:O	1:A:187:SER:HB2	1.98	0.63
1:G:179:VAL:O	1:G:183:LYS:HG3	1.98	0.63
1:A:179:VAL:O	1:A:183:LYS:HG3	2.03	0.58
1:D:144:LEU:O	1:D:147:GLU:HG2	2.03	0.57
1:A:141:LEU:CB	1:A:142:PRO:HD3	2.38	0.54
1:D:93:LEU:HG	1:D:134:MET:CE	2.37	0.54
1:A:93:LEU:HG	1:A:134:MET:CE	2.38	0.54
1:A:182:TRP:CD1	1:A:186:LEU:HD12	2.43	0.54
1:G:98:ALA:O	1:G:184:LEU:HD21	2.10	0.52
1:A:95:LEU:HD11	1:A:141:LEU:HD11	1.91	0.52
1:D:105:ILE:HD11	1:D:141:LEU:HD21	1.93	0.50
1:A:105:ILE:HD11	1:A:141:LEU:HD21	1.95	0.47
1:G:175:LEU:CD2	1:G:205:LYS:HA	2.38	0.46
1:G:196:TRP:HA	1:G:243:PHE:CE1	2.50	0.46
1:G:114:GLN:HA	1:G:164:PHE:CZ	2.51	0.46
1:G:122:PHE:HD2	1:G:123:LEU:HD12	1.80	0.46
1:B:141:LEU:HB2	1:B:142:PRO:HD3	1.98	0.46
1:A:108:LYS:HD2	1:A:108:LYS:HA	1.82	0.45
1:G:141:LEU:HB2	1:G:142:PRO:HD3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:183:LYS:O	1:G:187:SER:HB2	2.16	0.45
1:A:237:PRO:HD2	1:A:240:ILE:HD12	1.99	0.45
1:B:223:ILE:HA	1:B:229:ASN:HD21	1.81	0.45
1:A:230:TYR:CE1	1:A:236:TRP:CD1	3.05	0.44
1:G:167:ASN:O	1:G:170:GLN:HB2	2.17	0.44
1:G:204:HIS:O	1:G:204:HIS:ND1	2.50	0.44
1:G:94:SER:HB2	1:G:138:LYS:NZ	2.33	0.44
1:A:120:LYS:HB2	3:A:301:BR:BR	2.72	0.44
1:B:140:LEU:O	1:B:144:LEU:HG	2.18	0.44
1:B:167:ASN:OD1	1:B:167:ASN:N	2.50	0.44
1:D:93:LEU:HG	1:D:134:MET:HE1	1.99	0.43
1:A:124:ASP:O	1:A:128:GLU:HG3	2.18	0.43
1:A:136:LYS:O	1:A:140:LEU:HD13	2.19	0.43
1:D:191:LYS:HD2	1:D:192:PHE:CE2	2.53	0.43
1:B:175:LEU:HB2	1:B:206:ARG:O	2.19	0.43
1:B:248:ARG:HB2	1:B:249:PRO:HD3	2.01	0.42
1:B:167:ASN:HD21	1:D:150:ASP:CG	2.22	0.42
1:B:120:LYS:HE3	1:B:120:LYS:HB3	1.86	0.42
1:B:230:TYR:HB3	1:B:248:ARG:HH21	1.84	0.42
1:D:114:GLN:HA	1:D:164:PHE:CZ	2.55	0.42
1:A:64:LYS:HB3	1:A:132:ASP:HB2	2.01	0.41
1:A:196:TRP:HA	1:A:243:PHE:CE1	2.56	0.41
1:D:100:ILE:O	1:D:104:VAL:HG23	2.19	0.41
1:G:202:GLU:HB3	1:G:203:HIS:CD2	2.56	0.41
1:A:197:ASN:O	1:A:201:MET:HG3	2.20	0.41
1:B:232:GLU:C	1:B:234:GLY:H	2.24	0.41
1:B:179:VAL:O	1:B:183:LYS:HG3	2.21	0.40
1:B:222:MET:O	1:B:229:ASN:ND2	2.55	0.40
1:G:135:GLU:HG3	1:G:135:GLU:H	1.52	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	191/200 (96%)	182 (95%)	9 (5%)	0	100	100
1	B	190/200 (95%)	184 (97%)	6 (3%)	0	100	100
1	D	186/200 (93%)	182 (98%)	4 (2%)	0	100	100
1	G	191/200 (96%)	185 (97%)	6 (3%)	0	100	100
2	C	8/12 (67%)	8 (100%)	0	0	100	100
2	E	8/12 (67%)	8 (100%)	0	0	100	100
2	F	9/12 (75%)	9 (100%)	0	0	100	100
2	H	8/12 (67%)	8 (100%)	0	0	100	100
All	All	791/848 (93%)	766 (97%)	25 (3%)	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	153/175 (87%)	146 (95%)	7 (5%)	27	58
1	B	153/175 (87%)	147 (96%)	6 (4%)	32	62
1	D	156/175 (89%)	146 (94%)	10 (6%)	17	47
1	G	154/175 (88%)	145 (94%)	9 (6%)	20	50
2	C	3/11 (27%)	3 (100%)	0	100	100
2	E	4/11 (36%)	4 (100%)	0	100	100
2	F	2/11 (18%)	2 (100%)	0	100	100
2	H	3/11 (27%)	3 (100%)	0	100	100
All	All	628/744 (84%)	596 (95%)	32 (5%)	24	54

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	GLU
1	A	110	ARG

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Mol	Chain	Res	Type
1	A	187	SER
1	A	191	LYS
1	A	210	ARG
1	A	217	LEU
1	A	222	MET
1	B	145	GLU
1	B	150	ASP
1	B	167	ASN
1	B	215	LEU
1	B	217	LEU
1	B	222	MET
1	D	119	ARG
1	D	135	GLU
1	D	150	ASP
1	D	163	THR
1	D	187	SER
1	D	191	LYS
1	D	210	ARG
1	D	215	LEU
1	D	217	LEU
1	D	222	MET
1	G	73	LYS
1	G	134	MET
1	G	135	GLU
1	G	149	LYS
1	G	160	PHE
1	G	163	THR
1	G	187	SER
1	G	217	LEU
1	G	222	MET

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	203	HIS
1	G	159	GLN
1	G	203	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 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

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	193/200 (96%)	-0.11	0 100 100	25, 50, 83, 90	0
1	B	192/200 (96%)	-0.11	1 (0%) 91 91	25, 48, 76, 87	0
1	D	188/200 (94%)	-0.01	1 (0%) 91 91	27, 55, 84, 96	0
1	G	193/200 (96%)	-0.14	0 100 100	28, 44, 80, 92	0
2	C	9/12 (75%)	-0.49	0 100 100	44, 47, 50, 50	0
2	E	9/12 (75%)	-0.33	0 100 100	38, 46, 55, 56	0
2	F	10/12 (83%)	-0.60	0 100 100	40, 48, 55, 55	0
2	H	9/12 (75%)	-0.39	0 100 100	39, 46, 52, 52	0
All	All	803/848 (94%)	-0.11	2 (0%) 95 96	25, 49, 81, 96	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	227	MET	2.7
1	D	227	MET	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no carbohydrates in this entry.

6.4 Ligands

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, 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	B-factors(Å^2)	Q<0.9
3	BR	B	301	1/1	0.99	0.06	52,52,52,52	0
3	BR	A	301	1/1	0.99	0.05	46,46,46,46	0

6.5 Other polymers

There are no such residues in this entry.