Full wwPDB X-ray Structure Validation Report (i)

Sep 20, 2023 – 08:11 PM EDT

PDB ID	:	5K82
Title	:	Crystal Structure of a Primate APOBEC3G N-Terminal Domain
Authors	:	Xiao, X.; Li, S.-X.; Yang, H.; Chen, X.S.
Deposited on	:	2016-05-27
Resolution	:	2.91 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 (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

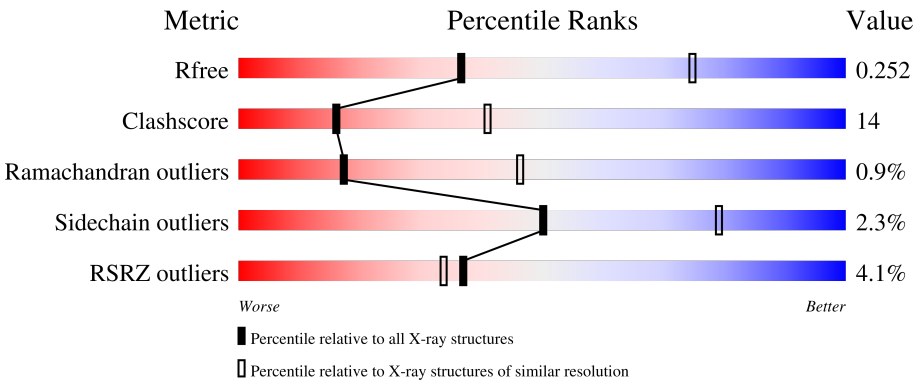
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.91 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	2307 (2.94-2.90)
Clashscore	141614	2531 (2.94-2.90)
Ramachandran outliers	138981	2462 (2.94-2.90)
Sidechain outliers	138945	2464 (2.94-2.90)
RSRZ outliers	127900	2248 (2.94-2.90)

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 of 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	196	4% 65% 28%
1	B	196	4% 66% 29%
1	C	196	4% 66% 26%
1	D	196	4% 69% 27%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 6342 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 Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G,Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	188	1579	1029	275	265	10	0	0	0
1	B	188	1578	1029	275	264	10	0	0	0
1	C	188	1578	1029	275	264	10	0	0	0
1	D	191	1603	1045	279	268	11	0	0	0

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP M1GSK9
A	-3	PRO	-	expression tag	UNP M1GSK9
A	-2	ALA	-	expression tag	UNP M1GSK9
A	-1	GLY	-	expression tag	UNP M1GSK9
A	0	SER	-	expression tag	UNP M1GSK9
A	143	ALA	-	linker	UNP M1GSK9
A	144	GLU	-	linker	UNP M1GSK9
A	145	ALA	-	linker	UNP M1GSK9
A	146	GLY	-	linker	UNP M1GSK9
B	-4	GLY	-	expression tag	UNP M1GSK9
B	-3	PRO	-	expression tag	UNP M1GSK9
B	-2	ALA	-	expression tag	UNP M1GSK9
B	-1	GLY	-	expression tag	UNP M1GSK9
B	0	SER	-	expression tag	UNP M1GSK9
B	143	ALA	-	linker	UNP M1GSK9
B	144	GLU	-	linker	UNP M1GSK9
B	145	ALA	-	linker	UNP M1GSK9
B	146	GLY	-	linker	UNP M1GSK9
C	-4	GLY	-	expression tag	UNP M1GSK9
C	-3	PRO	-	expression tag	UNP M1GSK9

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	ALA	-	expression tag	UNP M1GSK9
C	-1	GLY	-	expression tag	UNP M1GSK9
C	0	SER	-	expression tag	UNP M1GSK9
C	143	ALA	-	linker	UNP M1GSK9
C	144	GLU	-	linker	UNP M1GSK9
C	145	ALA	-	linker	UNP M1GSK9
C	146	GLY	-	linker	UNP M1GSK9
D	-4	GLY	-	expression tag	UNP M1GSK9
D	-3	PRO	-	expression tag	UNP M1GSK9
D	-2	ALA	-	expression tag	UNP M1GSK9
D	-1	GLY	-	expression tag	UNP M1GSK9
D	0	SER	-	expression tag	UNP M1GSK9
D	143	ALA	-	linker	UNP M1GSK9
D	144	GLU	-	linker	UNP M1GSK9
D	145	ALA	-	linker	UNP M1GSK9
D	146	GLY	-	linker	UNP M1GSK9

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

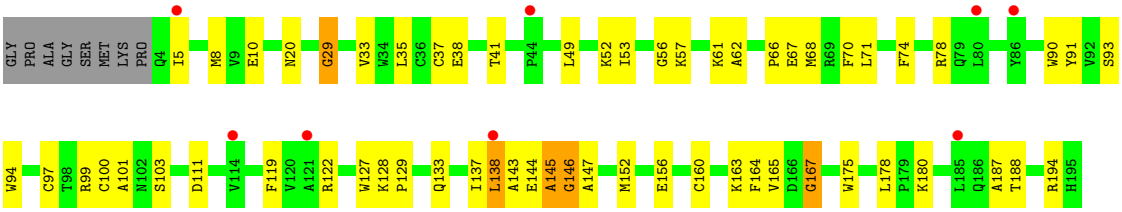
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
2	A	1	1	1	0	0
2	B	1	1	1	0	0
2	C	1	1	1	0	0
2	D	1	1	1	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

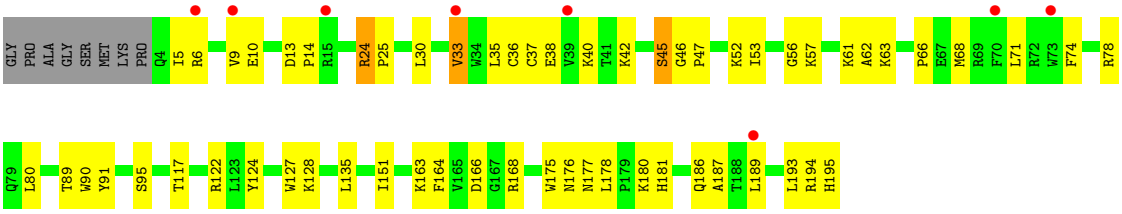
• Molecule 1: Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G,Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G

Chain A:



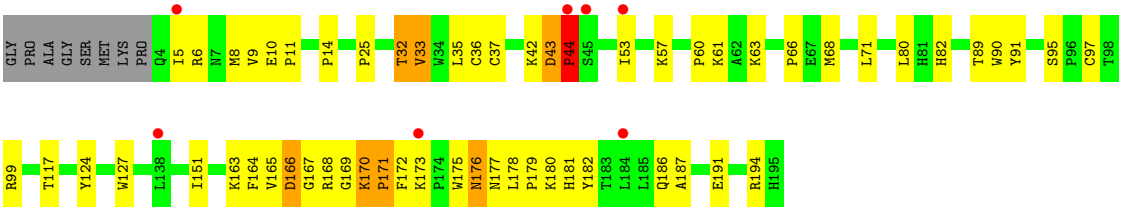
• Molecule 1: Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G,Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G

Chain B:



• Molecule 1: Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G,Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G

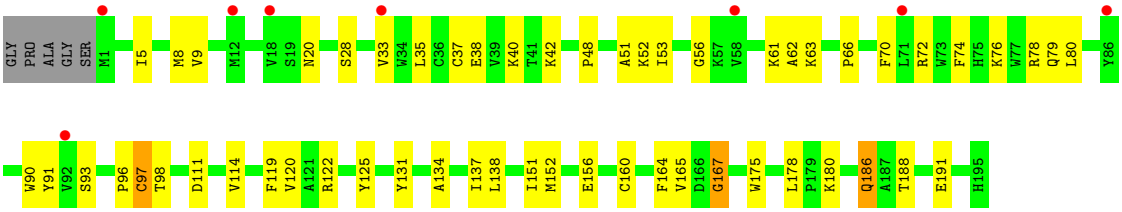
Chain C:



• Molecule 1: Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G,Apolipoprotein B mRNA editing enzyme, catalytic peptide-like 3G

Chain D:

4%
69%
27%


GLY PRO ALA GLY SER M1 I5 M8 V9 M12 V18 S19 N20 S28 V33 W34 L35 C36 C37 E38 V39 K40 T41 K42 P48 A51 K52 I53 G56 K57 V58 K61 A62 K63 P66 F70 L71 R72 W73 F74 H75 K76 W77 R78 Q79 L80 Y86
W90 Y91 V92 S93 P96 C97 T98 D111 V114 F119 V120 A121 R122 Y125 Y131 A134 I137 L138 I151 M152 E156 C160 F164 V165 D166 G167 W175 L178 P179 K180 Q186 A187 T188 E191 H195

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	152.40Å 152.40Å 79.78Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	42.30 – 2.91 49.88 – 2.91	Depositor EDS
% Data completeness (in resolution range)	98.4 (42.30-2.91) 91.3 (49.88-2.91)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.50 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.224 , 0.251 0.228 , 0.252	Depositor DCC
R_{free} test set	2000 reflections (4.48%)	wwPDB-VP
Wilson B-factor (Å^2)	69.0	Xtriage
Anisotropy	0.827	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 51.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.025 for -h,-k,l 0.477 for h,-h-k,-l 0.028 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	6342	wwPDB-VP
Average B, all atoms (Å^2)	90.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.39% 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 (i)

5.1 Standard geometry (i)

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

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	0.57	0/1634	0.80	3/2219 (0.1%)
1	B	0.56	1/1633 (0.1%)	0.83	4/2219 (0.2%)
1	C	0.76	3/1633 (0.2%)	0.85	7/2219 (0.3%)
1	D	0.53	0/1659	0.71	0/2252
All	All	0.61	4/6559 (0.1%)	0.80	14/8909 (0.2%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	44	PRO	N-CD	18.93	1.74	1.47
1	B	37	CYS	CB-SG	-5.14	1.73	1.81
1	C	171	PRO	N-CD	5.06	1.54	1.47
1	C	37	CYS	CB-SG	-5.06	1.73	1.81

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	45	SER	N-CA-C	14.13	149.15	111.00
1	A	145	ALA	CB-CA-C	-13.10	90.46	110.10
1	C	43	ASP	C-N-CD	-10.83	96.77	120.60
1	B	45	SER	CB-CA-C	-10.00	91.09	110.10
1	C	44	PRO	N-CA-CB	9.94	115.23	103.30
1	C	44	PRO	CA-N-CD	-8.78	99.21	111.50
1	C	43	ASP	CB-CA-C	8.60	127.59	110.40
1	A	146	GLY	N-CA-C	8.00	133.10	113.10
1	A	29	GLY	N-CA-C	-7.37	94.67	113.10
1	B	46	GLY	C-N-CD	6.53	142.11	128.40
1	C	43	ASP	N-CA-C	-6.09	94.55	111.00
1	B	24	ARG	NE-CZ-NH1	5.99	123.29	120.30
1	C	44	PRO	N-CA-C	-5.96	96.59	112.10

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	170	LYS	C-N-CD	5.95	140.89	128.40

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	1579	0	1556	59	0
1	B	1578	0	1556	42	0
1	C	1578	0	1555	49	0
1	D	1603	0	1588	41	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
All	All	6342	0	6255	182	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 14.

All (182) 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:C:44:PRO:N	1:C:44:PRO:CD	1.74	1.35
1:C:171:PRO:HD2	1:C:173:LYS:NZ	1.50	1.22
1:C:43:ASP:C	1:C:44:PRO:CD	2.33	0.98
1:C:171:PRO:HD2	1:C:173:LYS:HZ2	1.16	0.91
1:A:101:ALA:HB1	1:A:138:LEU:HD21	1.50	0.90
1:C:171:PRO:CD	1:C:173:LYS:NZ	2.36	0.89
1:D:78:ARG:NH2	1:D:111:ASP:OD2	2.06	0.88
1:A:101:ALA:CB	1:A:138:LEU:HD21	2.05	0.87
1:C:167:GLY:O	1:C:170:LYS:HB2	1.82	0.79
1:A:41:THR:HG23	1:A:49:LEU:HD11	1.65	0.77
1:C:53:ILE:HD11	1:C:164:PHE:HB3	1.68	0.76

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:LEU:HD11	1:B:193:LEU:HD11	1.69	0.74
1:A:74:PHE:O	1:A:78:ARG:HG3	1.91	0.71
1:B:56:GLY:HA3	1:B:66:PRO:HD3	1.73	0.70
1:C:171:PRO:CD	1:C:173:LYS:HZ2	2.00	0.69
1:A:144:GLU:HA	1:A:144:GLU:OE1	1.94	0.68
1:D:37:CYS:HG	1:D:70:PHE:HE2	1.42	0.68
1:A:101:ALA:CA	1:A:138:LEU:HD21	2.24	0.67
1:A:133:GLN:O	1:A:137:ILE:HG13	1.95	0.67
1:A:78:ARG:NH2	1:A:111:ASP:OD2	2.28	0.66
1:A:137:ILE:O	1:A:144:GLU:N	2.28	0.66
1:D:76:LYS:O	1:D:79:GLN:NE2	2.24	0.65
1:B:36:CYS:HB2	1:B:91:TYR:HB2	1.79	0.65
1:A:56:GLY:HA3	1:A:66:PRO:HD3	1.78	0.65
1:B:189:LEU:HD11	1:B:193:LEU:CD1	2.28	0.64
1:C:5:ILE:HA	1:C:8:MET:HG3	1.80	0.64
1:C:10:GLU:N	1:C:10:GLU:OE1	2.31	0.63
1:D:79:GLN:NE2	1:D:80:LEU:HD13	2.15	0.62
1:C:61:LYS:HG3	1:C:63:LYS:H	1.65	0.62
1:C:171:PRO:HD2	1:C:173:LYS:HZ3	1.58	0.61
1:A:37:CYS:HG	1:A:70:PHE:HE2	1.46	0.61
1:A:138:LEU:O	1:A:147:ALA:HB3	1.99	0.60
1:A:35:LEU:HD21	1:A:90:TRP:CD1	2.36	0.60
1:B:57:LYS:N	1:B:57:LYS:HD2	2.16	0.60
1:A:5:ILE:HG22	1:A:8:MET:SD	2.42	0.60
1:A:194:ARG:HH11	1:C:194:ARG:NH2	2.00	0.59
1:B:57:LYS:HD2	1:B:57:LYS:H	1.67	0.59
1:C:5:ILE:HD11	1:C:163:LYS:HB3	1.85	0.59
1:B:10:GLU:N	1:B:10:GLU:OE1	2.36	0.58
1:B:189:LEU:CD1	1:B:193:LEU:CD1	2.81	0.58
1:D:74:PHE:CE2	1:D:78:ARG:HD2	2.37	0.58
1:A:138:LEU:N	1:A:138:LEU:HD23	2.18	0.58
1:C:36:CYS:HB2	1:C:91:TYR:HB2	1.86	0.57
1:A:144:GLU:O	1:A:145:ALA:HB3	2.05	0.57
1:D:37:CYS:SG	1:D:38:GLU:N	2.78	0.57
1:C:5:ILE:HD11	1:C:163:LYS:HD3	1.87	0.56
1:D:35:LEU:HD21	1:D:90:TRP:CD1	2.40	0.56
1:D:37:CYS:SG	1:D:70:PHE:HE2	2.27	0.56
1:A:101:ALA:HA	1:A:138:LEU:HD21	1.88	0.56
1:A:5:ILE:HA	1:A:8:MET:HG3	1.87	0.56
1:A:101:ALA:HB1	1:A:138:LEU:CD2	2.32	0.56
1:B:42:LYS:HD2	1:B:42:LYS:O	2.06	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:74:PHE:O	1:D:78:ARG:HG3	2.06	0.55
1:B:189:LEU:CD1	1:B:193:LEU:HD11	2.37	0.54
1:B:5:ILE:HD11	1:B:163:LYS:HD3	1.88	0.54
1:C:89:THR:HG22	1:C:117:THR:HB	1.89	0.54
1:D:56:GLY:HA3	1:D:66:PRO:HD3	1.88	0.54
1:A:74:PHE:CE2	1:A:78:ARG:HD2	2.42	0.54
1:C:61:LYS:HD2	1:C:99:ARG:NH1	2.23	0.54
1:D:63:LYS:O	1:D:72:ARG:NH2	2.40	0.54
1:A:61:LYS:HE2	1:A:99:ARG:HH11	1.73	0.54
1:A:68:MET:HE1	1:A:103:SER:HB2	1.89	0.53
1:A:194:ARG:HD2	1:C:194:ARG:HH22	1.74	0.53
1:C:5:ILE:HG22	1:C:8:MET:SD	2.49	0.53
1:C:32:THR:HG23	1:C:57:LYS:HD3	1.91	0.53
1:B:68:MET:HE1	1:B:71:LEU:HD12	1.89	0.53
1:C:61:LYS:HD2	1:C:99:ARG:HH12	1.74	0.53
1:C:168:ARG:C	1:C:170:LYS:H	2.12	0.52
1:D:165:VAL:O	1:D:167:GLY:N	2.41	0.52
1:A:37:CYS:SG	1:A:38:GLU:N	2.83	0.52
1:C:9:VAL:O	1:C:11:PRO:HD3	2.09	0.52
1:B:6:ARG:NH2	1:B:166:ASP:OD1	2.42	0.52
1:D:119:PHE:HB3	1:D:152:MET:HG3	1.92	0.52
1:D:61:LYS:HG3	1:D:63:LYS:H	1.75	0.52
1:A:5:ILE:HD11	1:A:163:LYS:HD3	1.91	0.52
1:A:10:GLU:N	1:A:10:GLU:OE1	2.43	0.52
1:B:189:LEU:CD1	1:B:193:LEU:HD12	2.41	0.51
1:D:79:GLN:HE21	1:D:80:LEU:HD13	1.74	0.51
1:B:135:LEU:O	1:B:193:LEU:HD21	2.11	0.51
1:D:96:PRO:HG2	1:D:138:LEU:HD11	1.92	0.51
1:A:165:VAL:O	1:A:167:GLY:N	2.44	0.50
1:C:177:ASN:OD1	1:C:180:LYS:HD2	2.11	0.50
1:D:42:LYS:O	1:D:42:LYS:HD2	2.12	0.50
1:B:187:ALA:HA	1:D:191:GLU:HG3	1.94	0.50
1:A:119:PHE:HB3	1:A:152:MET:HG3	1.93	0.49
1:A:180:LYS:HE3	1:C:127:TRP:CE2	2.47	0.49
1:B:61:LYS:HG3	1:B:63:LYS:H	1.77	0.49
1:A:175:TRP:CE2	1:A:178:LEU:HD12	2.47	0.49
1:A:56:GLY:CA	1:A:66:PRO:HD3	2.41	0.49
1:C:35:LEU:HD21	1:C:90:TRP:CD1	2.48	0.49
1:B:53:ILE:HD11	1:B:164:PHE:HB3	1.94	0.48
1:B:89:THR:HG22	1:B:117:THR:HB	1.94	0.48
1:D:61:LYS:HD2	1:D:62:ALA:H	1.77	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:ILE:HG13	1:D:186:GLN:HA	1.95	0.48
1:D:9:VAL:HG12	1:D:51:ALA:O	2.13	0.48
1:C:171:PRO:CD	1:C:173:LYS:HZ1	2.23	0.48
1:C:42:LYS:O	1:C:43:ASP:HB2	2.14	0.48
1:A:53:ILE:HD11	1:A:164:PHE:HB3	1.94	0.47
1:D:53:ILE:HD11	1:D:164:PHE:HB3	1.96	0.47
1:A:57:LYS:N	1:A:57:LYS:HD2	2.28	0.47
1:C:43:ASP:CA	1:C:44:PRO:CD	2.92	0.47
1:A:187:ALA:HA	1:C:191:GLU:HG3	1.96	0.47
1:B:61:LYS:HD2	1:B:62:ALA:H	1.80	0.47
1:B:176:ASN:O	1:B:177:ASN:HB2	2.14	0.47
1:C:175:TRP:CE2	1:C:178:LEU:HD12	2.49	0.47
1:A:91:TYR:HD2	1:A:160:CYS:SG	2.38	0.46
1:C:172:PHE:CD1	1:C:173:LYS:N	2.82	0.46
1:B:5:ILE:HD11	1:B:163:LYS:HB3	1.97	0.46
1:A:20:ASN:O	1:A:93:SER:HB2	2.15	0.46
1:B:151:ILE:HG13	1:B:186:GLN:HA	1.98	0.46
1:C:71:LEU:HA	1:C:71:LEU:HD23	1.75	0.46
1:D:120:VAL:HG12	1:D:122:ARG:O	2.16	0.46
1:C:80:LEU:HD23	1:C:80:LEU:HA	1.67	0.46
1:C:151:ILE:HG13	1:C:186:GLN:HA	1.96	0.46
1:D:111:ASP:OD1	1:D:114:VAL:HG23	2.16	0.46
1:B:9:VAL:HG12	1:B:52:LYS:HA	1.96	0.46
1:D:52:LYS:HG2	1:D:53:ILE:H	1.81	0.46
1:D:175:TRP:CE2	1:D:178:LEU:HD12	2.51	0.46
1:A:91:TYR:CD2	1:A:160:CYS:HB2	2.50	0.45
1:C:60:PRO:HA	1:C:61:LYS:C	2.37	0.45
1:D:79:GLN:OE1	1:D:79:GLN:N	2.37	0.45
1:B:127:TRP:CE2	1:D:180:LYS:HE3	2.52	0.45
1:B:175:TRP:CE2	1:B:178:LEU:HD12	2.52	0.45
1:C:68:MET:HE1	1:C:71:LEU:HD12	1.99	0.44
1:B:38:GLU:OE2	1:B:40:LYS:HE3	2.16	0.44
1:C:176:ASN:O	1:C:177:ASN:HB2	2.16	0.44
1:D:33:VAL:O	1:D:66:PRO:HG3	2.17	0.44
1:A:57:LYS:HD2	1:A:57:LYS:H	1.81	0.44
1:B:95:SER:HB3	1:B:124:TYR:H	1.82	0.44
1:A:67:GLU:HG3	1:A:100:CYS:HB3	1.99	0.44
1:C:14:PRO:HD3	1:C:166:ASP:HB2	1.99	0.44
1:C:43:ASP:C	1:C:44:PRO:HD3	2.33	0.44
1:C:33:VAL:O	1:C:66:PRO:HG3	2.17	0.44
1:A:127:TRP:CZ2	1:C:180:LYS:HE2	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:177:ASN:OD1	1:B:180:LYS:HD2	2.18	0.44
1:C:95:SER:HB3	1:C:124:TYR:H	1.83	0.44
1:D:5:ILE:HA	1:D:8:MET:HE3	1.99	0.43
1:C:164:PHE:CD1	1:C:164:PHE:N	2.86	0.43
1:B:187:ALA:CB	1:D:188:THR:HA	2.48	0.43
1:A:37:CYS:SG	1:A:70:PHE:HE2	2.39	0.43
1:B:30:LEU:HD13	1:B:122:ARG:NH2	2.33	0.43
1:A:52:LYS:HG2	1:A:53:ILE:H	1.84	0.43
1:A:144:GLU:C	1:A:146:GLY:N	2.71	0.43
1:A:74:PHE:CD2	1:A:78:ARG:HD2	2.53	0.43
1:C:179:PRO:HA	1:C:182:TYR:HB3	2.00	0.43
1:D:5:ILE:HD11	1:D:48:PRO:HG3	2.00	0.43
1:D:20:ASN:O	1:D:93:SER:HB2	2.19	0.42
1:B:6:ARG:NH2	1:B:166:ASP:HA	2.34	0.42
1:A:52:LYS:HG2	1:A:53:ILE:N	2.34	0.42
1:B:80:LEU:HD23	1:B:80:LEU:HA	1.73	0.42
1:A:61:LYS:HD2	1:A:62:ALA:H	1.83	0.42
1:B:33:VAL:O	1:B:66:PRO:HG3	2.19	0.42
1:A:94:TRP:CZ3	1:A:122:ARG:HD2	2.55	0.42
1:A:188:THR:HA	1:C:187:ALA:CB	2.50	0.42
1:B:71:LEU:HD23	1:B:71:LEU:HA	1.75	0.42
1:B:35:LEU:HD21	1:B:90:TRP:CD1	2.54	0.42
1:D:56:GLY:CA	1:D:66:PRO:HD3	2.47	0.42
1:A:71:LEU:HD23	1:A:71:LEU:HA	1.82	0.42
1:B:168:ARG:HA	1:B:168:ARG:HD3	1.64	0.42
1:A:137:ILE:O	1:A:144:GLU:HB2	2.18	0.42
1:B:25:PRO:HD3	1:B:181:HIS:ND1	2.35	0.42
1:A:128:LYS:HB3	1:A:128:LYS:HE2	1.86	0.42
1:A:128:LYS:HA	1:A:129:PRO:HD3	1.87	0.41
1:D:134:ALA:HA	1:D:137:ILE:HD12	2.02	0.41
1:B:13:ASP:OD1	1:B:14:PRO:HD2	2.20	0.41
1:D:38:GLU:OE2	1:D:40:LYS:HE3	2.20	0.41
1:D:125:TYR:HD2	1:D:131:TYR:CE2	2.39	0.41
1:A:68:MET:HE1	1:A:103:SER:CB	2.50	0.41
1:C:25:PRO:HD3	1:C:181:HIS:ND1	2.35	0.41
1:C:165:VAL:HG12	1:C:166:ASP:N	2.35	0.41
1:D:91:TYR:CD2	1:D:160:CYS:HB2	2.56	0.41
1:D:52:LYS:HG2	1:D:53:ILE:N	2.35	0.41
1:A:119:PHE:CE1	1:A:156:GLU:HG2	2.56	0.41
1:A:138:LEU:HD23	1:A:138:LEU:H	1.86	0.41
1:B:56:GLY:CA	1:B:66:PRO:HD3	2.46	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:97:CYS:SG	1:D:98:THR:N	2.94	0.41
1:A:33:VAL:O	1:A:66:PRO:HG3	2.20	0.41
1:B:24:ARG:HH11	1:B:24:ARG:CG	2.33	0.40
1:A:137:ILE:C	1:A:143:ALA:N	2.73	0.40
1:D:119:PHE:CE1	1:D:156:GLU:HG2	2.56	0.40
1:A:5:ILE:HD13	1:A:5:ILE:HG21	1.88	0.40
1:B:74:PHE:CE2	1:B:78:ARG:HD2	2.57	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	186/196 (95%)	176 (95%)	8 (4%)	2 (1%)	14	41
1	B	186/196 (95%)	176 (95%)	8 (4%)	2 (1%)	14	41
1	C	186/196 (95%)	175 (94%)	9 (5%)	2 (1%)	14	41
1	D	189/196 (96%)	183 (97%)	5 (3%)	1 (0%)	29	60
All	All	747/784 (95%)	710 (95%)	30 (4%)	7 (1%)	17	46

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	44	PRO
1	B	45	SER
1	D	167	GLY
1	A	29	GLY
1	A	167	GLY
1	B	47	PRO
1	C	169	GLY

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	170/175 (97%)	168 (99%)	2 (1%)	71	90
1	B	170/175 (97%)	166 (98%)	4 (2%)	49	78
1	C	170/175 (97%)	163 (96%)	7 (4%)	30	63
1	D	173/175 (99%)	170 (98%)	3 (2%)	60	84
All	All	683/700 (98%)	667 (98%)	16 (2%)	50	79

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	97	CYS
1	A	138	LEU
1	B	33	VAL
1	B	128	LYS
1	B	194	ARG
1	B	195	HIS
1	C	6	ARG
1	C	32	THR
1	C	33	VAL
1	C	82	HIS
1	C	97	CYS
1	C	166	ASP
1	C	176	ASN
1	D	28	SER
1	D	97	CYS
1	D	186	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 4 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

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	188/196 (95%)	0.69	8 (4%)	35	32	50, 94, 126, 141	0
1	B	188/196 (95%)	0.74	8 (4%)	35	32	52, 85, 123, 148	0
1	C	188/196 (95%)	0.74	7 (3%)	41	38	51, 84, 126, 150	0
1	D	191/196 (97%)	0.69	8 (4%)	36	33	48, 93, 130, 170	0
All	All	755/784 (96%)	0.71	31 (4%)	37	34	48, 88, 127, 170	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	44	PRO	4.5
1	C	5	ILE	4.5
1	D	1	MET	4.5
1	B	15	ARG	3.7
1	C	45	SER	3.3
1	D	86	TYR	3.1
1	C	173	LYS	3.1
1	D	33	VAL	2.7
1	A	86	TYR	2.5
1	A	80	LEU	2.5
1	B	33	VAL	2.5
1	C	138	LEU	2.5
1	A	138	LEU	2.5
1	A	5	ILE	2.5
1	C	53	ILE	2.4
1	A	44	PRO	2.4
1	D	58	VAL	2.4
1	B	39	VAL	2.4
1	B	70	PHE	2.3
1	D	92	VAL	2.2
1	D	71	LEU	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	12	MET	2.1
1	B	189	LEU	2.1
1	A	185	LEU	2.1
1	B	73	TRP	2.1
1	C	184	LEU	2.1
1	A	114	VAL	2.0
1	B	9	VAL	2.0
1	D	18	VAL	2.0
1	A	121	ALA	2.0
1	B	6	ARG	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ZN	A	401	1/1	0.95	0.31	92,92,92,92	0
2	ZN	D	401	1/1	0.96	0.28	92,92,92,92	0
2	ZN	C	401	1/1	0.98	0.32	73,73,73,73	0
2	ZN	B	401	1/1	0.99	0.31	78,78,78,78	0

6.5 Other polymers (i)

There are no such residues in this entry.