



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 5, 2023 – 12:07 PM JST

PDB ID : 7XYQ
Title : Crystal structure of PD-L1 and the computationally designed DBL1_03 protein binder
Authors : Liu, K.; Xu, Z.; Han, P.; Pacesa, M.; Gao, G.F.; Chai, Y.; Tan, S.
Deposited on : 2022-06-02
Resolution : 2.85 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.32.2
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) : 2.32.2

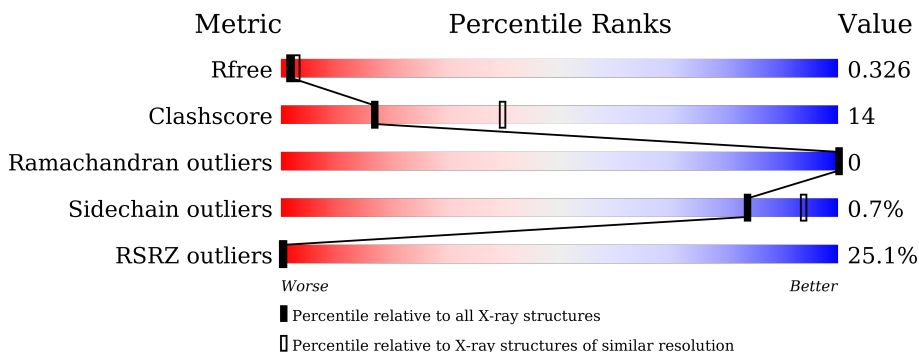
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 $\leq 5\%$. 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	207	
2	B	124	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 2620 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.

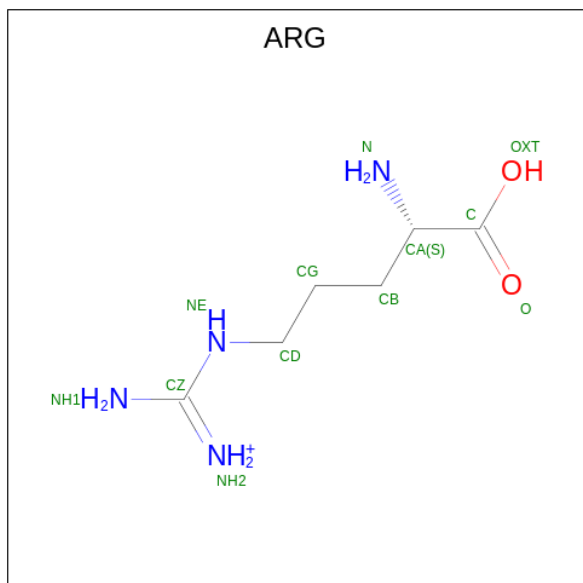
- Molecule 1 is a protein called CD274 molecule.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	203	1633	1033	276	317	7	0	0	0

- Molecule 2 is a protein called DBL1_03.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	124	974	613	159	193	9	0	0	0

- Molecule 3 is ARGinine (three-letter code: ARG) (formula: C₆H₁₅N₄O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	12	6	4	2	0	0

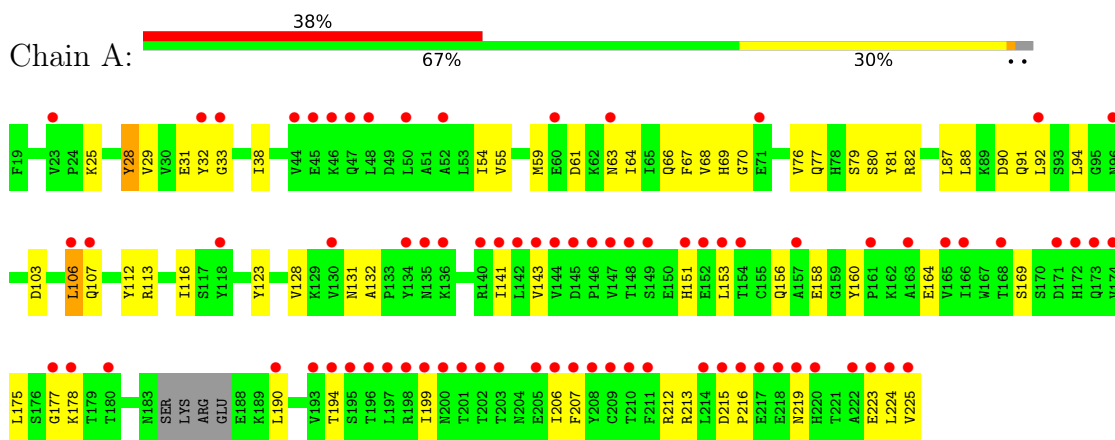
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total O 1 1	0	0

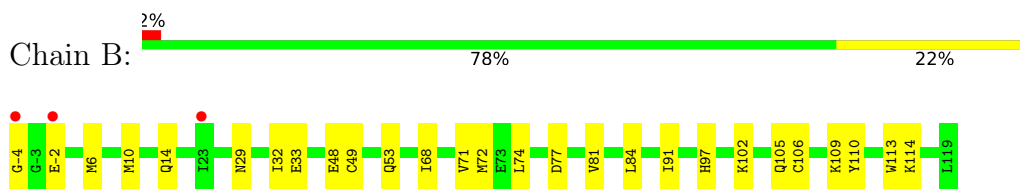
3 Residue-property plots [i](#)

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: CD274 molecule



- Molecule 2: DBL1_03



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	97.93Å 97.93Å 106.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.97 – 2.85 48.96 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.97-2.85) 99.9 (48.96-2.85)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 2.86Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.300 , 0.318 0.296 , 0.326	Depositor DCC
R_{free} test set	630 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	98.5	Xtrriage
Anisotropy	0.219	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 88.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	2620	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% 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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.49	0/1662	0.72	0/2255
2	B	0.49	0/985	0.71	0/1321
All	All	0.49	0/2647	0.72	0/3576

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 [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	1633	0	1617	54	0
2	B	974	0	987	24	0
3	A	12	0	12	2	0
4	B	1	0	0	0	0
All	All	2620	0	2616	74	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 (74) 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:113:ARG:HD2	1:A:123:TYR:HD2	1.28	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ILE:HG23	1:A:68:VAL:HG22	1.66	0.77
1:A:54:ILE:HG12	1:A:68:VAL:HG13	1.67	0.75
1:A:113:ARG:HD2	1:A:123:TYR:CD2	2.19	0.75
2:B:6:MET:HE2	2:B:71:VAL:HG13	1.72	0.71
1:A:59:MET:HG3	1:A:112:TYR:CE1	2.26	0.70
1:A:59:MET:HB2	1:A:64:ILE:HD11	1.76	0.67
2:B:48:GLU:OE1	2:B:97:HIS:ND1	2.26	0.66
1:A:177:GLY:O	3:A:301:ARG:NH1	2.29	0.65
2:B:106:CYS:O	2:B:109:LYS:HG2	1.97	0.64
1:A:25:LYS:HB2	1:A:28:TYR:CE1	2.34	0.64
1:A:28:TYR:CD2	1:A:38:ILE:HG22	2.33	0.63
2:B:77:ASP:O	2:B:81:VAL:HG23	2.00	0.61
1:A:215:ASP:HB2	1:A:216:PRO:HD3	1.82	0.61
2:B:109:LYS:HE3	2:B:110:TYR:HE1	1.66	0.60
1:A:206:ILE:HG12	1:A:225:VAL:HG22	1.83	0.59
1:A:77:GLN:NE2	1:A:81:TYR:O	2.37	0.58
1:A:141:ILE:HG12	1:A:153:LEU:HG	1.86	0.57
1:A:61:ASP:HA	2:B:-4:GLY:H2	1.69	0.57
1:A:67:PHE:HE1	1:A:70:GLY:C	2.09	0.56
2:B:77:ASP:OD1	2:B:77:ASP:N	2.38	0.55
1:A:141:ILE:HD11	1:A:224:LEU:HB3	1.90	0.54
1:A:131:ASN:OD1	1:A:213:ARG:NH1	2.37	0.54
1:A:68:VAL:HG12	1:A:69:HIS:CD2	2.45	0.52
1:A:29:VAL:CG1	1:A:131:ASN:HB2	2.41	0.51
1:A:90:ASP:OD1	1:A:91:GLN:N	2.44	0.51
1:A:80:SER:HB2	1:A:107:GLN:HE22	1.76	0.51
1:A:79:SER:HA	1:A:82:ARG:HB2	1.94	0.50
1:A:156:GLN:HG3	1:A:194:THR:OG1	2.11	0.49
1:A:29:VAL:HG13	1:A:131:ASN:HB2	1.95	0.48
2:B:6:MET:HG2	2:B:74:LEU:HD12	1.96	0.48
1:A:90:ASP:OD1	1:A:91:GLN:HG3	2.14	0.48
1:A:132:ALA:HB3	1:A:160:TYR:H	1.77	0.48
1:A:178:LYS:HA	3:A:301:ARG:HD3	1.96	0.48
1:A:55:VAL:HG22	1:A:116:ILE:HD12	1.96	0.47
2:B:72:MET:CE	2:B:113:TRP:HE1	2.27	0.47
1:A:63:ASN:HD22	2:B:-2:GLU:HB3	1.80	0.47
1:A:158:GLU:OE2	1:A:190:LEU:HD23	2.15	0.47
1:A:212:ARG:NE	1:A:219:ASN:OD1	2.44	0.47
2:B:84:LEU:HA	2:B:110:TYR:CE2	2.50	0.47
1:A:141:ILE:CG1	1:A:224:LEU:HD23	2.44	0.47
1:A:63:ASN:HB2	2:B:-2:GLU:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:MET:HA	2:B:72:MET:HE2	1.97	0.47
1:A:77:GLN:HE21	1:A:81:TYR:C	2.17	0.46
1:A:28:TYR:HB2	1:A:128:VAL:HG22	1.97	0.46
1:A:32:TYR:CE2	1:A:190:LEU:HD22	2.50	0.46
1:A:106:LEU:H	1:A:106:LEU:HG	1.53	0.46
1:A:66:GLN:OE1	1:A:76:VAL:HG21	2.16	0.45
2:B:102:LYS:O	2:B:105:GLN:HB3	2.16	0.45
2:B:91:ILE:HD11	2:B:106:CYS:HB2	1.97	0.45
1:A:143:VAL:HG22	1:A:151:HIS:CD2	2.52	0.45
2:B:72:MET:HE1	2:B:113:TRP:NE1	2.32	0.44
1:A:164:GLU:HG3	1:A:212:ARG:HB3	2.00	0.44
2:B:29:ASN:O	2:B:33:GLU:N	2.47	0.44
2:B:109:LYS:HG3	2:B:110:TYR:HD1	1.82	0.44
1:A:67:PHE:HE2	1:A:92:LEU:CD1	2.31	0.44
1:A:206:ILE:HG23	1:A:223:GLU:HG3	2.00	0.44
2:B:49:CYS:O	2:B:53:GLN:HG2	2.17	0.44
2:B:10:MET:O	2:B:14:GLN:HG3	2.18	0.43
1:A:33:GLY:O	1:A:103:ASP:HA	2.18	0.43
2:B:109:LYS:HG3	2:B:110:TYR:CD1	2.54	0.43
1:A:87:LEU:HD21	1:A:92:LEU:HD21	1.99	0.43
1:A:28:TYR:CE2	1:A:38:ILE:HA	2.54	0.43
1:A:199:ILE:HD13	1:A:207:PHE:CZ	2.53	0.43
1:A:199:ILE:HD13	1:A:207:PHE:CE1	2.54	0.42
1:A:94:LEU:HD23	1:A:94:LEU:HA	1.85	0.42
1:A:88:LEU:HD23	1:A:88:LEU:HA	1.85	0.42
1:A:158:GLU:CD	1:A:190:LEU:HD23	2.40	0.41
1:A:31:GLU:HA	1:A:131:ASN:O	2.21	0.41
1:A:63:ASN:HD22	2:B:-2:GLU:CB	2.33	0.41
2:B:32:ILE:HG22	2:B:114:LYS:HB2	2.03	0.41
1:A:169:SER:HB3	1:A:175:LEU:HD11	2.04	0.40
2:B:68:ILE:HD12	2:B:68:ILE:HA	1.96	0.40
1:A:67:PHE:HE1	1:A:70:GLY:CA	2.34	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	199/207 (96%)	183 (92%)	16 (8%)	0	100	100
2	B	122/124 (98%)	118 (97%)	4 (3%)	0	100	100
All	All	321/331 (97%)	301 (94%)	20 (6%)	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	184/188 (98%)	182 (99%)	2 (1%)	73	90
2	B	114/114 (100%)	114 (100%)	0	100	100
All	All	298/302 (99%)	296 (99%)	2 (1%)	84	94

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	TYR
1	A	106	LEU

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

Mol	Chain	Res	Type
1	A	77	GLN
1	A	220	HIS
2	B	55	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ARG	A	301	-	10,11,11	0.78	1 (10%)	11,13,13	1.33	2 (18%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ARG	A	301	-	-	2/11/11/11	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	301	ARG	OXT-C	-2.13	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	301	ARG	OXT-C-CA	2.86	123.13	113.38
3	A	301	ARG	OXT-C-O	-2.78	117.78	124.09

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	301	ARG	OXT-C-CA-N
3	A	301	ARG	O-C-CA-N

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	ARG	2	0

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	203/207 (98%)	2.21	79 (38%) 0 0	79, 128, 220, 305	0
2	B	124/124 (100%)	0.38	3 (2%) 59 56	63, 95, 130, 169	0
All	All	327/331 (98%)	1.52	82 (25%) 0 0	63, 115, 206, 305	0

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	149	SER	10.6
1	A	197	LEU	9.6
1	A	148	THR	9.3
1	A	146	PRO	8.7
1	A	202	THR	8.0
1	A	147	VAL	8.0
1	A	199	ILE	7.7
1	A	173	GLN	7.1
1	A	144	VAL	7.0
1	A	214	LEU	6.3
1	A	152	GLU	6.2
1	A	208	TYR	6.1
1	A	134	TYR	5.9
1	A	198	ARG	5.8
1	A	210	THR	5.8
1	A	168	THR	5.7
1	A	141	ILE	5.4
1	A	193	VAL	5.4
1	A	201	THR	5.3
1	A	151	HIS	5.2
1	A	224	LEU	5.1
1	A	154	THR	5.1
1	A	166	ILE	4.9
1	A	47	GLN	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	130	VAL	4.7
1	A	142	LEU	4.7
1	A	195	SER	4.7
1	A	46	LYS	4.7
1	A	140	ARG	4.5
1	A	200	ASN	4.4
1	A	48	LEU	4.3
1	A	220	HIS	4.2
1	A	153	LEU	4.1
1	A	172	HIS	4.1
1	A	207	PHE	4.1
1	A	157	ALA	3.9
1	A	118	TYR	3.8
1	A	196	THR	3.8
1	A	222	ALA	3.8
2	B	-2	GLU	3.7
1	A	143	VAL	3.7
1	A	211	PHE	3.6
1	A	190	LEU	3.5
1	A	225	VAL	3.5
1	A	165	VAL	3.3
1	A	203	THR	3.2
1	A	145	ASP	3.1
1	A	217	GLU	3.1
2	B	-4	GLY	3.1
1	A	33	GLY	3.1
1	A	218	GLU	3.1
1	A	180	THR	2.9
1	A	44	VAL	2.9
1	A	161	PRO	2.9
1	A	163	ALA	2.8
1	A	206	ILE	2.8
1	A	92	LEU	2.6
1	A	194	THR	2.6
1	A	107	GLN	2.6
1	A	63	ASN	2.6
1	A	60	GLU	2.4
1	A	45	GLU	2.4
1	A	209	CYS	2.4
1	A	216	PRO	2.4
1	A	136	LYS	2.4
1	A	96	ASN	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	223	GLU	2.3
1	A	174	VAL	2.3
1	A	171	ASP	2.2
1	A	135	ASN	2.2
1	A	219	ASN	2.2
1	A	177	GLY	2.2
1	A	71	GLU	2.2
1	A	106	LEU	2.1
1	A	215	ASP	2.1
2	B	23	ILE	2.1
1	A	50	LEU	2.1
1	A	178	LYS	2.1
1	A	32	TYR	2.1
1	A	52	ALA	2.0
1	A	205	GLU	2.0
1	A	23	VAL	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
3	ARG	A	301	12/12	0.80	0.20	121,130,142,143	0

6.5 Other polymers [i](#)

There are no such residues in this entry.