



wwPDB X-ray Structure Validation Summary Report ⓘ

May 26, 2020 – 01:23 am BST

PDB ID : 5O4Y
Title : Structure of human PD-L1 in complex with inhibitor
Authors : Magiera, K.; Grudnik, P.; Dubin, G.; Holak, T.A.
Deposited on : 2017-05-31
Resolution : 2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

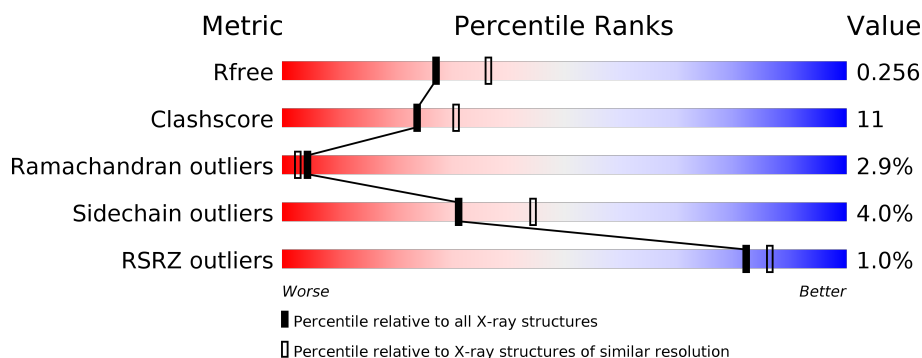
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 $\leq 5\%$. 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	B	118	<div> <div>88%</div> <div>12%</div> </div>
1	C	118	<div> <div>82%</div> <div>17%</div> <div>•</div> </div>
1	E	118	<div> <div>85%</div> <div>14%</div> <div>•</div> </div>
2	A	16	<div> <div>6%</div> <div>19%</div> <div>31%</div> <div>19%</div> <div>31%</div> </div>
2	D	16	<div> <div>38%</div> <div>38%</div> <div>19%</div> <div>6%</div> </div>
2	F	16	<div> <div>6%</div> <div>19%</div> <div>38%</div> <div>31%</div> <div>13%</div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 6160 atoms, of which 2950 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 Programmed cell death 1 ligand 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	B	118	Total	C	H	N	O	S	0	0	0
			1778	580	872	150	171	5			
1	C	118	Total	C	H	N	O	S	0	0	0
			1722	570	831	148	168	5			
1	E	118	Total	C	H	N	O	S	1	1	0
			1787	582	878	150	172	5			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	133	ALA	-	expression tag	UNP Q9NZQ7
B	134	TYR	-	expression tag	UNP Q9NZQ7
B	135	ALA	-	expression tag	UNP Q9NZQ7
C	133	ALA	-	expression tag	UNP Q9NZQ7
C	134	TYR	-	expression tag	UNP Q9NZQ7
C	135	ALA	-	expression tag	UNP Q9NZQ7
E	133	ALA	-	expression tag	UNP Q9NZQ7
E	134	TYR	-	expression tag	UNP Q9NZQ7
E	135	ALA	-	expression tag	UNP Q9NZQ7

- Molecule 2 is a protein called PHE-MAA-ASN-PRO-HIS-LEU-SER-TRP-SER-TRP-9KK-9 KK-ARG-CCS-GLY-NH2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	A	16	Total	C	H	N	O	S	0	0	1
			256	89	123	24	19	1			
2	D	16	Total	C	H	N	O	S	0	0	1
			256	89	123	24	19	1			
2	F	16	Total	C	H	N	O	S	0	0	1
			256	89	123	24	19	1			

- Molecule 3 is water.

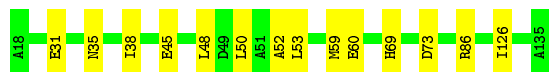
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	39	Total 39	O 39	0	0
3	C	25	Total 25	O 25	0	0
3	E	35	Total 35	O 35	0	0
3	A	3	Total 3	O 3	0	0
3	D	2	Total 2	O 2	0	0
3	F	1	Total 1	O 1	0	0

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: Programmed cell death 1 ligand 1

Chain B: 




- Molecule 1: Programmed cell death 1 ligand 1

Chain C: 



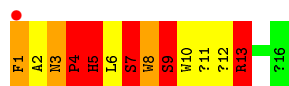
- Molecule 1: Programmed cell death 1 ligand 1

Chain E: 



- Molecule 2: PHE-MAA-ASN-PRO-HIS-LEU-SER-TRP-SER-TRP-9KK-9KK-ARG-CCS-GLY-NH2

Chain A: 




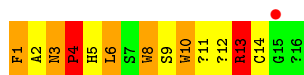
- Molecule 2: PHE-MAA-ASN-PRO-HIS-LEU-SER-TRP-SER-TRP-9KK-9KK-ARG-CCS-GLY-NH2

Chain D: 



- Molecule 2: PHE-MAA-ASN-PRO-HIS-LEU-SER-TRP-SER-TRP-9KK-9KK-ARG-CCS-GLY-NH2

Chain F: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.55Å 80.95Å 54.23Å 90.00° 104.49° 90.00°	Depositor
Resolution (Å)	29.78 – 2.30 29.78 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.9 (29.78-2.30) 98.1 (29.78-2.30)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.02 (at 2.31Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.198 , 0.262 0.199 , 0.256	Depositor DCC
R_{free} test set	941 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.708	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 47.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6160	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.71% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 9KK, MAA, CCS, NH2

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	B	0.61	0/922	0.75	0/1249
1	C	0.65	1/907 (0.1%)	0.74	0/1231
1	E	0.61	0/933	0.67	0/1267
2	A	2.53	3/102 (2.9%)	3.13	15/134 (11.2%)
2	D	2.57	3/102 (2.9%)	3.08	11/134 (8.2%)
2	F	2.23	2/102 (2.0%)	2.59	8/134 (6.0%)
All	All	0.97	9/3068 (0.3%)	1.14	34/4149 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	A	0	1

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	13	ARG	CZ-NH1	-10.13	1.19	1.33
2	D	13	ARG	CZ-NH1	-9.97	1.20	1.33
2	D	8	TRP	NE1-CE2	-7.78	1.27	1.37
2	A	13	ARG	CZ-NH1	-7.08	1.23	1.33
2	A	9	SER	CA-CB	-6.75	1.42	1.52

The worst 5 of 34 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4	PRO	CA-C-N	12.24	144.13	117.20
2	D	5	HIS	N-CA-CB	11.94	132.09	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	4	PRO	CA-C-N	11.43	142.34	117.20
2	D	4	PRO	C-N-CA	10.85	148.82	121.70
2	F	13	ARG	NE-CZ-NH2	10.72	125.66	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	1	PHE	Peptide

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	B	906	872	870	10	0
1	C	891	831	834	16	0
1	E	909	878	864	13	2
2	A	133	123	96	18	1
2	D	133	123	95	2	0
2	F	133	123	98	11	3
3	A	3	0	0	0	0
3	B	39	0	0	7	0
3	C	25	0	0	4	0
3	D	2	0	0	0	0
3	E	35	0	0	4	0
3	F	1	0	0	0	0
All	All	3210	2950	2857	66	3

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 11.

The worst 5 of 66 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)
2:A:9:SER:OG	2:A:13:ARG:HB2	1.76	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:13:ARG:O	2:D:14:CCS:HD3	1.77	0.83
2:A:9:SER:HG	2:A:13:ARG:HB2	1.48	0.79
1:B:52:ALA:O	3:B:301:HOH:O	2.01	0.77
1:B:31:GLU:OE1	3:B:302:HOH:O	2.03	0.76

All (3) 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:E:134:TYR:HH	2:F:13:ARG:HH21[1_556]	1.34	0.26
1:E:134:TYR:OH	2:F:13:ARG:HH21[1_556]	1.40	0.20
2:A:12:9KK:O	2:F:13:ARG:HE[2_555]	1.57	0.03

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	B	116/118 (98%)	108 (93%)	8 (7%)	0	100	100
1	C	116/118 (98%)	107 (92%)	9 (8%)	0	100	100
1	E	117/118 (99%)	110 (94%)	6 (5%)	1 (1%)	17	20
2	A	10/16 (62%)	4 (40%)	1 (10%)	5 (50%)	0	0
2	D	10/16 (62%)	7 (70%)	1 (10%)	2 (20%)	0	0
2	F	10/16 (62%)	6 (60%)	1 (10%)	3 (30%)	0	0
All	All	379/402 (94%)	342 (90%)	26 (7%)	11 (3%)	4	3

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	133	ALA
2	A	7	SER

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Mol	Chain	Res	Type
2	A	9	SER
2	A	13	ARG
2	D	5	HIS

5.3.2 Protein sidechains ⓘ

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	B	90/101 (89%)	88 (98%)	2 (2%)	52	69
1	C	87/101 (86%)	87 (100%)	0	100	100
1	E	93/101 (92%)	92 (99%)	1 (1%)	73	86
2	A	10/10 (100%)	8 (80%)	2 (20%)	1	1
2	D	10/10 (100%)	7 (70%)	3 (30%)	0	0
2	F	10/10 (100%)	6 (60%)	4 (40%)	0	0
All	All	300/333 (90%)	288 (96%)	12 (4%)	31	44

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	D	3	ASN
2	D	6	LEU
2	F	4	PRO
2	A	9	SER
2	F	3	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	3	ASN
2	D	5	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

12 non-standard protein/DNA/RNA residues are 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$
2	CCS	F	14	2	7,8,10	1.21	1 (14%)	3,8,12	0.91	0
2	9KK	D	12	2	7,8,9	0.75	0	5,8,10	1.43	1 (20%)
2	9KK	F	12	2	7,8,9	1.05	0	5,8,10	1.76	2 (40%)
2	9KK	A	12	2	7,8,9	0.90	0	5,8,10	1.42	2 (40%)
2	MAA	F	2	2	4,5,6	1.43	1 (25%)	1,5,7	1.17	0
2	9KK	D	11	2	7,8,9	1.10	0	5,8,10	2.10	1 (20%)
2	MAA	D	2	2	4,5,6	1.29	0	1,5,7	0.58	0
2	9KK	F	11	2	7,8,9	1.23	2 (28%)	5,8,10	1.90	1 (20%)
2	9KK	A	11	2	7,8,9	0.72	0	5,8,10	1.14	0
2	MAA	A	2	2	4,5,6	1.07	0	1,5,7	2.38	1 (100%)
2	CCS	D	14	2	7,8,10	1.49	2 (28%)	3,8,12	1.77	1 (33%)
2	CCS	A	14	2	7,8,10	2.81	5 (71%)	4,8,12	1.78	1 (25%)

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
2	CCS	F	14	2	-	1/4/7/10	-
2	9KK	D	12	2	-	3/5/8/10	-
2	9KK	F	12	2	-	1/5/8/10	-
2	9KK	A	12	2	-	2/5/8/10	-
2	MAA	F	2	2	-	1/1/4/6	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	9KK	D	11	2	-	1/5/8/10	-
2	MAA	D	2	2	-	0/1/4/6	-
2	9KK	F	11	2	-	0/5/8/10	-
2	9KK	A	11	2	-	3/5/8/10	-
2	MAA	A	2	2	-	1/1/4/6	-
2	CCS	D	14	2	-	2/4/7/10	-
2	CCS	A	14	2	-	1/5/7/10	-

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	14	CCS	OZ2-CE	-5.22	1.15	1.42
2	A	14	CCS	CD-SG	-2.97	1.70	1.81
2	A	14	CCS	CB-SG	-2.68	1.70	1.80
2	A	14	CCS	CA-N	-2.66	1.40	1.48
2	F	14	CCS	CD-SG	-2.51	1.73	1.81

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	11	9KK	O-C-CA	-4.28	113.56	124.78
2	F	11	9KK	O-C-CA	-3.12	116.60	124.78
2	A	14	CCS	CB-SG-CD	3.10	111.57	102.27
2	F	12	9KK	O-C-CA	-2.79	117.48	124.78
2	F	12	9KK	CM-N-CA	2.59	121.69	113.64

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	14	CCS	CA-CB-SG-CD
2	D	12	9KK	C-CA-CB-CG
2	A	12	9KK	O-C-CA-CB
2	A	2	MAA	CB-CA-N-CM
2	D	14	CCS	CA-CB-SG-CD

There are no ring outliers.

8 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	14	CCS	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	12	9KK	1	0
2	A	12	9KK	1	1
2	F	2	MAA	1	0
2	F	11	9KK	1	0
2	A	11	9KK	2	0
2	A	2	MAA	2	0
2	D	14	CCS	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	B	118/118 (100%)	-0.44	0 100 100	26, 35, 49, 58	0
1	C	118/118 (100%)	0.06	1 (0%) 86 89	20, 46, 71, 86	0
1	E	118/118 (100%)	-0.04	1 (0%) 86 89	30, 43, 57, 70	0
2	A	11/16 (68%)	0.40	1 (9%) 9 12	41, 49, 56, 57	0
2	D	11/16 (68%)	-0.06	0 100 100	29, 37, 42, 53	0
2	F	11/16 (68%)	0.42	1 (9%) 9 12	41, 50, 62, 81	0
All	All	387/402 (96%)	-0.11	4 (1%) 82 86	20, 42, 62, 86	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	15	GLY	4.5
1	E	18	ALA	3.0
2	A	1	PHE	2.1
1	C	18	ALA	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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	9KK	A	11	9/10	0.90	0.21	42,52,60,62	0
2	MAA	A	2	6/7	0.92	0.15	36,53,66,66	0
2	MAA	F	2	6/7	0.93	0.14	39,48,59,59	0
2	9KK	F	11	9/10	0.93	0.17	43,57,82,82	0
2	CCS	F	14	9/11	0.93	0.13	42,62,74,79	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	9KK	A	12	9/10	0.93	0.18	40,53,66,66	0
2	9KK	F	12	9/10	0.94	0.12	39,51,72,72	0
2	9KK	D	12	9/10	0.94	0.13	34,44,52,55	0
2	9KK	D	11	9/10	0.95	0.15	25,33,45,45	0
2	CCS	D	14	9/11	0.95	0.13	34,45,54,57	0
2	CCS	A	14	9/11	0.96	0.11	33,48,56,60	0
2	MAA	D	2	6/7	0.97	0.10	30,37,42,42	0

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.