



wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 08:30 PM GMT

PDB ID : 1KJ2
Title : Murine Alloreactive ScFv TCR-Peptide-MHC Class I Molecule Complex
Authors : Reiser, J.-B.; Gregoire, C.; Darnault, C.; Mosser, T.; Guimezanes, A.; Schmitt-Verhulst, A.-M.; Fontecilla-Camps, J.C.; Mazza, G.; Malissen, B.; Housset, D.
Deposited on : 2001-12-04
Resolution : 2.71 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
<http://wwpdb.org/validation/2016/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 : 1.7 (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

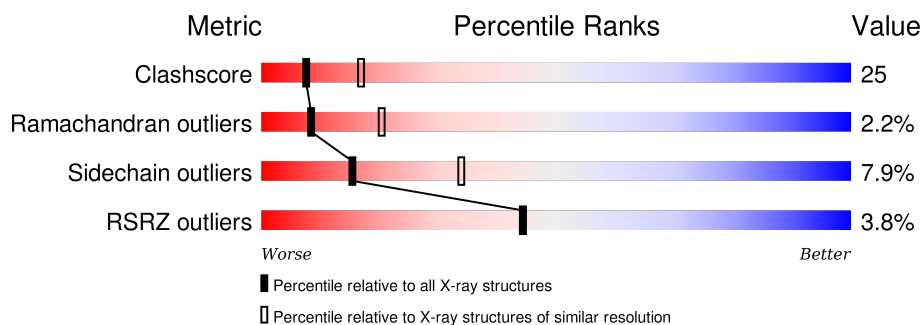
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.71 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))
Clashscore	102246	2771 (2.74-2.70)
Ramachandran outliers	100387	2726 (2.74-2.70)
Sidechain outliers	100360	2727 (2.74-2.70)
RSRZ outliers	91569	2443 (2.74-2.70)

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 $\leq 5\%$. 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	H	277	<div> <div>5%</div> <div>66%</div> <div>30%</div> <div>.</div> </div>
1	I	277	<div> <div>4%</div> <div>61%</div> <div>34%</div> <div>5%</div> </div>
2	P	8	<div> <div>50%</div> <div>38%</div> <div>13%</div> </div>
2	Q	8	<div> <div>25%</div> <div>63%</div> <div>13%</div> </div>
3	L	99	<div> <div>2%</div> <div>59%</div> <div>39%</div> <div>.</div> </div>
3	M	99	<div> <div>4%</div> <div>52%</div> <div>42%</div> <div>6%</div> </div>
4	A	111	<div> <div>2%</div> <div>53%</div> <div>40%</div> <div>7%</div> </div>

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Mol	Chain	Length	Quality of chain
4	D	111	
5	B	117	
5	E	117	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	MAN	A	203	X	-	-	-
6	GAL	A	206	-	-	-	X
6	MAN	A	208	X	-	-	-
7	NAG	E	401	X	-	-	-

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 10144 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 Allogeneic H-2Kb MHC Class I Molecule.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	H	276	Total	C	N	O	S	0	0	0
			2247	1418	395	425	9			
1	I	277	Total	C	N	O	S	0	0	0
			2254	1423	396	426	9			

- Molecule 2 is a protein called Naturally processed octapeptide PKB1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	P	8	Total	C	N	O	0	0	0
			67	46	9	12			
2	Q	8	Total	C	N	O	0	0	0
			67	46	9	12			

- Molecule 3 is a protein called Beta-2 microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			
3	M	99	Total	C	N	O	S	0	0	0
			821	524	138	152	7			

- Molecule 4 is a protein called KB5-C20 T-Cell receptor alpha-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	111	Total	C	N	O	S	0	0	0
			881	560	149	170	2			
4	D	111	Total	C	N	O	S	0	0	0
			881	560	149	170	2			

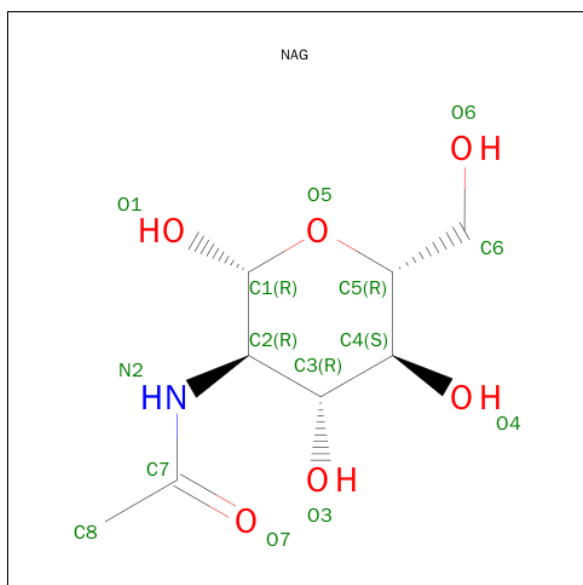
- Molecule 5 is a protein called KB5-C20 T-Cell receptor beta-chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	B	117	Total	C	N	O	S	0	0	0
			940	596	167	172	5			
5	E	117	Total	C	N	O	S	0	0	0
			940	596	167	172	5			

- Molecule 6 is a polymer of unknown type called SUGAR (8-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	8	Total	C	N	O	0	0
			106	59	4	43		

- Molecule 7 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	B	1	Total	C	N	O	0	0
			14	8	1	5		
7	E	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	5	Total	O	0	0
			5	5		
8	B	10	Total	O	0	0
			10	10		

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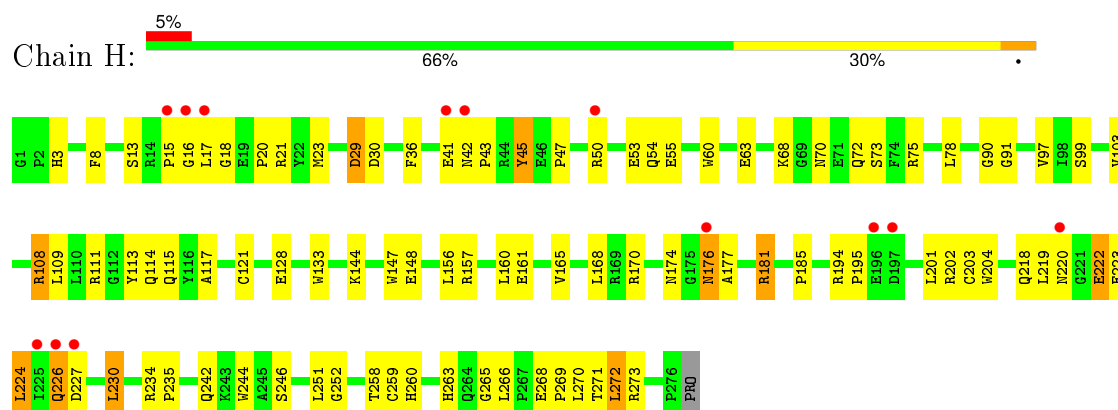
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	D	6	Total 6	O 6	0	0
8	E	7	Total 7	O 7	0	0
8	H	22	Total 22	O 22	0	0
8	I	18	Total 18	O 18	0	0
8	L	12	Total 12	O 12	0	0
8	M	6	Total 6	O 6	0	0
8	P	2	Total 2	O 2	0	0
8	Q	3	Total 3	O 3	0	0

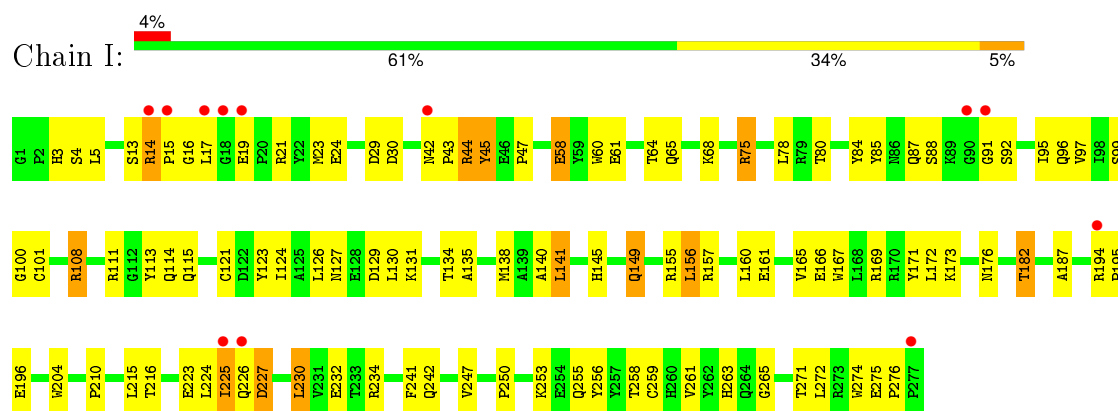
3 Residue-property plots

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: Allogeneic H-2Kb MHC Class I Molecule



• Molecule 1: Allogeneic H-2Kb MHC Class I Molecule



• Molecule 2: Naturally processed octapeptide PKB1

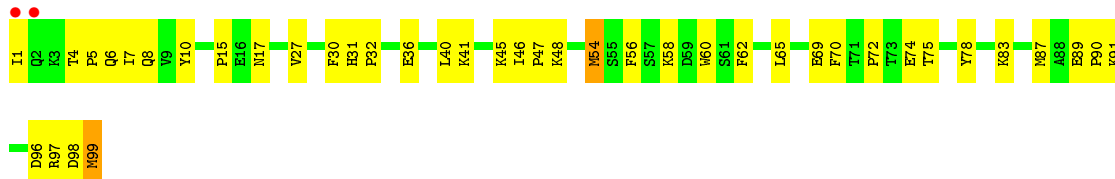


• Molecule 2: Naturally processed octapeptide PKB1

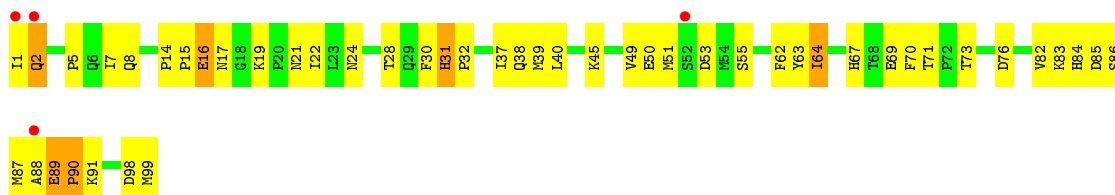




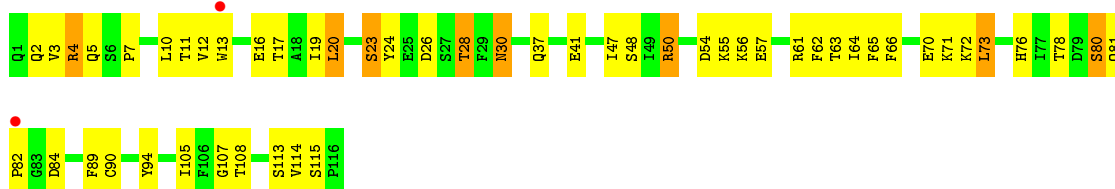
• Molecule 3: Beta-2 microglobulin



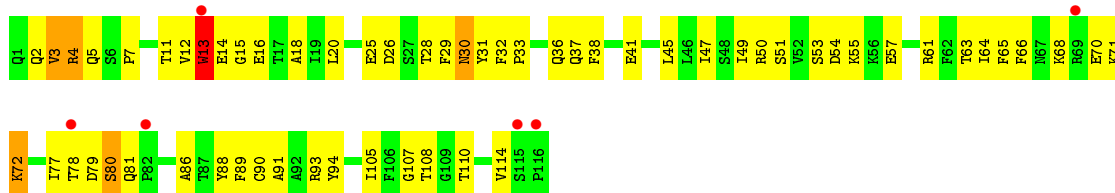
• Molecule 3: Beta-2 microglobulin



• Molecule 4: KB5-C20 T-Cell receptor alpha-chain



• Molecule 4: KB5-C20 T-Cell receptor alpha-chain

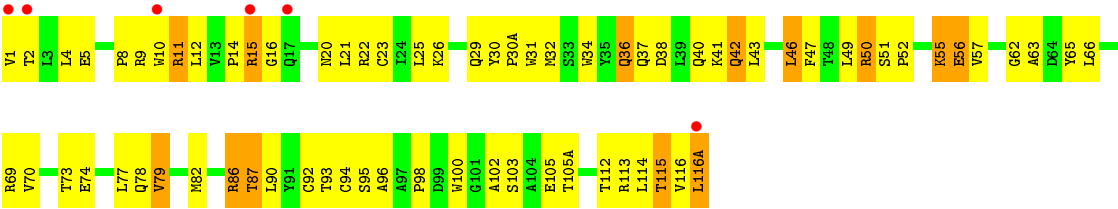


• Molecule 5: KB5-C20 T-Cell receptor beta-chain





• Molecule 5: KB5-C20 T-Cell receptor beta-chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.20Å 77.92Å 132.96Å 90.00° 108.23° 90.00°	Depositor
Resolution (Å)	12.00 – 2.71 14.99 – 2.71	Depositor EDS
% Data completeness (in resolution range)	(Not available) (12.00-2.71) 95.5 (14.99-2.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.19 (at 2.73Å)	Xtriage
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.220 , 0.278 0.230 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	42.4	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 54.1	EDS
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 45992 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10144	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 32.74 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 8.9477e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: SIA, GAL, NAG, MAN

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	H	0.45	0/2309	0.71	0/3137
1	I	0.45	0/2317	0.70	0/3149
2	P	0.68	0/67	0.81	0/88
2	Q	0.62	0/67	0.79	0/88
3	L	0.45	0/847	0.73	0/1148
3	M	0.41	0/847	0.71	1/1148 (0.1%)
4	A	0.43	0/904	0.66	0/1225
4	D	0.41	0/904	0.67	0/1225
5	B	0.43	0/962	0.80	0/1310
5	E	0.43	0/962	0.77	0/1310
All	All	0.44	0/10186	0.72	1/13828 (0.0%)

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
6	A	2	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	2	GLN	N-CA-C	-5.46	96.26	111.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	203	MAN	C1

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Mol	Chain	Res	Type	Atom
6	A	208	MAN	C1

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	H	2247	0	2136	81	0
1	I	2254	0	2143	99	0
2	P	67	0	77	3	0
2	Q	67	0	77	5	0
3	L	821	0	796	32	0
3	M	821	0	796	44	0
4	A	881	0	844	53	0
4	D	881	0	845	74	0
5	B	940	0	936	70	0
5	E	940	0	936	77	0
6	A	106	0	89	7	0
7	B	14	0	13	0	0
7	E	14	0	13	0	0
8	A	5	0	0	1	0
8	B	10	0	0	1	0
8	D	6	0	0	2	0
8	E	7	0	0	4	0
8	H	22	0	0	2	0
8	I	18	0	0	3	0
8	L	12	0	0	0	0
8	M	6	0	0	0	0
8	P	2	0	0	0	0
8	Q	3	0	0	0	0
All	All	10144	0	9701	502	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 25.

The worst 5 of 502 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:I:14:ARG:HB3	1:I:15:PRO:HD2	1.33	1.09
4:D:108:THR:HA	5:E:42:GLN:HE22	1.22	1.02
4:D:13:TRP:HB2	4:D:16:GLU:HG3	1.46	0.96
1:I:138:MET:HA	1:I:141:LEU:HD12	1.45	0.95
5:E:36:GLN:HB3	5:E:46:LEU:HD11	1.49	0.93

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	H	274/277 (99%)	247 (90%)	21 (8%)	6 (2%)	8	20
1	I	275/277 (99%)	248 (90%)	23 (8%)	4 (2%)	13	31
2	P	6/8 (75%)	4 (67%)	1 (17%)	1 (17%)	0	0
2	Q	6/8 (75%)	4 (67%)	1 (17%)	1 (17%)	0	0
3	L	97/99 (98%)	90 (93%)	5 (5%)	2 (2%)	9	21
3	M	97/99 (98%)	81 (84%)	10 (10%)	6 (6%)	2	2
4	A	109/111 (98%)	97 (89%)	11 (10%)	1 (1%)	21	47
4	D	109/111 (98%)	88 (81%)	19 (17%)	2 (2%)	11	25
5	B	115/117 (98%)	106 (92%)	7 (6%)	2 (2%)	11	27
5	E	115/117 (98%)	104 (90%)	10 (9%)	1 (1%)	21	47
All	All	1203/1224 (98%)	1069 (89%)	108 (9%)	26 (2%)	8	20

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	17	LEU
1	H	226	GLN
4	A	80	SER

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Mol	Chain	Res	Type
1	I	225	ILE
3	M	53	ASP

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	H	234/235 (100%)	224 (96%)	10 (4%)	35	65
1	I	235/235 (100%)	219 (93%)	16 (7%)	20	43
2	P	8/8 (100%)	8 (100%)	0	100	100
2	Q	8/8 (100%)	8 (100%)	0	100	100
3	L	94/94 (100%)	88 (94%)	6 (6%)	22	46
3	M	94/94 (100%)	89 (95%)	5 (5%)	28	56
4	A	96/96 (100%)	86 (90%)	10 (10%)	9	19
4	D	96/96 (100%)	90 (94%)	6 (6%)	22	47
5	B	102/102 (100%)	90 (88%)	12 (12%)	6	14
5	E	102/102 (100%)	83 (81%)	19 (19%)	2	4
All	All	1069/1070 (100%)	985 (92%)	84 (8%)	15	34

5 of 84 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	116(A)	LEU
1	I	149	GLN
5	E	70	VAL
1	I	44	ARG
1	I	65	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
5	B	29	GLN

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Mol	Chain	Res	Type
5	B	44	GLN
4	D	37	GLN
5	B	37	GLN
5	B	78	GLN

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 ⓘ

8 carbohydrates 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	$\# Z > 2$
6	NAG	A	201	4,6	14,14,15	0.62	0	15,19,21	0.84	1 (6%)
6	NAG	A	202	6	14,14,15	0.71	1 (7%)	15,19,21	0.77	0
6	MAN	A	203	6	11,11,12	0.61	0	14,15,17	1.78	2 (14%)
6	MAN	A	204	6	11,11,12	0.77	0	14,15,17	0.71	0
6	NAG	A	205	6	14,14,15	0.64	0	15,19,21	1.13	2 (13%)
6	GAL	A	206	6	11,11,12	0.67	0	14,15,17	0.45	0
6	SIA	A	207	6	16,20,21	0.57	0	18,28,31	0.71	0
6	MAN	A	208	6	11,11,12	0.61	0	14,15,17	1.59	2 (14%)

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
6	NAG	A	201	4,6	-	0/6/23/26	0/1/1/1
6	NAG	A	202	6	-	0/6/23/26	0/1/1/1
6	MAN	A	203	6	1/1/4/5	0/2/19/22	0/1/1/1
6	MAN	A	204	6	-	0/2/19/22	0/1/1/1
6	NAG	A	205	6	-	0/6/23/26	0/1/1/1
6	GAL	A	206	6	-	0/2/19/22	0/1/1/1
6	SIA	A	207	6	-	0/14/34/38	0/1/1/1
6	MAN	A	208	6	1/1/4/5	0/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	202	NAG	C1-C2	2.07	1.55	1.52

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	A	201	NAG	C2-N2-C7	-2.74	119.52	123.04
6	A	203	MAN	O3-C3-C2	-2.36	105.73	110.00
6	A	205	NAG	C2-N2-C7	-2.10	120.35	123.04
6	A	205	NAG	C4-C3-C2	2.92	115.76	111.23
6	A	208	MAN	C1-O5-C5	3.82	117.10	112.25

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
6	A	208	MAN	C1
6	A	203	MAN	C1

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	201	NAG	1	0
6	A	202	NAG	4	0
6	A	203	MAN	2	0
6	A	204	MAN	2	0
6	A	205	NAG	4	0

5.6 Ligand geometry

2 ligands 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	$\# Z > 2$
7	NAG	B	301	5	14,14,15	0.60	0	15,19,21	0.94	1 (6%)
7	NAG	E	401	5	14,14,15	1.19	1 (7%)	15,19,21	0.93	1 (6%)

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
7	NAG	B	301	5	-	0/6/23/26	0/1/1/1
7	NAG	E	401	5	1/1/5/7	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	E	401	NAG	C1-C2	3.94	1.57	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	301	NAG	C2-N2-C7	-2.81	119.42	123.04
7	E	401	NAG	C3-C4-C5	-2.32	106.15	110.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	E	401	NAG	C1

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 ⓘ

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	H	276/277 (99%)	-0.20	13 (4%) 35 34	13, 35, 78, 101	7 (2%)
1	I	277/277 (100%)	-0.09	12 (4%) 39 39	23, 40, 76, 102	10 (3%)
2	P	8/8 (100%)	-1.10	0 100 100	16, 19, 29, 31	0
2	Q	8/8 (100%)	-1.06	0 100 100	23, 29, 38, 42	0
3	L	99/99 (100%)	-0.26	2 (2%) 68 69	22, 36, 58, 88	2 (2%)
3	M	99/99 (100%)	0.28	4 (4%) 42 42	26, 55, 86, 98	3 (3%)
4	A	111/111 (100%)	-0.12	2 (1%) 71 72	17, 43, 71, 82	1 (0%)
4	D	111/111 (100%)	0.35	6 (5%) 29 28	23, 58, 89, 104	1 (0%)
5	B	117/117 (100%)	-0.11	1 (0%) 85 86	20, 44, 77, 86	1 (0%)
5	E	117/117 (100%)	-0.06	6 (5%) 32 31	23, 45, 81, 92	3 (2%)
All	All	1223/1224 (99%)	-0.08	46 (3%) 44 44	13, 42, 80, 104	28 (2%)

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	116	PRO	5.8
1	I	17	LEU	4.8
4	D	13	TRP	4.5
1	I	225	ILE	4.4
4	D	115	SER	4.3

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

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, 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	LLDF	B-factors(Å ²)	Q<0.9
6	GAL	A	206	11/12	0.79	0.33	3.81	97,101,102,104	0
6	SIA	A	207	20/21	0.81	0.30	-	99,102,104,104	0
6	MAN	A	208	11/12	0.79	0.48	-	102,104,105,106	0
6	NAG	A	205	14/15	0.84	0.23	-	96,98,100,100	0
6	NAG	A	201	14/15	0.87	0.27	-	62,72,74,76	0
6	MAN	A	203	11/12	0.77	0.25	-	92,94,96,100	0
6	MAN	A	204	11/12	0.81	0.35	-	96,98,99,100	0
6	NAG	A	202	14/15	0.89	0.26	-	80,83,85,88	0

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. 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, 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	LLDF	B-factors(Å ²)	Q<0.9
7	NAG	E	401	14/15	0.84	0.30	-	63,67,70,70	0
7	NAG	B	301	14/15	0.85	0.31	-	68,70,72,72	0

6.5 Other polymers

There are no such residues in this entry.