



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:50 PM UTC

PDB ID : 6Y6C / pdb_00006y6c
Title : TREM2 extracellular domain (19-174) in complex with single-chain variable fragment (scFv-4)
Authors : Szykowska, A.; Preger, C.; Williams, E.; Mukhopadhyay, S.M.M.; McKinley, G.; Gruslund, S.; Wigren, E.; Persson, H.; Arrowsmith, C.H.; Edwards, A.; von Delft, F.; Bountra, C.; Davis, J.B.; Di Daniel, E.; Burgess-Brown, N.; Bullock, A.
Deposited on : 2020-02-26
Resolution : 2.26 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)

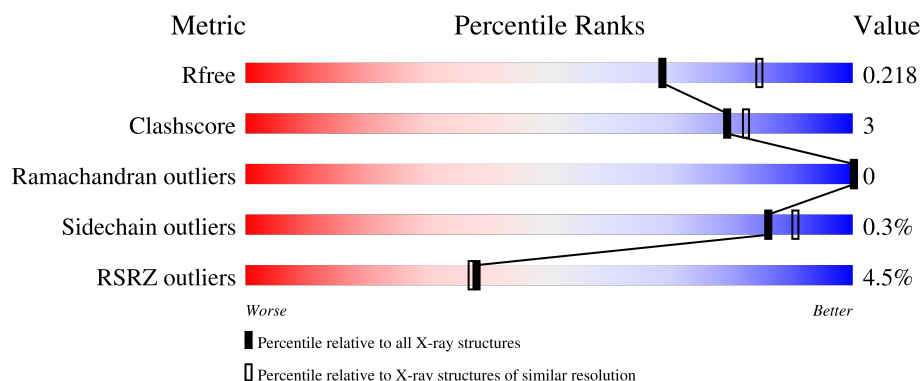
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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}	180053	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	202	 2% 56% 42%
1	B	202	 3% 55% 42%
2	C	245	 3% 86% 7% 7%
2	D	245	 5% 84% 10% 7%

Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5771 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 Triggering receptor expressed on myeloid cells 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	118	Total	C	N	O	S	0	0	0
			915	572	169	169	5			
1	B	118	Total	C	N	O	S	0	0	0
			930	578	175	172	5			

There are 92 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	GLU	-	expression tag	UNP Q9NZC2
A	-5	THR	-	expression tag	UNP Q9NZC2
A	-4	GLY	-	expression tag	UNP Q9NZC2
A	-3	HIS	-	expression tag	UNP Q9NZC2
A	-2	HIS	-	expression tag	UNP Q9NZC2
A	-1	HIS	-	expression tag	UNP Q9NZC2
A	0	HIS	-	expression tag	UNP Q9NZC2
A	1	HIS	-	expression tag	UNP Q9NZC2
A	2	HIS	-	expression tag	UNP Q9NZC2
A	3	SER	-	expression tag	UNP Q9NZC2
A	4	SER	-	expression tag	UNP Q9NZC2
A	5	GLY	-	expression tag	UNP Q9NZC2
A	6	VAL	-	expression tag	UNP Q9NZC2
A	7	ASP	-	expression tag	UNP Q9NZC2
A	8	LEU	-	expression tag	UNP Q9NZC2
A	9	GLY	-	expression tag	UNP Q9NZC2
A	10	THR	-	expression tag	UNP Q9NZC2
A	11	GLU	-	expression tag	UNP Q9NZC2
A	12	ASN	-	expression tag	UNP Q9NZC2
A	13	LEU	-	expression tag	UNP Q9NZC2
A	14	TYR	-	expression tag	UNP Q9NZC2
A	15	PHE	-	expression tag	UNP Q9NZC2
A	16	GLN	-	expression tag	UNP Q9NZC2
A	17	SER	-	expression tag	UNP Q9NZC2
A	18	MET	-	expression tag	UNP Q9NZC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	175	SER	-	expression tag	UNP Q9NZC2
A	176	SER	-	expression tag	UNP Q9NZC2
A	177	LYS	-	expression tag	UNP Q9NZC2
A	178	GLY	-	expression tag	UNP Q9NZC2
A	179	GLY	-	expression tag	UNP Q9NZC2
A	180	TYR	-	expression tag	UNP Q9NZC2
A	181	GLY	-	expression tag	UNP Q9NZC2
A	182	LEU	-	expression tag	UNP Q9NZC2
A	183	ASN	-	expression tag	UNP Q9NZC2
A	184	ASP	-	expression tag	UNP Q9NZC2
A	185	ILE	-	expression tag	UNP Q9NZC2
A	186	PHE	-	expression tag	UNP Q9NZC2
A	187	GLU	-	expression tag	UNP Q9NZC2
A	188	ALA	-	expression tag	UNP Q9NZC2
A	189	GLN	-	expression tag	UNP Q9NZC2
A	190	LYS	-	expression tag	UNP Q9NZC2
A	191	ILE	-	expression tag	UNP Q9NZC2
A	192	GLU	-	expression tag	UNP Q9NZC2
A	193	TRP	-	expression tag	UNP Q9NZC2
A	194	HIS	-	expression tag	UNP Q9NZC2
A	195	GLU	-	expression tag	UNP Q9NZC2
B	-6	GLU	-	expression tag	UNP Q9NZC2
B	-5	THR	-	expression tag	UNP Q9NZC2
B	-4	GLY	-	expression tag	UNP Q9NZC2
B	-3	HIS	-	expression tag	UNP Q9NZC2
B	-2	HIS	-	expression tag	UNP Q9NZC2
B	-1	HIS	-	expression tag	UNP Q9NZC2
B	0	HIS	-	expression tag	UNP Q9NZC2
B	1	HIS	-	expression tag	UNP Q9NZC2
B	2	HIS	-	expression tag	UNP Q9NZC2
B	3	SER	-	expression tag	UNP Q9NZC2
B	4	SER	-	expression tag	UNP Q9NZC2
B	5	GLY	-	expression tag	UNP Q9NZC2
B	6	VAL	-	expression tag	UNP Q9NZC2
B	7	ASP	-	expression tag	UNP Q9NZC2
B	8	LEU	-	expression tag	UNP Q9NZC2
B	9	GLY	-	expression tag	UNP Q9NZC2
B	10	THR	-	expression tag	UNP Q9NZC2
B	11	GLU	-	expression tag	UNP Q9NZC2
B	12	ASN	-	expression tag	UNP Q9NZC2
B	13	LEU	-	expression tag	UNP Q9NZC2
B	14	TYR	-	expression tag	UNP Q9NZC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	15	PHE	-	expression tag	UNP Q9NZC2
B	16	GLN	-	expression tag	UNP Q9NZC2
B	17	SER	-	expression tag	UNP Q9NZC2
B	18	MET	-	expression tag	UNP Q9NZC2
B	175	SER	-	expression tag	UNP Q9NZC2
B	176	SER	-	expression tag	UNP Q9NZC2
B	177	LYS	-	expression tag	UNP Q9NZC2
B	178	GLY	-	expression tag	UNP Q9NZC2
B	179	GLY	-	expression tag	UNP Q9NZC2
B	180	TYR	-	expression tag	UNP Q9NZC2
B	181	GLY	-	expression tag	UNP Q9NZC2
B	182	LEU	-	expression tag	UNP Q9NZC2
B	183	ASN	-	expression tag	UNP Q9NZC2
B	184	ASP	-	expression tag	UNP Q9NZC2
B	185	ILE	-	expression tag	UNP Q9NZC2
B	186	PHE	-	expression tag	UNP Q9NZC2
B	187	GLU	-	expression tag	UNP Q9NZC2
B	188	ALA	-	expression tag	UNP Q9NZC2
B	189	GLN	-	expression tag	UNP Q9NZC2
B	190	LYS	-	expression tag	UNP Q9NZC2
B	191	ILE	-	expression tag	UNP Q9NZC2
B	192	GLU	-	expression tag	UNP Q9NZC2
B	193	TRP	-	expression tag	UNP Q9NZC2
B	194	HIS	-	expression tag	UNP Q9NZC2
B	195	GLU	-	expression tag	UNP Q9NZC2

- Molecule 2 is a protein called Single chain variable.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	228	Total	C	N	O	S	0	0	0
			1758	1114	289	347	8			
2	D	229	Total	C	N	O	S	0	0	0
			1765	1119	289	349	8			

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

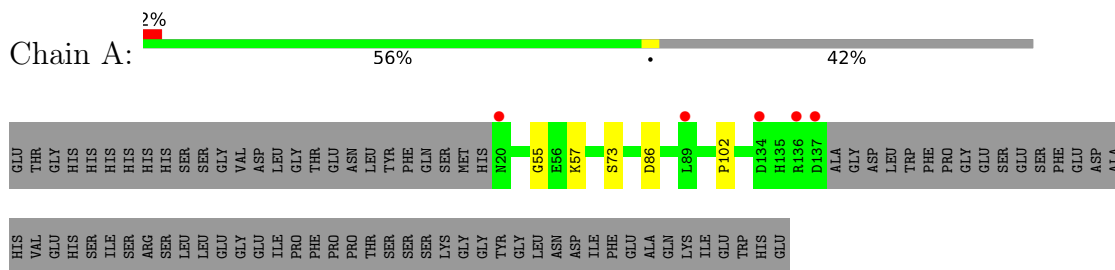
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	74	Total	O	0	0
			74	74		
4	B	74	Total	O	0	0
			74	74		
4	C	112	Total	O	0	0
			112	112		
4	D	115	Total	O	0	0
			115	115		

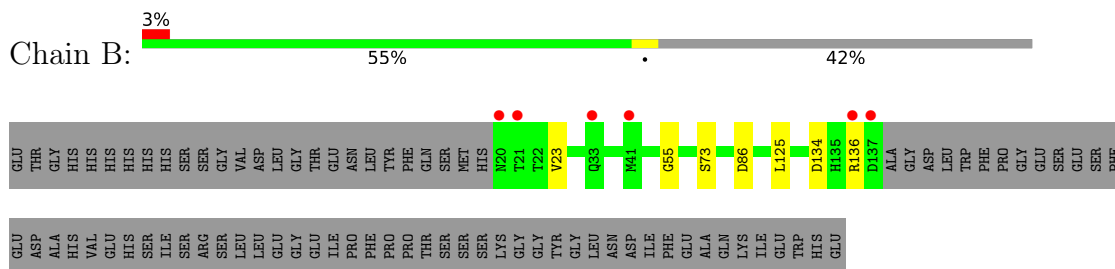
3 Residue-property plots [i](#)

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.

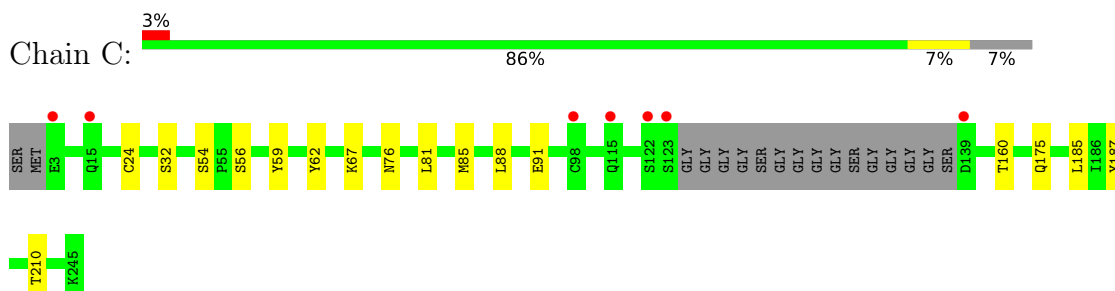
- Molecule 1: Triggering receptor expressed on myeloid cells 2



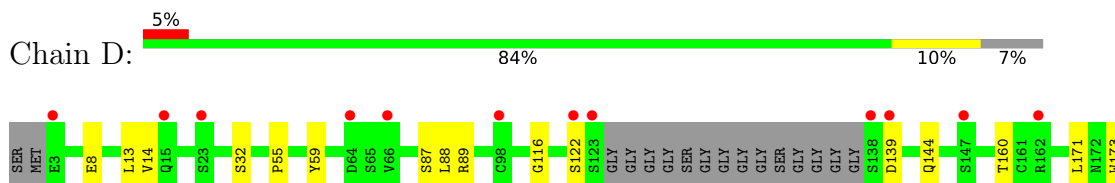
- Molecule 1: Triggering receptor expressed on myeloid cells 2

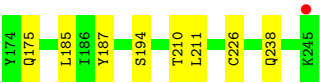


- Molecule 2: Single chain variable



- Molecule 2: Single chain variable





4 Data and refinement statistics

Property	Value	Source
Space group	P 41 2 2	Depositor
Cell constants a, b, c, α , β , γ	111.66Å 111.66Å 232.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.63 – 2.26 100.63 – 2.26	Depositor EDS
% Data completeness (in resolution range)	99.7 (100.63-2.26) 91.9 (100.63-2.26)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.82 (at 2.25Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.191 , 0.216 0.193 , 0.218	Depositor DCC
R_{free} test set	3452 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	33.9	Xtriage
Anisotropy	0.484	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5771	wwPDB-VP
Average B, all atoms (Å ²)	42.0	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 41.16 % 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 2.4589e-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, 0.333 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: NAG

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	0.11	0/935	0.31	0/1271
1	B	0.09	0/950	0.30	0/1290
2	C	0.10	0/1802	0.32	0/2443
2	D	0.11	0/1809	0.34	0/2451
All	All	0.10	0/5496	0.32	0/7455

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	915	0	887	5	0
1	B	930	0	909	5	0
2	C	1758	0	1660	9	0
2	D	1765	0	1670	14	0
3	A	14	0	13	0	0
3	B	14	0	13	0	0
4	A	74	0	0	0	0
4	B	74	0	0	1	0
4	C	112	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	115	0	0	0	0
All	All	5771	0	5152	28	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 3.

All (28) 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:C:175:GLN:HB2	2:C:185:LEU:HD11	1.82	0.62
2:C:160:THR:HG22	2:C:210:THR:HG22	1.87	0.57
1:B:134:ASP:OD2	1:B:136:ARG:NH1	2.39	0.56
2:D:175:GLN:HB2	2:D:185:LEU:HD11	1.88	0.56
1:A:73:SER:HB3	1:A:86:ASP:HB3	1.90	0.53
2:D:160:THR:HG22	2:D:210:THR:HG22	1.90	0.52
2:D:87:SER:OG	2:D:89:ARG:NH1	2.43	0.52
2:D:171:LEU:HD11	2:D:226:CYS:HB2	1.92	0.50
2:C:85:MET:HB3	2:C:88:LEU:HD21	1.94	0.48
2:D:144:GLN:O	2:D:238:GLN:NE2	2.39	0.48
2:C:32:SER:HB3	2:C:76:ASN:HB3	1.96	0.47
2:D:32:SER:O	2:D:55:PRO:HB3	2.14	0.47
1:A:55:GLY:HA3	2:D:187:TYR:CZ	2.52	0.45
1:A:57:LYS:HD3	2:D:194:SER:HB3	1.99	0.44
2:D:8:GLU:CD	2:D:116:GLY:H	2.25	0.44
1:B:55:GLY:HA3	2:C:187:TYR:CZ	2.53	0.44
1:A:55:GLY:HA3	2:D:187:TYR:CE1	2.53	0.43
2:D:14:VAL:HG11	2:D:88:LEU:HD13	2.00	0.43
2:C:54:SER:HB3	2:C:59:TYR:HB2	2.00	0.43
2:C:24:CYS:HB3	2:C:81:LEU:HB3	2.01	0.42
1:A:102:PRO:HG3	2:D:59:TYR:CZ	2.54	0.42
1:B:73:SER:HB3	1:B:86:ASP:HB3	2.00	0.42
4:B:329:HOH:O	2:C:56:SER:HB3	2.19	0.42
1:B:134:ASP:OD1	1:B:136:ARG:HG3	2.20	0.42
2:D:13:LEU:HD11	2:D:122:SER:HB3	2.02	0.41
2:D:173:TRP:CD2	2:D:211:LEU:HB2	2.55	0.41
1:B:23:VAL:HG22	1:B:125:LEU:HD23	2.01	0.41
2:C:62:TYR:HB2	2:C:67:LYS:HG3	2.03	0.41

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	116/202 (57%)	112 (97%)	4 (3%)	0	100	100
1	B	116/202 (57%)	116 (100%)	0	0	100	100
2	C	224/245 (91%)	216 (96%)	8 (4%)	0	100	100
2	D	225/245 (92%)	218 (97%)	7 (3%)	0	100	100
All	All	681/894 (76%)	662 (97%)	19 (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	98/174 (56%)	98 (100%)	0	100	100
1	B	102/174 (59%)	102 (100%)	0	100	100
2	C	187/196 (95%)	186 (100%)	1 (0%)	81	87
2	D	189/196 (96%)	188 (100%)	1 (0%)	81	87
All	All	576/740 (78%)	574 (100%)	2 (0%)	86	90

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

Mol	Chain	Res	Type
2	C	91	GLU
2	D	139	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	43	HIS
1	A	68	ASN
1	B	43	HIS
2	C	84	GLN
2	C	86	ASN
2	C	115	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	NAG	A	201	1	14,14,15	0.32	0	17,19,21	0.39	0
3	NAG	B	201	1	14,14,15	0.32	0	17,19,21	0.53	0

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	NAG	A	201	1	-	0/6/23/26	0/1/1/1
3	NAG	B	201	1	-	0/6/23/26	0/1/1/1

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

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	118/202 (58%)	0.23	5 (4%) 40 40	28, 39, 58, 97	0
1	B	118/202 (58%)	0.39	6 (5%) 33 32	33, 42, 62, 113	0
2	C	228/245 (93%)	0.26	7 (3%) 51 51	28, 40, 59, 89	0
2	D	229/245 (93%)	0.25	13 (5%) 29 27	28, 39, 61, 93	0
All	All	693/894 (77%)	0.28	31 (4%) 38 37	28, 40, 62, 113	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	137	ASP	8.1
2	C	123	SER	6.6
2	D	123	SER	5.9
1	B	137	ASP	5.8
1	A	136	ARG	5.1
2	D	139	ASP	4.8
1	B	20	ASN	4.1
2	D	138	SER	4.1
2	C	139	ASP	4.0
1	A	20	ASN	3.9
1	B	136	ARG	3.9
2	C	15	GLN	3.5
2	D	15	GLN	3.5
2	D	66	VAL	2.9
2	C	122	SER	2.8
1	A	134	ASP	2.6
2	D	64	ASP	2.6
1	B	21	THR	2.4
1	B	41	MET	2.4
2	D	98	CYS	2.4
2	D	3	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
2	C	3	GLU	2.4
2	C	115	GLN	2.3
2	D	147	SER	2.1
2	D	245	LYS	2.1
2	D	162	ARG	2.1
2	D	122	SER	2.0
1	B	33	GLN	2.0
1	A	89	LEU	2.0
2	D	23	SER	2.0
2	C	98	CYS	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
3	NAG	B	201	14/15	0.75	0.20	54,68,80,82	0
3	NAG	A	201	14/15	0.78	0.22	50,64,76,78	0

6.5 Other polymers [i](#)

There are no such residues in this entry.