



Full wwPDB X-ray Structure Validation Report ⓘ

Dec 1, 2022 – 12:04 PM EST

PDB ID : 7N2N
Title : TCR-antigen complex AS4.2-PRPF3-HLA*B27
Authors : Yang, X.; Jude, K.M.; Garcia, K.C.
Deposited on : 2021-05-29
Resolution : 2.60 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 : 2.31.2
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) : 2.31.2

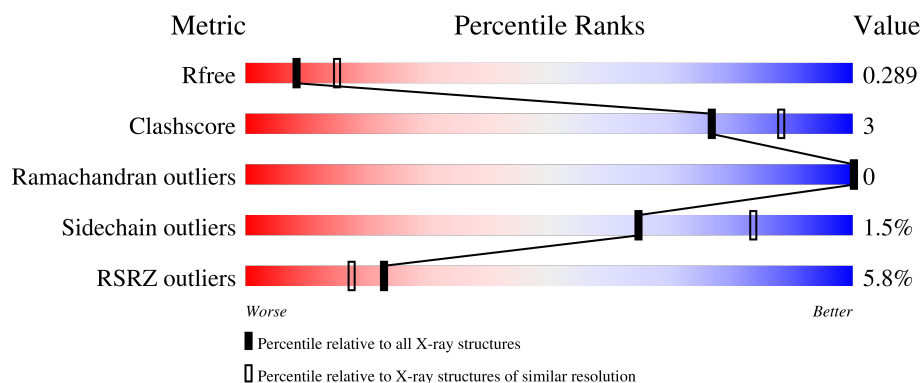
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	C	9	100%
2	A	278	5% 90% 9% .
3	B	100	4% 89% 11%
4	D	210	11% 85% 8% 7%
5	F	242	3% 90% 9% .

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 6700 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 Pre-mRNA Processing Factor 3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	C	9	Total	C	N	O	0	0	0
			69	45	13	11			

- Molecule 2 is a protein called Human leukocyte antigen (HLA) B27.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	275	Total	C	N	O	S	0	1	0
			2241	1392	406	437	6			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	SER	CYS	conflict	UNP A3F718

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 4 is a protein called T cell receptor alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	196	Total	C	N	O	S	0	0	0
			1500	930	252	311	7			

- Molecule 5 is a protein called T cell receptor beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	241	Total	C	N	O	S	0	0	0
			1916	1212	332	367	5			

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		
6	B	1	Total	C	O	0	0
			6	3	3		
6	D	1	Total	C	O	0	0
			6	3	3		
6	F	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 8 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	C	3	Total 3	O 3	0	0
9	A	26	Total 26	O 26	0	0
9	B	12	Total 12	O 12	0	0
9	D	11	Total 11	O 11	0	0
9	F	14	Total 14	O 14	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.

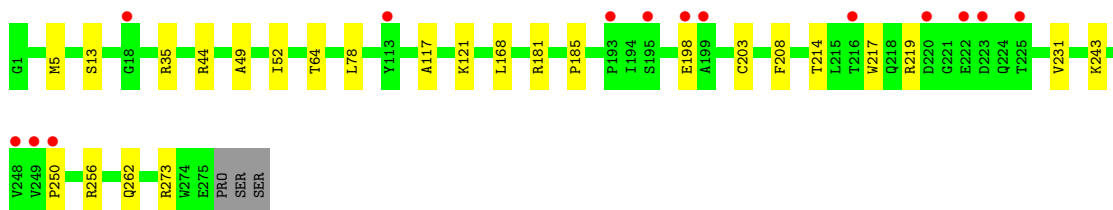
- Molecule 1: Pre-mRNA Processing Factor 3

Chain C:  100%


There are no outlier residues recorded for this chain.

- Molecule 2: Human leukocyte antigen (HLA) B27

Chain A:  5% 90% 9%




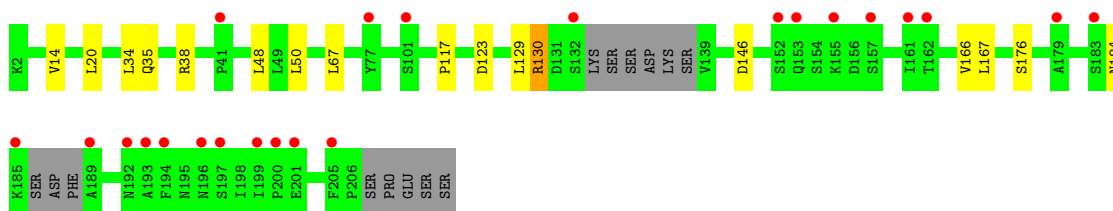
- Molecule 3: Beta-2-microglobulin

Chain B:  4% 89% 11%




- Molecule 4: T cell receptor alpha chain

Chain D:  11% 85% 8% 7%



- Molecule 5: T cell receptor beta chain

Chain F:  3% 90% 9%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.11Å 53.15Å 106.82Å 90.00° 98.48° 90.00°	Depositor
Resolution (Å)	47.48 – 2.60 47.48 – 2.34	Depositor EDS
% Data completeness (in resolution range)	95.9 (47.48-2.60) 96.2 (47.48-2.34)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.29 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.19.1_4122+SVN	Depositor
R, R_{free}	0.248 , 0.291 0.246 , 0.289	Depositor DCC
R_{free} test set	1278 reflections (3.37%)	wwPDB-VP
Wilson B-factor (Å ²)	39.2	Xtriage
Anisotropy	0.255	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 37.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	6700	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.36% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, 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	C	0.28	0/69	0.62	0/91
2	A	0.24	0/2303	0.51	0/3131
3	B	0.24	0/860	0.47	0/1162
4	D	0.25	0/1525	0.49	0/2072
5	F	0.25	0/1967	0.49	0/2680
All	All	0.25	0/6724	0.49	0/9136

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	C	69	0	85	0	0
2	A	2241	0	2100	12	0
3	B	837	0	803	6	0
4	D	1500	0	1436	12	0
5	F	1916	0	1824	15	0
6	B	12	0	16	0	0
6	D	6	0	8	0	0
6	F	6	0	8	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	D	28	0	26	0	0
7	F	14	0	13	1	0
8	F	5	0	0	0	0
9	A	26	0	0	0	0
9	B	12	0	0	1	0
9	C	3	0	0	0	0
9	D	11	0	0	0	0
9	F	14	0	0	0	0
All	All	6700	0	6319	39	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 (39) 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:5:MET:HB2	2:A:168:LEU:HD13	1.73	0.70
5:F:204:PRO:HG2	5:F:205:ARG:HH12	1.61	0.65
2:A:13:SER:HB3	2:A:78:LEU:HD13	1.79	0.63
4:D:117:PRO:HG3	4:D:166:VAL:HG11	1.80	0.62
2:A:214:THR:HB	2:A:262:GLN:HB2	1.80	0.62
4:D:14:VAL:HG21	4:D:20:LEU:HD21	1.84	0.58
2:A:44:ARG:HD2	2:A:64:THR:HG21	1.86	0.58
5:F:67:GLN:NE2	7:F:301:NAG:O7	2.39	0.55
3:B:17:ASN:HD21	3:B:74:GLU:HG2	1.73	0.53
5:F:21:LEU:HD22	5:F:109:THR:HG21	1.92	0.52
2:A:185:PRO:HB3	2:A:208:PHE:HB3	1.93	0.51
2:A:219:ARG:CZ	2:A:256:ARG:HH12	2.24	0.51
4:D:35:GLN:HG2	4:D:50:LEU:HG	1.94	0.50
5:F:52:GLY:HA2	5:F:68:GLN:HB3	1.94	0.49
4:D:184:ASN:OD1	4:D:184:ASN:N	2.45	0.48
4:D:50:LEU:HD12	5:F:102:THR:HB	1.95	0.48
5:F:160:TRP:HB2	5:F:209:ARG:HB3	1.95	0.48
3:B:6:LYS:HG2	3:B:28:SER:O	2.14	0.47
5:F:103:GLN:HG3	6:F:302:GOL:H31	1.95	0.47
4:D:167:LEU:HB3	5:F:171:CYS:HB3	1.97	0.47
2:A:219:ARG:NH2	2:A:256:ARG:HH12	2.13	0.47
3:B:24:ASN:HB3	3:B:65:LEU:HD11	1.96	0.46
4:D:129:LEU:HB3	5:F:128:PHE:HB3	1.97	0.46
5:F:17:GLN:HG3	5:F:18:ARG:H	1.82	0.44
4:D:130:ARG:HB3	5:F:129:GLU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:130:PRO:HD3	5:F:143:LEU:HG	1.98	0.44
4:D:34:LEU:HD13	4:D:67:LEU:HD13	1.99	0.43
4:D:38:ARG:HB3	4:D:48:LEU:HD11	1.99	0.43
2:A:203:CYS:HB2	2:A:217:TRP:CZ2	2.54	0.43
2:A:231:VAL:O	2:A:243:LYS:NZ	2.36	0.43
4:D:146:ASP:OD1	4:D:146:ASP:N	2.52	0.42
3:B:47:GLU:HG2	3:B:48:LYS:H	1.84	0.42
5:F:22:ARG:HG2	5:F:75:GLU:HG2	2.02	0.42
3:B:6:LYS:HG3	9:B:203:HOH:O	2.18	0.42
2:A:49:ALA:O	2:A:52:ILE:HG22	2.20	0.42
4:D:123:ASP:OD2	5:F:137:HIS:NE2	2.52	0.42
2:A:198:GLU:HA	2:A:250:PRO:HA	2.02	0.42
5:F:127:VAL:HG13	5:F:237:ALA:HB3	2.02	0.41
2:A:117:ALA:HB2	3:B:60:TRP:CE2	2.56	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	C	7/9 (78%)	7 (100%)	0	0	100	100
2	A	274/278 (99%)	265 (97%)	9 (3%)	0	100	100
3	B	98/100 (98%)	96 (98%)	2 (2%)	0	100	100
4	D	190/210 (90%)	184 (97%)	6 (3%)	0	100	100
5	F	239/242 (99%)	228 (95%)	11 (5%)	0	100	100
All	All	808/839 (96%)	780 (96%)	28 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	C	7/7 (100%)	7 (100%)	0	100	100
2	A	234/237 (99%)	230 (98%)	4 (2%)	60	81
3	B	95/95 (100%)	93 (98%)	2 (2%)	53	77
4	D	173/187 (92%)	171 (99%)	2 (1%)	71	87
5	F	209/211 (99%)	206 (99%)	3 (1%)	67	85
All	All	718/737 (97%)	707 (98%)	11 (2%)	65	83

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	35	ARG
2	A	121	LYS
2	A	181	ARG
2	A	273	ARG
3	B	70	PHE
3	B	75	LYS
4	D	130	ARG
4	D	176	SER
5	F	171	CYS
5	F	205	ARG
5	F	242	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	180	GLN

5.3.3 RNA ⓘ

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](#)

8 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	$\# Z > 2$
6	GOL	D	303	-	5,5,5	0.93	0	5,5,5	1.14	1 (20%)
7	NAG	D	302	4	14,14,15	0.24	0	17,19,21	0.52	0
8	SO4	F	303	-	4,4,4	0.14	0	6,6,6	0.05	0
7	NAG	D	301	4	14,14,15	0.26	0	17,19,21	0.39	0
6	GOL	B	102	-	5,5,5	0.94	0	5,5,5	1.04	0
7	NAG	F	301	5	14,14,15	0.27	0	17,19,21	0.52	0
6	GOL	F	302	-	5,5,5	0.99	0	5,5,5	0.89	0
6	GOL	B	101	-	5,5,5	0.93	0	5,5,5	0.98	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
6	GOL	D	303	-	-	2/4/4/4	-
7	NAG	D	302	4	-	2/6/23/26	0/1/1/1
7	NAG	D	301	4	-	2/6/23/26	0/1/1/1
6	GOL	B	102	-	-	0/4/4/4	-
7	NAG	F	301	5	-	3/6/23/26	0/1/1/1
6	GOL	F	302	-	-	3/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	B	101	-	-	0/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
6	D	303	GOL	C3-C2-C1	-2.12	103.48	111.70

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	D	303	GOL	O1-C1-C2-O2
6	D	303	GOL	O1-C1-C2-C3
6	F	302	GOL	C1-C2-C3-O3
7	D	301	NAG	O5-C5-C6-O6
7	D	301	NAG	C4-C5-C6-O6
7	F	301	NAG	O5-C5-C6-O6
7	F	301	NAG	C4-C5-C6-O6
6	F	302	GOL	O2-C2-C3-O3
7	D	302	NAG	O5-C5-C6-O6
7	F	301	NAG	C3-C2-N2-C7
6	F	302	GOL	O1-C1-C2-C3
7	D	302	NAG	C3-C2-N2-C7

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	F	301	NAG	1	0
6	F	302	GOL	1	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	C	9/9 (100%)	0.08	0 100 100	23, 25, 31, 33	0
2	A	275/278 (98%)	0.35	14 (5%) 28 22	19, 39, 89, 107	0
3	B	100/100 (100%)	0.15	4 (4%) 38 31	24, 39, 65, 104	0
4	D	196/210 (93%)	0.68	23 (11%) 4 3	27, 53, 98, 123	0
5	F	241/242 (99%)	0.25	7 (2%) 51 45	23, 45, 73, 100	0
All	All	821/839 (97%)	0.37	48 (5%) 23 17	19, 44, 89, 123	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	F	3	GLY	7.9
4	D	200	PRO	5.7
4	D	132	SER	4.7
5	F	185	ASP	4.5
2	A	222	GLU	3.6
2	A	248	VAL	3.6
5	F	182	ALA	3.5
4	D	196	ASN	3.5
2	A	223	ASP	3.4
3	B	0	MET	3.4
4	D	152	SER	3.4
4	D	185	LYS	3.3
4	D	155	LYS	3.2
4	D	189	ALA	3.2
5	F	183	LEU	3.2
4	D	194	PHE	3.1
5	F	243	ALA	3.1
2	A	249	VAL	3.1
4	D	157	SER	3.1
4	D	192	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
4	D	183	SER	2.8
4	D	205	PHE	2.8
2	A	195	SER	2.8
2	A	250	PRO	2.7
4	D	162	THR	2.6
3	B	87	LEU	2.6
4	D	77	TYR	2.5
3	B	15	ALA	2.4
2	A	198	GLU	2.4
4	D	161	ILE	2.4
3	B	74	GLU	2.4
4	D	201	GLU	2.4
2	A	113	TYR	2.3
4	D	101	SER	2.3
4	D	179	ALA	2.3
4	D	153	GLN	2.3
2	A	220	ASP	2.3
2	A	193	PRO	2.3
5	F	238	GLU	2.2
4	D	193	ALA	2.2
2	A	18	GLY	2.2
5	F	181	PRO	2.1
2	A	216	THR	2.1
2	A	225	THR	2.1
4	D	199	ILE	2.0
2	A	199	ALA	2.0
4	D	197	SER	2.0
4	D	41	PRO	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
7	NAG	D	302	14/15	0.61	0.26	62,82,93,99	0
7	NAG	D	301	14/15	0.76	0.23	48,55,60,62	0
7	NAG	F	301	14/15	0.76	0.30	39,59,66,67	0
6	GOL	D	303	6/6	0.79	0.27	56,61,74,79	0
6	GOL	B	102	6/6	0.79	0.25	41,52,55,56	0
6	GOL	F	302	6/6	0.80	0.25	23,33,50,51	0
6	GOL	B	101	6/6	0.90	0.32	29,38,47,48	0
8	SO4	F	303	5/5	0.91	0.26	70,70,76,89	0

6.5 Other polymers [i](#)

There are no such residues in this entry.