



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2024 – 01:00 PM EDT

PDB ID : 6BXB  
Title : Crystal structure of an extended b3 integrin P33  
Authors : Zhou, D.; Zhu, J.  
Deposited on : 2017-12-18  
Resolution : 2.39 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

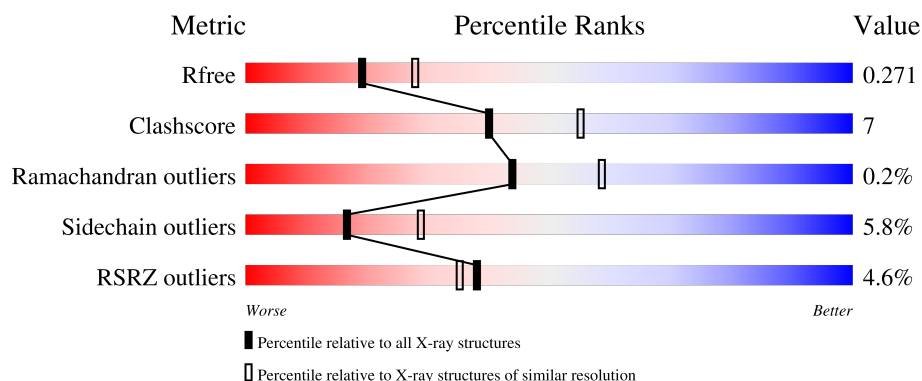
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

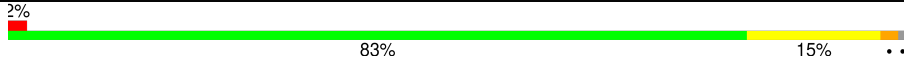

The reported resolution of this entry is 2.39 Å.

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))
$R_{free}$	164625	4642 (2.40-2.40)
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

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  $\geq 3$ , 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	466	
1	B	466	

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7469 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 Chimera protein of Integrin beta-3 and Integrin alpha-L.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	463	Total	C	N	O	S	0	1	0
			3598	2242	612	712	32			
1	B	465	Total	C	N	O	S	0	0	0
			3617	2256	614	715	32			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	PRO	LEU	conflict	UNP P05106
A	171	TRP	ARG	conflict	UNP P20701
A	460	THR	-	expression tag	UNP P05106
A	461	ARG	-	expression tag	UNP P05106
A	462	GLU	-	expression tag	UNP P05106
A	463	LEU	-	expression tag	UNP P05106
A	464	TYR	-	expression tag	UNP P05106
A	465	PHE	-	expression tag	UNP P05106
A	466	GLN	-	expression tag	UNP P05106
B	33	PRO	LEU	conflict	UNP P05106
B	171	TRP	ARG	conflict	UNP P20701
B	460	THR	-	expression tag	UNP P05106
B	461	ARG	-	expression tag	UNP P05106
B	462	GLU	-	expression tag	UNP P05106
B	463	LEU	-	expression tag	UNP P05106
B	464	TYR	-	expression tag	UNP P05106
B	465	PHE	-	expression tag	UNP P05106
B	466	GLN	-	expression tag	UNP P05106

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Ca	0	0
			1	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
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		
3	B	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 GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



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

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Mg	0	0
			1	1		

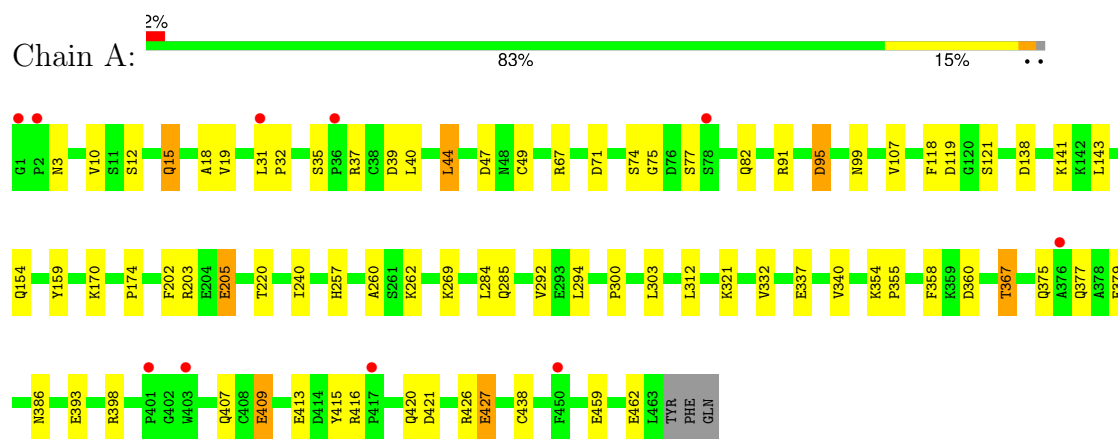
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	91	Total	O	0	0
			91	91		
6	B	79	Total	O	0	0
			79	79		

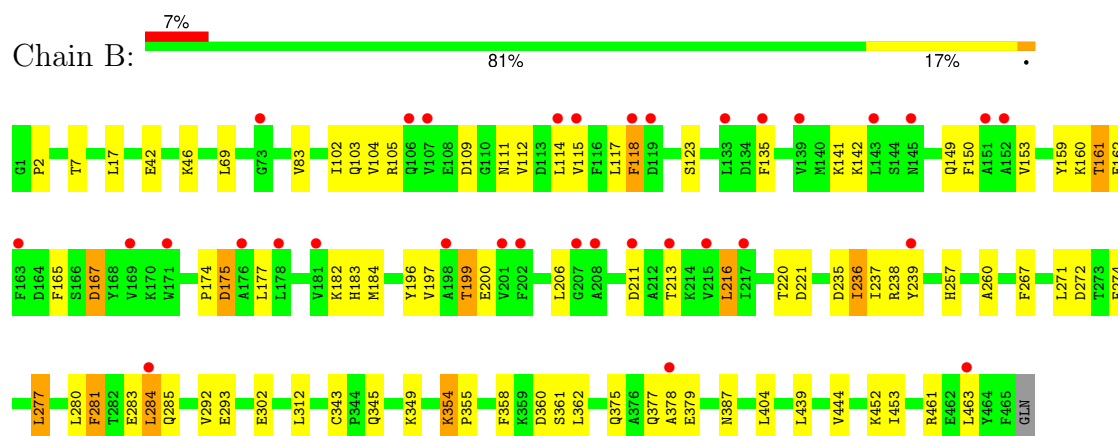
### 3 Residue-property plots [i](#)

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: Chimera protein of Integrin beta-3 and Integrin alpha-L



- Molecule 1: Chimera protein of Integrin beta-3 and Integrin alpha-L



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.56Å 79.84Å 116.16Å 90.00° 91.42° 90.00°	Depositor
Resolution (Å)	53.52 – 2.39 53.52 – 2.39	Depositor EDS
% Data completeness (in resolution range)	99.4 (53.52-2.39) 99.4 (53.52-2.39)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.11 (at 2.39Å)	Xtriage
Refinement program	PHENIX 1.12_2829	Depositor
R, $R_{free}$	0.221 , 0.268 0.224 , 0.271	Depositor DCC
$R_{free}$ test set	2139 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	62.8	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 64.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.033 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7469	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	86.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, CA, NAG, MG

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	0.25	0/3666	0.45	0/4947
1	B	0.27	0/3684	0.49	0/4971
All	All	0.26	0/7350	0.47	0/9918

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
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	281	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	A	3598	0	3503	45	0
1	B	3617	0	3511	48	0
2	A	1	0	0	0	0
3	A	28	0	26	1	0
3	B	42	0	39	2	0
4	A	12	0	16	1	0
5	B	1	0	0	0	0
6	A	91	0	0	4	0
6	B	79	0	0	0	0
All	All	7469	0	7095	94	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 7.

All (94) 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:B:135:PHE:HB2	1:B:277:LEU:HD13	1.64	0.80
1:A:67:ARG:NH2	6:A:602:HOH:O	2.17	0.76
1:A:205:GLU:OE2	6:A:601:HOH:O	2.07	0.71
1:B:271:LEU:HD21	1:B:280:LEU:HD22	1.75	0.69
1:B:161:THR:OG1	1:B:196:TYR:OH	2.10	0.66
1:B:387:ASN:HB3	3:B:504:NAG:H2	1.79	0.65
1:B:118:PHE:HD1	1:B:118:PHE:H	1.44	0.64
1:A:3:ASN:ND2	6:A:604:HOH:O	2.33	0.61
1:A:141:LYS:HG3	1:A:174:PRO:HG2	1.85	0.59
1:B:260:ALA:HB1	1:B:267:PHE:HB2	1.86	0.58
3:B:504:NAG:H83	3:B:504:NAG:H3	1.86	0.57
1:B:404:LEU:HD13	1:B:439:LEU:HD13	1.87	0.57
1:B:199:THR:OG1	1:B:200:GLU:OE1	2.23	0.56
1:B:354:LYS:NZ	1:B:358:PHE:O	2.37	0.56
1:A:71:ASP:O	1:A:74:SER:OG	2.22	0.56
1:B:302:GLU:OE1	1:B:349:LYS:NZ	2.38	0.56
1:B:141:LYS:HG2	1:B:174:PRO:HG3	1.88	0.55
1:A:240:ILE:HG22	1:A:260:ALA:HB2	1.89	0.55
1:A:143:LEU:HD21	1:A:285:GLN:NE2	2.23	0.54
1:B:199:THR:OG1	1:B:200:GLU:N	2.41	0.54
1:A:202:PHE:HB3	4:A:505:GOL:H11	1.89	0.54
1:A:337:GLU:HB2	3:A:502:NAG:H83	1.90	0.53
1:B:281:PHE:HB3	1:B:284:LEU:HD12	1.89	0.53
1:A:10:VAL:HB	1:A:15:GLN:NE2	2.24	0.53
1:A:99:ASN:ND2	6:A:609:HOH:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:VAL:HB	1:A:15:GLN:HE22	1.75	0.51
1:A:39:ASP:HB3	1:A:44:LEU:HD13	1.91	0.51
1:A:413:GLU:HG2	1:A:415:TYR:H	1.75	0.51
1:A:12:SER:O	1:A:15:GLN:NE2	2.43	0.51
1:A:82:GLN:HG2	1:A:107[A]:VAL:HG12	1.92	0.51
1:B:83:VAL:HB	1:B:360:ASP:HB3	1.93	0.51
1:A:393:GLU:OE2	1:A:398:ARG:NH1	2.43	0.51
1:A:377:GLN:HG2	1:A:379:GLU:HG3	1.92	0.50
1:B:111:ASN:ND2	1:B:211:ASP:OD2	2.44	0.50
1:B:167:ASP:N	1:B:167:ASP:OD1	2.44	0.50
1:A:31:LEU:HD12	1:A:32:PRO:HD2	1.94	0.50
1:A:426:ARG:HG3	1:A:427:GLU:H	1.78	0.49
1:A:407:GLN:O	1:A:409:GLU:N	2.46	0.48
1:B:355:PRO:HB2	1:B:358:PHE:CD1	2.48	0.48
1:A:15:GLN:HA	1:A:18:ALA:HB3	1.95	0.48
1:B:2:PRO:HB3	1:B:452:LYS:HE2	1.95	0.48
1:B:284:LEU:HD13	1:B:285:GLN:N	2.27	0.48
1:A:354:LYS:HG3	1:A:360:ASP:O	2.14	0.48
1:B:216:LEU:O	1:B:239:TYR:HB2	2.14	0.47
1:A:118:PHE:CZ	1:A:154:GLN:HB2	2.50	0.47
1:B:69:LEU:HD13	1:B:105:ARG:HB2	1.97	0.47
1:A:15:GLN:O	1:A:19:VAL:HG23	2.14	0.47
1:B:7:THR:HG22	1:B:452:LYS:HB2	1.96	0.47
1:B:272:ASP:OD1	1:B:272:ASP:N	2.47	0.47
1:B:312:LEU:HA	1:B:312:LEU:HD23	1.68	0.47
1:B:439:LEU:HD12	1:B:444:VAL:HG21	1.96	0.47
1:B:117:LEU:HD22	1:B:197:VAL:HG21	1.97	0.46
1:A:119:ASP:HB2	1:A:220:THR:HA	1.96	0.46
1:B:123:SER:OG	1:B:221:ASP:OD2	2.33	0.46
1:B:149:GLN:HB3	1:B:165:PHE:CD1	2.51	0.46
1:A:12:SER:H	1:A:15:GLN:NE2	2.13	0.46
1:B:102:ILE:HG21	1:B:362:LEU:HD22	1.98	0.45
1:B:153:VAL:HG22	1:B:161:THR:HG23	1.98	0.45
1:A:386:ASN:HD21	1:A:409:GLU:HA	1.82	0.45
1:B:141:LYS:CG	1:B:174:PRO:HG3	2.46	0.45
1:B:260:ALA:HB1	1:B:267:PHE:CB	2.46	0.45
1:B:42:GLU:O	1:B:46:LYS:HG2	2.16	0.45
1:A:420:GLN:HG3	1:A:438:CYS:SG	2.57	0.45
1:B:274:PHE:O	1:B:277:LEU:HG	2.17	0.44
1:A:294:LEU:HB2	1:A:321:LYS:HB2	2.00	0.44
1:B:69:LEU:HD11	1:B:103:GLN:HB3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:12:SER:H	1:A:15:GLN:HE22	1.66	0.43
1:B:42:GLU:OE2	1:B:42:GLU:N	2.47	0.43
1:B:153:VAL:HG13	1:B:160:LYS:O	2.18	0.43
1:B:453:ILE:HG12	1:B:461:ARG:HG3	2.01	0.43
1:A:203:ARG:NH2	1:A:205:GLU:OE2	2.51	0.43
1:A:300:PRO:HD2	1:A:303:LEU:HD12	2.01	0.43
1:A:170:LYS:HE3	1:A:170:LYS:HB2	1.75	0.43
1:A:39:ASP:OD1	1:A:40:LEU:N	2.45	0.42
1:A:292:VAL:HG21	1:A:332:VAL:HG21	2.02	0.42
1:B:112:VAL:HA	1:B:213:THR:OG1	2.19	0.42
1:B:281:PHE:HD2	1:B:284:LEU:HG	1.84	0.42
1:A:269:LYS:HE3	1:A:284:LEU:HD21	2.01	0.42
1:B:114:LEU:HD21	1:B:150:PHE:CE1	2.55	0.42
1:B:375:GLN:O	1:B:378:ALA:HB2	2.20	0.42
1:B:104:VAL:HG11	1:B:292:VAL:HG11	2.02	0.41
1:A:95:ASP:HA	1:A:340:VAL:O	2.20	0.41
1:A:355:PRO:HB2	1:A:358:PHE:CD1	2.56	0.41
1:A:32:PRO:HG2	1:A:35:SER:OG	2.20	0.41
1:B:236:ILE:H	1:B:236:ILE:HG22	1.57	0.41
1:A:119:ASP:OD1	1:A:121:SER:OG	2.39	0.41
1:A:15:GLN:H	1:A:15:GLN:HG3	1.57	0.41
1:B:175:ASP:OD1	1:B:175:ASP:N	2.52	0.41
1:B:184:MET:H	1:B:184:MET:HG2	1.65	0.41
1:A:262:LYS:HD2	1:A:262:LYS:N	2.34	0.41
1:B:293:GLU:O	1:B:355:PRO:HA	2.21	0.41
1:A:91:ARG:HA	1:A:367:THR:O	2.21	0.40
1:A:75:GLY:O	1:A:77:SER:N	2.55	0.40
1:B:354:LYS:HB3	1:B:361:SER:HB2	2.04	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	462/466 (99%)	427 (92%)	34 (7%)	1 (0%)	44	59
1	B	463/466 (99%)	430 (93%)	32 (7%)	1 (0%)	44	59
All	All	925/932 (99%)	857 (93%)	66 (7%)	2 (0%)	44	59

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	162	GLU
1	A	312	LEU

### 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	A	412/414 (100%)	394 (96%)	18 (4%)	24	41
1	B	413/414 (100%)	383 (93%)	30 (7%)	11	20
All	All	825/828 (100%)	777 (94%)	48 (6%)	17	29

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	GLN
1	A	37	ARG
1	A	44	LEU
1	A	47	ASP
1	A	49	CYS
1	A	95	ASP
1	A	138	ASP
1	A	159	TYR
1	A	205	GLU
1	A	257	HIS
1	A	367	THR
1	A	375	GLN
1	A	409	GLU
1	A	416	ARG

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Mol	Chain	Res	Type
1	A	421	ASP
1	A	427	GLU
1	A	459	GLU
1	A	462	GLU
1	B	17	LEU
1	B	109	ASP
1	B	115	VAL
1	B	118	PHE
1	B	142	LYS
1	B	159	TYR
1	B	161	THR
1	B	167	ASP
1	B	175	ASP
1	B	177	LEU
1	B	182	LYS
1	B	183	HIS
1	B	199	THR
1	B	206	LEU
1	B	216	LEU
1	B	220	THR
1	B	235	ASP
1	B	236	ILE
1	B	237	ILE
1	B	238	ARG
1	B	257	HIS
1	B	277	LEU
1	B	283	GLU
1	B	284	LEU
1	B	343	CYS
1	B	345	GLN
1	B	354	LYS
1	B	377	GLN
1	B	379	GLU
1	B	463	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	14	GLN
1	A	375	GLN
1	B	111	ASN

### 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 ⓘ

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 for Mogul analysis.

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	502	1	14,14,15	0.28	0	17,19,21	0.40	0
3	NAG	A	503	1	14,14,15	0.20	0	17,19,21	0.42	0
3	NAG	B	502	1	14,14,15	0.26	0	17,19,21	0.50	0
3	NAG	B	504	1	14,14,15	0.28	0	17,19,21	1.37	2 (11%)
3	NAG	B	503	1	14,14,15	0.27	0	17,19,21	0.35	0
4	GOL	A	505	-	5,5,5	0.92	0	5,5,5	1.15	1 (20%)
4	GOL	A	504	-	5,5,5	0.91	0	5,5,5	1.13	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	502	1	-	0/6/23/26	0/1/1/1
3	NAG	A	503	1	-	2/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	B	502	1	-	2/6/23/26	0/1/1/1
3	NAG	B	504	1	-	4/6/23/26	0/1/1/1
3	NAG	B	503	1	-	4/6/23/26	0/1/1/1
4	GOL	A	505	-	-	0/4/4/4	-
4	GOL	A	504	-	-	0/4/4/4	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	504	NAG	C2-N2-C7	4.40	128.79	122.90
3	B	504	NAG	C1-C2-N2	2.24	113.96	110.43
4	A	505	GOL	C3-C2-C1	-2.09	104.12	111.80

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	NAG	C4-C5-C6-O6
3	A	503	NAG	O5-C5-C6-O6
3	B	503	NAG	O5-C5-C6-O6
3	B	503	NAG	C4-C5-C6-O6
3	B	503	NAG	C8-C7-N2-C2
3	B	503	NAG	O7-C7-N2-C2
3	B	504	NAG	C8-C7-N2-C2
3	B	504	NAG	O7-C7-N2-C2
3	B	502	NAG	C4-C5-C6-O6
3	B	502	NAG	O5-C5-C6-O6
3	B	504	NAG	C1-C2-N2-C7
3	B	504	NAG	C3-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	502	NAG	1	0
3	B	504	NAG	2	0
4	A	505	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	463/466 (99%)	0.22	10 (2%) 62 59	39, 72, 155, 219	1 (0%)
1	B	465/466 (99%)	0.58	33 (7%) 23 21	49, 85, 138, 226	0
All	All	928/932 (99%)	0.40	43 (4%) 38 35	39, 80, 146, 226	1 (0%)

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	201	VAL	4.7
1	B	169	VAL	3.9
1	B	202	PHE	3.5
1	B	163	PHE	3.5
1	A	401	PRO	3.4
1	B	118	PHE	3.3
1	B	181	VAL	3.2
1	B	198	ALA	3.2
1	A	36	PRO	3.2
1	B	463	LEU	3.2
1	B	115	VAL	3.1
1	B	139	VAL	3.1
1	B	151	ALA	3.1
1	A	1	GLY	3.0
1	A	450	PHE	3.0
1	B	213	THR	2.9
1	B	171	TRP	2.8
1	B	107	VAL	2.7
1	A	2	PRO	2.7
1	B	208	ALA	2.7
1	B	133	LEU	2.6
1	B	152	ALA	2.6
1	B	378	ALA	2.5
1	B	143	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	114	LEU	2.4
1	B	135	PHE	2.4
1	A	403	TRP	2.3
1	A	417	PRO	2.3
1	B	284	LEU	2.3
1	B	217	ILE	2.3
1	B	239	TYR	2.3
1	B	73	GLY	2.2
1	B	176	ALA	2.2
1	B	215	VAL	2.2
1	B	106	GLN	2.2
1	B	207	GLY	2.2
1	B	211	ASP	2.1
1	A	376	ALA	2.1
1	A	78	SER	2.1
1	B	178	LEU	2.1
1	B	119	ASP	2.1
1	B	145	ASN	2.1
1	A	31	LEU	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, 95<sup>th</sup> 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
4	GOL	A	504	6/6	0.77	0.16	88,101,110,114	0
3	NAG	A	502	14/15	0.80	0.10	89,108,114,115	0
3	NAG	A	503	14/15	0.83	0.13	87,107,122,133	0
4	GOL	A	505	6/6	0.85	0.15	79,83,90,97	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAG	B	503	14/15	0.86	0.10	81,90,103,109	0
3	NAG	B	502	14/15	0.94	0.08	42,54,64,70	0
3	NAG	B	504	14/15	0.95	0.08	46,57,67,70	0
2	CA	A	501	1/1	0.96	0.05	69,69,69,69	0
5	MG	B	501	1/1	0.99	0.04	62,62,62,62	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.