



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:01 PM GMT

PDB ID : 3VSX  
Title : Human renin in complex with compound 18  
Authors : Takahashi, M.; Hanzawa, H.  
Deposited on : 2012-05-11  
Resolution : 2.80 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 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

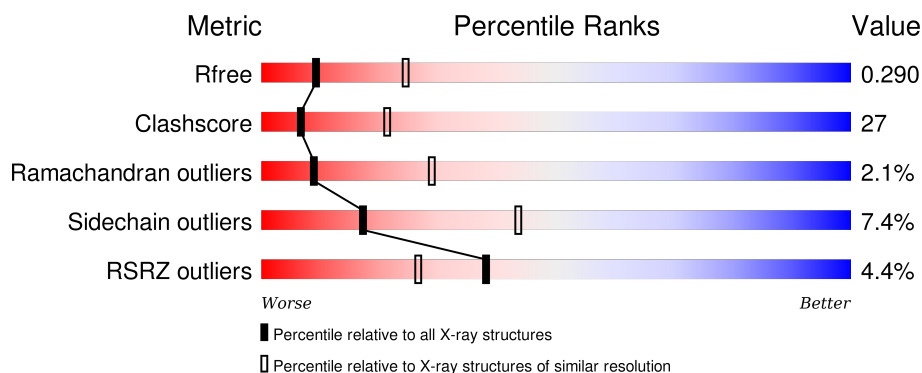
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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))
$R_{free}$	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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  $\geq 3$ , 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	A	340	<div> <div>5%</div> <div>56%</div> <div>40%</div> <div>.</div> </div>
1	B	340	<div> <div>4%</div> <div>57%</div> <div>36%</div> <div>7%</div> </div>

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5340 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 Renin.

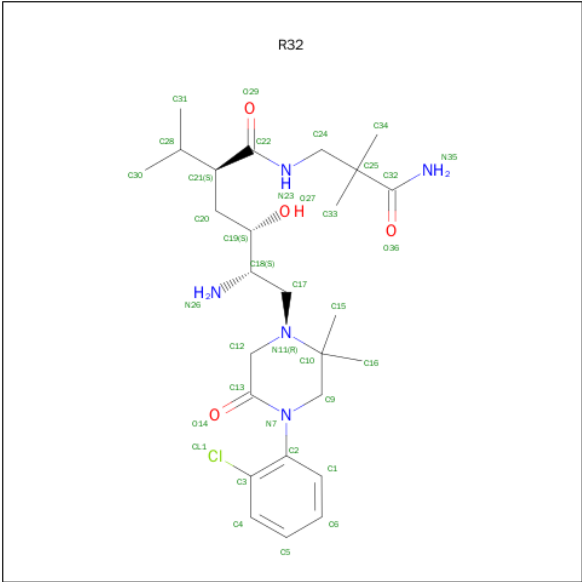
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	340	Total	C	N	O	S	0	0	0
			2620	1672	424	510	14			
1	B	340	Total	C	N	O	S	0	0	0
			2620	1672	424	510	14			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



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

- Molecule 3 is (2S,4S,5S)-5-AMINO-N-(3-AMINO-2,2-DIMETHYL-3-OXOPROPYL)-6-[4-(2-CHLOROPHENYL)-2,2-DIMETHYL-5-OXOPIPERAZIN-1-YL]-4-HYDROXY-2-(PROPAN-2-YL)HEXANAMIDE (three-letter code: R32) (formula:  $C_{26}H_{42}ClN_5O_4$ ).

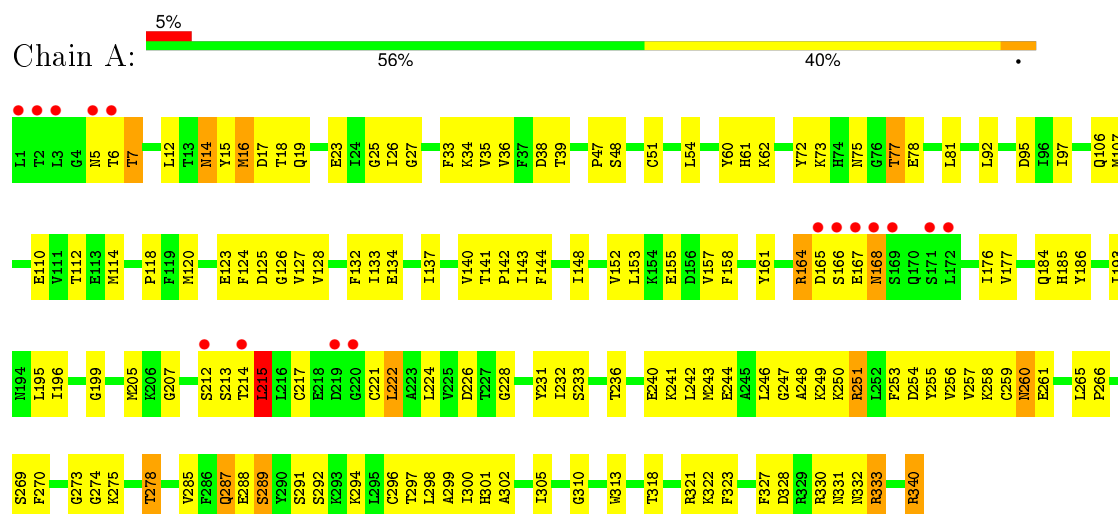


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 36	C 26	Cl 1	N 5	O 4	0	0
3	B	1	Total 36	C 26	Cl 1	N 5	O 4	0	0

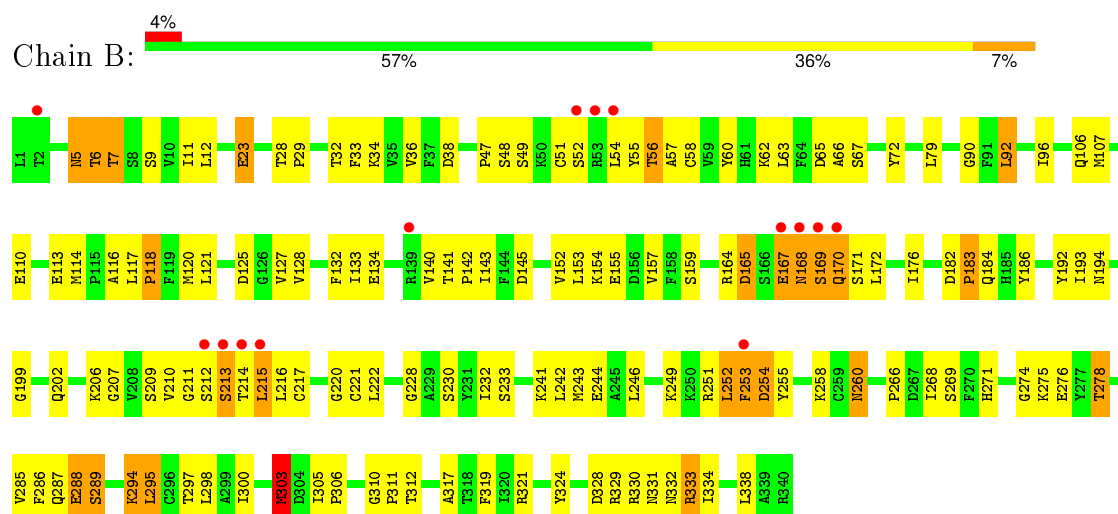
### 3 Residue-property plots

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 ( $\text{RSRZ} > 2$ ). 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: Renin



#### • Molecule 1: Renin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	138.19Å 138.19Å 138.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.74 – 2.80 27.10 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.0 (19.74-2.80) 99.0 (27.10-2.80)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	7.00 (at 2.80Å)	Xtriage
Refinement program	CNX 2000.1	Depositor
R, $R_{free}$	0.237 , 0.301 0.232 , 0.290	Depositor DCC
$R_{free}$ test set	2165 reflections (11.10%)	DCC
Wilson B-factor (Å <sup>2</sup> )	40.9	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 24.3	EDS
Estimated twinning fraction	0.055 for l,-k,h	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 21747 reflections	Xtriage
$F_o, F_c$ correlation	0.89	EDS
Total number of atoms	5340	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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, 0.375 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: NAG, R32

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	0.44	0/2680	0.68	0/3636
1	B	0.44	0/2680	0.71	0/3636
All	All	0.44	0/5360	0.69	0/7272

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

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	2620	0	2561	131	0
1	B	2620	0	2561	152	0
2	A	14	0	13	1	0
2	B	14	0	13	1	0
3	A	36	0	42	2	0
3	B	36	0	42	2	0
All	All	5340	0	5232	280	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 27.

All (280) 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:A:48:SER:HB2	1:A:110:GLU:HB3	1.49	0.93
1:A:157:VAL:HG12	1:A:328:ASP:HA	1.50	0.93
1:B:48:SER:HB2	1:B:110:GLU:HG2	1.52	0.91
1:A:215:LEU:H	1:A:215:LEU:HD23	1.38	0.88
1:A:75:ASN:OD1	1:A:77:THR:HG22	1.74	0.87
1:B:12:LEU:HD11	1:B:176:ILE:HG13	1.58	0.84
1:B:215:LEU:HD23	1:B:215:LEU:H	1.45	0.82
1:B:92:LEU:HD11	1:B:140:VAL:HG21	1.60	0.81
1:A:251:ARG:CB	1:A:251:ARG:HH11	1.95	0.79
1:A:250:LYS:HB2	1:A:255:TYR:CE2	2.20	0.76
1:B:79:LEU:HD13	1:B:92:LEU:HD21	1.67	0.76
1:A:166:SER:OG	1:B:170:GLN:HG2	1.87	0.75
1:A:14:ASN:HD21	1:A:17:ASP:H	1.30	0.75
1:A:77:THR:HG23	1:A:92:LEU:HD23	1.67	0.75
1:B:252:LEU:CG	1:B:253:PHE:H	1.99	0.74
1:B:252:LEU:HG	1:B:253:PHE:H	1.51	0.74
1:A:259:CYS:SG	1:A:294:LYS:HB3	2.27	0.74
1:B:6:THR:HB	1:B:152:VAL:O	1.88	0.73
1:A:251:ARG:HB3	1:A:251:ARG:HH11	1.53	0.73
1:B:210:VAL:HB	1:B:215:LEU:HD21	1.71	0.72
1:A:260:ASN:N	1:A:260:ASN:HD22	1.85	0.71
1:B:48:SER:CB	1:B:110:GLU:HG2	2.20	0.71
1:A:288:GLU:O	1:A:289:SER:HB3	1.91	0.70
1:B:294:LYS:HG3	1:B:295:LEU:H	1.57	0.70
1:B:96:ILE:O	1:B:96:ILE:HD12	1.92	0.70
1:A:164:ARG:HH11	1:A:164:ARG:HB3	1.57	0.69
1:B:258:LYS:HB3	1:B:260:ASN:ND2	2.08	0.69
1:B:155:GLU:HB2	1:B:157:VAL:HG22	1.73	0.68
1:A:14:ASN:HD22	1:A:14:ASN:C	1.95	0.68
1:B:154:LYS:NZ	1:B:154:LYS:HB3	2.09	0.68
1:B:194:ASN:HD22	1:B:333:ARG:HB3	1.58	0.67
1:B:249:LYS:NZ	1:B:251:ARG:HB3	2.09	0.67
1:A:106:GLN:OE1	1:A:143:ILE:HA	1.95	0.67
1:A:14:ASN:HD22	1:A:15:TYR:N	1.94	0.66
1:B:183:PRO:HA	1:B:186:TYR:CE1	2.31	0.66
1:B:157:VAL:HG12	1:B:328:ASP:HA	1.77	0.66
1:B:55:TYR:OH	1:B:113:GLU:HG2	1.95	0.66
1:A:213:SER:OG	1:A:215:LEU:HD22	1.96	0.66
1:A:92:LEU:HD11	1:A:140:VAL:HG21	1.77	0.66
1:A:148:ILE:HD12	1:A:153:LEU:HD12	1.77	0.65
1:A:243:MET:HG3	1:A:255:TYR:CD2	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:47:PRO:HG2	1:A:62:LYS:O	1.97	0.64
1:B:117:LEU:HD12	1:B:118:PRO:HA	1.78	0.64
1:A:269:SER:OG	1:A:278:THR:HB	1.97	0.64
1:B:32:THR:O	1:B:62:LYS:HD3	1.98	0.63
1:A:207:GLY:HA2	1:A:217:CYS:SG	2.38	0.63
1:A:231:TYR:CD2	1:A:301:HIS:CE1	2.88	0.62
1:A:265:LEU:CD1	1:A:266:PRO:HD2	2.29	0.62
1:B:258:LYS:HB3	1:B:260:ASN:HD21	1.61	0.62
1:A:26:ILE:HG12	1:A:97:ILE:HG12	1.81	0.62
1:B:286:PHE:HD2	1:B:297:THR:HG23	1.64	0.62
1:A:236:THR:O	1:A:240:GLU:HG3	1.99	0.62
1:B:258:LYS:HE3	1:B:260:ASN:HD21	1.65	0.61
1:B:260:ASN:N	1:B:260:ASN:HD22	1.98	0.61
1:B:206:LYS:HZ3	1:B:206:LYS:HB2	1.65	0.61
1:B:294:LYS:HA	1:B:294:LYS:HE3	1.83	0.61
1:B:11:ILE:HG23	1:B:172:LEU:CD1	2.31	0.61
1:A:143:ILE:HG23	1:A:144:PHE:N	2.16	0.61
1:A:14:ASN:HD21	1:A:17:ASP:N	1.99	0.60
1:A:196:ILE:HD12	1:A:222:LEU:HD23	1.82	0.60
1:B:328:ASP:HB3	1:B:333:ARG:HG3	1.83	0.60
1:B:133:ILE:HG22	1:B:134:GLU:OE1	2.01	0.60
1:B:133:ILE:HG13	1:B:142:PRO:HD3	1.84	0.60
1:B:269:SER:OG	1:B:278:THR:HB	2.02	0.59
1:A:288:GLU:O	1:A:289:SER:CB	2.50	0.59
1:A:260:ASN:H	1:A:260:ASN:HD22	1.50	0.59
1:B:56:THR:HG1	1:B:60:TYR:HE2	1.49	0.59
1:B:164:ARG:O	1:B:165:ASP:C	2.41	0.59
1:B:169:SER:O	1:B:170:GLN:C	2.41	0.59
1:B:217:CYS:O	1:B:217:CYS:SG	2.60	0.59
1:B:65:ASP:OD1	1:B:67:SER:HB3	2.03	0.58
1:A:305:ILE:O	1:A:310:GLY:HA3	2.03	0.58
1:B:331:ASN:HB2	1:B:333:ARG:CG	2.33	0.58
1:B:164:ARG:HA	1:B:321:ARG:HD2	1.84	0.58
1:A:14:ASN:ND2	1:A:17:ASP:H	2.00	0.58
1:B:165:ASP:OD2	1:B:168:ASN:HB3	2.04	0.58
1:A:12:LEU:HD11	1:A:176:ILE:HG13	1.86	0.57
1:B:5:ASN:ND2	1:B:5:ASN:O	2.38	0.56
1:A:213:SER:O	1:A:215:LEU:HD23	2.05	0.56
2:B:401:NAG:H83	2:B:401:NAG:O3	2.05	0.56
1:A:265:LEU:HD13	1:A:266:PRO:HD2	1.87	0.56
1:B:331:ASN:HB2	1:B:333:ARG:HG2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:ASN:HA	1:B:154:LYS:HG2	1.87	0.56
1:A:27:GLY:HA2	1:A:95:ASP:OD1	2.05	0.56
1:B:96:ILE:HD12	1:B:96:ILE:C	2.26	0.56
1:A:260:ASN:ND2	1:A:261:GLU:H	2.04	0.56
1:B:243:MET:HG3	1:B:255:TYR:CD2	2.41	0.56
1:A:231:TYR:HB3	1:A:299:ALA:O	2.06	0.56
1:B:142:PRO:HB2	1:B:145:ASP:OD2	2.06	0.56
1:A:236:THR:HA	1:A:302:ALA:HB1	1.88	0.55
1:A:132:PHE:HB2	1:A:199:GLY:HA2	1.87	0.55
1:B:246:LEU:HD11	1:B:268:ILE:HD11	1.86	0.55
1:B:252:LEU:HD12	1:B:253:PHE:N	2.21	0.55
1:A:287:GLN:O	1:A:296:CYS:SG	2.65	0.55
1:A:260:ASN:ND2	1:A:260:ASN:N	2.54	0.55
1:A:205:MET:HG2	1:A:221:CYS:SG	2.47	0.55
1:A:72:TYR:O	1:A:73:LYS:HD3	2.06	0.55
1:B:47:PRO:HB3	1:B:114:MET:CE	2.37	0.55
1:A:34:LYS:NZ	1:A:123:GLU:OE1	2.40	0.54
1:A:6:THR:HG22	1:A:7:THR:N	2.21	0.54
1:A:38:ASP:OD1	1:A:228:GLY:HA3	2.07	0.54
1:B:57:ALA:HB3	1:B:114:MET:HG3	1.89	0.54
1:A:248:ALA:HA	1:A:257:VAL:HG12	1.89	0.54
1:A:14:ASN:ND2	1:A:14:ASN:C	2.61	0.54
1:B:329:ARG:HG2	1:B:329:ARG:HH11	1.73	0.54
1:A:195:LEU:HG	1:A:332:ASN:O	2.08	0.54
1:B:249:LYS:HZ3	1:B:251:ARG:HB3	1.71	0.54
1:A:251:ARG:HG2	1:A:254:ASP:OD1	2.08	0.54
1:B:6:THR:CG2	1:B:7:THR:N	2.71	0.54
1:B:36:VAL:HG21	3:B:402:R32:H12	1.89	0.53
1:B:211:GLY:HA2	1:B:266:PRO:HB2	1.89	0.53
1:B:159:SER:HB3	1:B:324:TYR:CE1	2.43	0.53
1:B:118:PRO:HA	1:B:121:LEU:HD12	1.90	0.53
1:A:133:ILE:HG22	1:A:134:GLU:OE1	2.10	0.52
1:B:285:VAL:HG22	1:B:298:LEU:CD2	2.38	0.52
1:A:256:VAL:HG12	1:A:297:THR:HA	1.92	0.52
1:B:285:VAL:HG22	1:B:298:LEU:HD21	1.91	0.52
1:A:232:ILE:HG13	1:A:318:THR:HB	1.90	0.52
1:A:260:ASN:ND2	1:A:260:ASN:H	2.07	0.52
1:B:305:ILE:O	1:B:310:GLY:HA3	2.10	0.52
1:A:155:GLU:HB2	1:A:157:VAL:HG22	1.92	0.52
1:A:17:ASP:O	1:A:321:ARG:NH1	2.43	0.52
1:B:243:MET:HG3	1:B:255:TYR:CG	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:132:PHE:CB	1:A:199:GLY:HA2	2.40	0.51
1:A:259:CYS:HB2	1:A:291:SER:O	2.09	0.51
1:B:249:LYS:O	1:B:255:TYR:HA	2.10	0.51
1:A:81:LEU:HA	1:A:137:ILE:HD12	1.92	0.51
1:B:116:ALA:O	1:B:120:MET:HB2	2.10	0.51
1:A:340:ARG:HH12	1:B:7:THR:CG2	2.23	0.51
1:A:81:LEU:HD23	1:A:137:ILE:HD12	1.92	0.51
1:B:252:LEU:O	1:B:254:ASP:N	2.44	0.51
1:B:164:ARG:HG2	1:B:321:ARG:HG2	1.93	0.51
1:A:260:ASN:HD22	1:A:261:GLU:H	1.58	0.51
1:A:39:THR:HG21	1:A:327:PHE:CZ	2.45	0.51
1:A:328:ASP:OD2	1:A:333:ARG:HD2	2.10	0.51
1:B:154:LYS:HZ2	1:B:154:LYS:HB3	1.75	0.51
1:B:249:LYS:HZ2	1:B:251:ARG:HB3	1.76	0.51
1:A:15:TYR:HB3	1:A:19:GLN:HB2	1.91	0.51
1:A:260:ASN:OD1	1:A:292:SER:HB3	2.11	0.51
1:A:215:LEU:H	1:A:215:LEU:CD2	2.16	0.50
1:B:252:LEU:CG	1:B:253:PHE:N	2.71	0.50
1:B:252:LEU:CD1	1:B:253:PHE:H	2.24	0.50
1:B:58:CYS:O	1:B:63:LEU:HD21	2.12	0.50
1:A:6:THR:CG2	1:A:7:THR:N	2.75	0.50
1:A:242:LEU:O	1:A:246:LEU:HG	2.11	0.50
1:B:55:TYR:CZ	1:B:113:GLU:HG2	2.46	0.50
1:A:195:LEU:HG	1:A:332:ASN:C	2.32	0.49
1:A:6:THR:HB	1:A:152:VAL:O	2.12	0.49
1:B:216:LEU:HD21	1:B:241:LYS:HB2	1.93	0.49
1:B:194:ASN:ND2	1:B:333:ARG:HB3	2.25	0.49
1:B:213:SER:O	1:B:215:LEU:HD23	2.12	0.49
1:B:92:LEU:HD12	1:B:107:MET:HG3	1.93	0.49
2:A:401:NAG:O3	2:A:401:NAG:H83	2.13	0.49
1:B:132:PHE:HB2	1:B:199:GLY:O	2.12	0.49
1:A:265:LEU:HD12	1:A:266:PRO:HD2	1.95	0.49
1:B:206:LYS:NZ	1:B:271:HIS:CG	2.80	0.49
1:A:331:ASN:HB2	1:A:333:ARG:CG	2.43	0.49
1:B:206:LYS:NZ	1:B:271:HIS:CE1	2.81	0.49
1:A:241:LYS:O	1:A:244:GLU:HB3	2.14	0.48
1:A:166:SER:HG	1:B:170:GLN:HG2	1.79	0.48
1:B:206:LYS:HZ3	1:B:271:HIS:CE1	2.32	0.48
1:B:54:LEU:HD12	1:B:54:LEU:HA	1.61	0.48
1:B:118:PRO:CA	1:B:121:LEU:HD12	2.43	0.48
1:A:331:ASN:HB2	1:A:333:ARG:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:LEU:HD11	1:B:176:ILE:CG1	2.37	0.48
1:B:331:ASN:CB	1:B:333:ARG:HG2	2.43	0.48
1:B:48:SER:HB2	1:B:110:GLU:CG	2.35	0.48
1:B:269:SER:HB3	1:B:276:GLU:OE2	2.14	0.48
1:B:23:GLU:OE1	1:B:34:LYS:HG2	2.14	0.47
1:A:17:ASP:HB3	1:A:321:ARG:NH1	2.29	0.47
1:A:288:GLU:N	1:B:167:GLU:HG3	2.29	0.47
1:B:11:ILE:HG23	1:B:172:LEU:HD11	1.96	0.47
1:A:322:LYS:HG2	1:A:323:PHE:CE2	2.49	0.47
1:A:16:MET:O	1:A:18:THR:HG23	2.13	0.47
1:B:47:PRO:HB3	1:B:114:MET:HE1	1.95	0.47
1:A:39:THR:HG21	1:A:327:PHE:CE2	2.49	0.47
1:A:214:THR:O	1:A:214:THR:HG23	2.13	0.47
1:B:298:LEU:C	1:B:300:ILE:H	2.16	0.47
1:B:230:SER:O	1:B:317:ALA:HB3	2.14	0.47
1:A:224:LEU:C	1:A:224:LEU:HD23	2.34	0.47
1:B:106:GLN:OE1	1:B:143:ILE:HA	2.15	0.47
1:B:6:THR:HG22	1:B:153:LEU:HD23	1.96	0.47
1:A:305:ILE:HD12	1:A:305:ILE:N	2.29	0.47
1:A:193:ILE:HG13	1:A:273:GLY:HA3	1.96	0.47
1:A:167:GLU:O	1:A:168:ASN:HB2	2.15	0.47
1:A:242:LEU:O	1:A:242:LEU:HD23	2.14	0.47
1:A:328:ASP:HB3	1:A:333:ARG:HG3	1.97	0.47
1:B:285:VAL:O	1:B:287:GLN:N	2.48	0.46
1:B:168:ASN:O	1:B:170:GLN:N	2.48	0.46
1:B:311:PRO:O	1:B:312:THR:HB	2.15	0.46
1:A:186:TYR:N	1:A:340:ARG:HG2	2.31	0.46
1:B:232:ILE:HD11	1:B:319:PHE:HB2	1.97	0.46
1:A:287:GLN:HB3	1:B:167:GLU:CD	2.36	0.46
1:A:258:LYS:CB	1:A:260:ASN:HD21	2.29	0.46
1:B:212:SER:C	1:B:213:SER:OG	2.54	0.46
1:B:288:GLU:O	1:B:289:SER:HB3	2.16	0.46
1:B:6:THR:HG23	1:B:7:THR:N	2.32	0.45
1:A:242:LEU:C	1:A:242:LEU:HD23	2.36	0.45
1:B:206:LYS:HB2	1:B:206:LYS:NZ	2.30	0.45
1:A:258:LYS:HB2	1:A:260:ASN:HD21	1.82	0.45
1:A:259:CYS:CB	1:A:296:CYS:HG	2.26	0.45
1:B:209:SER:HA	1:B:214:THR:HA	1.98	0.45
1:B:215:LEU:H	1:B:215:LEU:CD2	2.24	0.45
1:A:253:PHE:O	1:A:254:ASP:HB3	2.17	0.45
1:B:328:ASP:OD2	1:B:333:ARG:HD2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:PRO:HD3	1:B:125:ASP:O	2.17	0.45
1:A:196:ILE:CD1	1:A:222:LEU:HD23	2.45	0.45
1:B:260:ASN:HD22	1:B:260:ASN:H	1.63	0.44
1:B:66:ALA:HB1	1:B:72:TYR:CD1	2.52	0.44
1:A:243:MET:O	1:A:247:GLY:N	2.48	0.44
1:B:206:LYS:HE2	1:B:274:GLY:H	1.81	0.44
1:A:60:TYR:CG	1:A:120:MET:HE3	2.52	0.44
1:A:92:LEU:HD12	1:A:107:MET:HG3	2.00	0.44
1:A:51:CYS:HB2	1:A:112:THR:HA	2.00	0.44
1:A:205:MET:HE3	1:A:270:PHE:HD2	1.83	0.44
1:A:274:GLY:O	1:A:275:LYS:HD2	2.18	0.44
1:A:243:MET:HG3	1:A:255:TYR:CE2	2.53	0.44
1:B:305:ILE:HG12	3:B:402:R32:H31	2.00	0.44
1:B:92:LEU:HD12	1:B:107:MET:CG	2.48	0.44
1:A:47:PRO:HD3	1:A:125:ASP:O	2.18	0.44
1:A:155:GLU:CB	1:A:157:VAL:HG22	2.49	0.43
1:B:275:LYS:HG2	1:B:276:GLU:N	2.33	0.43
1:B:193:ILE:HD12	1:B:193:ILE:N	2.33	0.43
1:B:317:ALA:O	1:B:321:ARG:HB2	2.19	0.43
1:B:182:ASP:HA	1:B:183:PRO:HD2	1.87	0.43
1:A:165:ASP:OD2	1:A:168:ASN:HB2	2.18	0.43
1:B:186:TYR:HA	1:B:338:LEU:O	2.18	0.43
1:B:206:LYS:HZ3	1:B:271:HIS:CG	2.36	0.43
1:B:23:GLU:HA	1:B:33:PHE:O	2.19	0.43
1:B:252:LEU:HD12	1:B:253:PHE:H	1.84	0.43
1:B:331:ASN:O	1:B:332:ASN:C	2.57	0.43
1:A:217:CYS:SG	1:A:217:CYS:O	2.76	0.43
1:A:184:GLN:O	1:A:340:ARG:HD2	2.19	0.43
1:A:166:SER:H	1:B:170:GLN:HB3	1.84	0.43
1:A:251:ARG:NH2	1:A:256:VAL:HG11	2.34	0.42
1:A:35:VAL:HA	1:A:126:GLY:O	2.19	0.42
1:B:207:GLY:H	1:B:271:HIS:HB3	1.84	0.42
1:A:233:SER:O	1:A:313:TRP:HA	2.19	0.42
1:A:226:ASP:C	1:A:228:GLY:H	2.21	0.42
1:B:329:ARG:NH1	1:B:329:ARG:HG2	2.32	0.42
1:B:305:ILE:HA	1:B:306:PRO:HD3	1.86	0.42
1:B:233:SER:HB2	1:B:303:MET:HB3	2.00	0.42
1:B:92:LEU:HD11	1:B:140:VAL:CG2	2.40	0.42
1:B:118:PRO:O	1:B:121:LEU:HD12	2.19	0.42
1:B:294:LYS:HG3	1:B:295:LEU:N	2.29	0.42
1:B:118:PRO:O	1:B:121:LEU:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:206:LYS:CE	1:B:274:GLY:H	2.32	0.42
1:A:161:TYR:CD1	1:A:185:HIS:HB3	2.54	0.42
1:B:47:PRO:HG2	1:B:62:LYS:O	2.20	0.42
1:B:127:VAL:HG12	1:B:128:VAL:N	2.35	0.42
1:A:285:VAL:HG22	1:A:298:LEU:HD22	2.02	0.42
1:B:79:LEU:HB2	1:B:92:LEU:HD23	2.01	0.42
1:B:159:SER:HB3	1:B:324:TYR:HE1	1.84	0.42
1:B:28:THR:HA	1:B:29:PRO:C	2.38	0.42
1:B:182:ASP:C	1:B:184:GLN:H	2.23	0.41
1:B:202:GLN:NE2	1:B:222:LEU:HB3	2.36	0.41
1:A:127:VAL:HG12	1:A:128:VAL:N	2.35	0.41
1:B:79:LEU:N	1:B:90:GLY:O	2.49	0.41
1:A:260:ASN:ND2	1:A:261:GLU:N	2.67	0.41
1:A:251:ARG:NH1	1:A:251:ARG:HB3	2.29	0.41
1:A:133:ILE:HG23	1:A:134:GLU:N	2.36	0.41
1:A:143:ILE:CG2	1:A:144:PHE:N	2.81	0.41
1:B:310:GLY:HA2	1:B:311:PRO:C	2.41	0.41
1:B:298:LEU:HD23	1:B:298:LEU:HA	1.81	0.41
1:A:23:GLU:HA	1:A:33:PHE:O	2.21	0.41
3:A:402:R32:H10	3:A:402:R32:H16	1.85	0.41
1:A:141:THR:HA	1:A:142:PRO:HD3	1.88	0.41
1:A:298:LEU:C	1:A:300:ILE:H	2.24	0.41
1:B:38:ASP:OD1	1:B:228:GLY:HA3	2.20	0.41
1:B:192:TYR:HA	1:B:334:ILE:O	2.21	0.41
1:B:220:GLY:O	1:B:221:CYS:HB3	2.21	0.40
1:A:25:GLY:O	1:A:97:ILE:HA	2.21	0.40
1:A:36:VAL:HG21	3:A:402:R32:H12	2.04	0.40
1:A:158:PHE:HA	1:A:177:VAL:O	2.21	0.40
1:B:252:LEU:C	1:B:254:ASP:H	2.25	0.40
1:B:254:ASP:OD1	1:B:254:ASP:N	2.53	0.40
1:B:167:GLU:OE1	1:B:167:GLU:HA	2.22	0.40
1:B:141:THR:HA	1:B:142:PRO:HD3	1.94	0.40
1:B:49:SER:C	1:B:51:CYS:H	2.24	0.40
1:A:61:HIS:CD2	1:A:124:PHE:O	2.75	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	338/340 (99%)	310 (92%)	23 (7%)	5 (2%)	13	40
1	B	338/340 (99%)	309 (91%)	20 (6%)	9 (3%)	6	21
All	All	676/680 (99%)	619 (92%)	43 (6%)	14 (2%)	9	29

All (14) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	168	ASN
1	A	212	SER
1	A	287	GLN
1	A	289	SER
1	B	168	ASN
1	B	170	GLN
1	A	215	LEU
1	B	169	SER
1	B	253	PHE
1	B	303	MET
1	B	165	ASP
1	B	289	SER
1	B	171	SER
1	B	183	PRO

### 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	290/290 (100%)	271 (93%)	19 (7%)	21	51
1	B	290/290 (100%)	266 (92%)	24 (8%)	14	38
All	All	580/580 (100%)	537 (93%)	43 (7%)	17	43

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	7	THR
1	A	14	ASN
1	A	16	MET
1	A	54	LEU
1	A	77	THR
1	A	78	GLU
1	A	114	MET
1	A	118	PRO
1	A	164	ARG
1	A	215	LEU
1	A	222	LEU
1	A	249	LYS
1	A	251	ARG
1	A	260	ASN
1	A	278	THR
1	A	330	ARG
1	A	333	ARG
1	A	340	ARG
1	B	5	ASN
1	B	6	THR
1	B	7	THR
1	B	9	SER
1	B	23	GLU
1	B	52	SER
1	B	56	THR
1	B	92	LEU
1	B	118	PRO
1	B	167	GLU
1	B	213	SER
1	B	215	LEU
1	B	242	LEU
1	B	244	GLU
1	B	252	LEU
1	B	254	ASP

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Mol	Chain	Res	Type
1	B	260	ASN
1	B	278	THR
1	B	288	GLU
1	B	294	LYS
1	B	295	LEU
1	B	303	MET
1	B	330	ARG
1	B	333	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	ASN
1	A	14	ASN
1	A	150	GLN
1	A	170	GLN
1	A	175	GLN
1	A	185	HIS
1	A	191	HIS
1	A	260	ASN
1	B	5	ASN
1	B	168	ASN
1	B	194	ASN
1	B	202	GLN
1	B	204	GLN
1	B	260	ASN
1	B	301	HIS

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry

4 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$
2	NAG	A	401	1	14,14,15	0.64	0	15,19,21	0.93	1 (6%)
3	R32	A	402	-	36,37,37	0.99	3 (8%)	34,55,55	1.14	3 (8%)
2	NAG	B	401	1	14,14,15	0.63	0	15,19,21	0.67	0
3	R32	B	402	-	36,37,37	1.13	3 (8%)	34,55,55	1.11	2 (5%)

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	NAG	A	401	1	-	0/6/23/26	0/1/1/1
3	R32	A	402	-	-	0/35/55/55	0/2/2/2
2	NAG	B	401	1	-	0/6/23/26	0/1/1/1
3	R32	B	402	-	-	0/35/55/55	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	R32	C10-N11	-3.53	1.44	1.49
3	B	402	R32	C12-N11	-3.34	1.44	1.47
3	B	402	R32	C2-N7	-3.26	1.39	1.44
3	A	402	R32	C2-N7	-3.13	1.39	1.44
3	A	402	R32	C12-N11	-2.90	1.45	1.47
3	A	402	R32	C10-N11	-2.37	1.46	1.49

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	402	R32	C24-N23-C22	-3.42	117.21	122.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	R32	C24-N23-C22	-3.34	117.33	122.77
2	A	401	NAG	C2-N2-C7	-2.45	119.89	123.04
3	A	402	R32	C25-C24-N23	-2.16	109.87	113.99
3	A	402	R32	C12-N11-C17	3.11	116.12	111.05
3	B	402	R32	C12-N11-C17	3.42	116.62	111.05

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	NAG	1	0
3	A	402	R32	2	0
2	B	401	NAG	1	0
3	B	402	R32	2	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	340/340 (100%)	-0.00	16 (4%) 35 24	14, 31, 51, 65	0
1	B	340/340 (100%)	0.05	14 (4%) 41 29	14, 32, 50, 67	0
All	All	680/680 (100%)	0.02	30 (4%) 38 26	14, 31, 50, 67	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	167	GLU	5.9
1	A	214	THR	4.4
1	B	212	SER	4.3
1	A	165	ASP	4.2
1	B	54	LEU	4.2
1	B	253	PHE	3.8
1	A	167	GLU	3.8
1	B	169	SER	3.6
1	B	214	THR	3.6
1	B	52	SER	3.3
1	B	170	GLN	3.1
1	A	5	ASN	2.9
1	A	169	SER	2.8
1	B	213	SER	2.8
1	B	215	LEU	2.7
1	A	1	LEU	2.6
1	A	2	THR	2.5
1	A	172	LEU	2.5
1	B	168	ASN	2.5
1	A	212	SER	2.4
1	A	171	SER	2.2
1	A	220	GLY	2.2
1	A	3	LEU	2.2
1	A	166	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	219	ASP	2.1
1	A	168	ASN	2.1
1	B	2	THR	2.0
1	B	53	ARG	2.0
1	A	6	THR	2.0
1	B	139	ARG	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 carbohydrates 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. 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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	R32	B	402	36/36	0.92	0.20	0.34	19,34,43,46	0
3	R32	A	402	36/36	0.95	0.15	-0.64	20,25,29,33	0
2	NAG	B	401	14/15	0.71	0.30	-	51,54,55,55	0
2	NAG	A	401	14/15	0.84	0.24	-	40,42,43,46	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.