



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 10:11 pm GMT

PDB ID : 1R1H  
Title : STRUCTURAL ANALYSIS OF NEPRILYSIN WITH VARIOUS SPECIFIC  
AND POTENT INHIBITORS  
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Deposited on : 2003-09-24  
Resolution : 1.95 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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

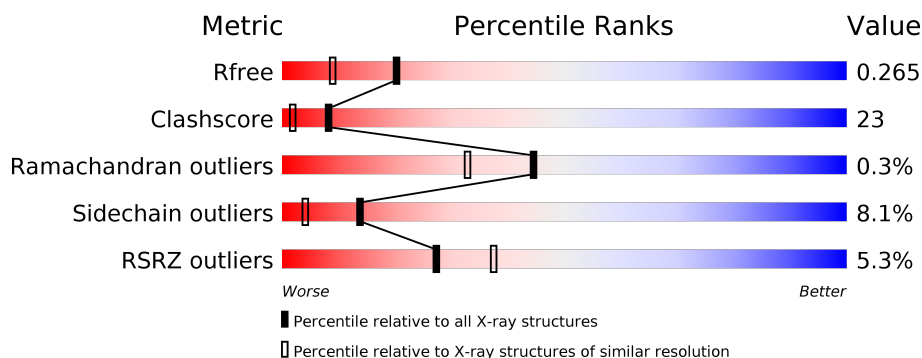
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.95 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))
$R_{free}$	100719	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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	696	<div> <div>5%</div> <div>68%</div> <div>28%</div> <div>.</div> </div>

## 2 Entry composition [i](#)

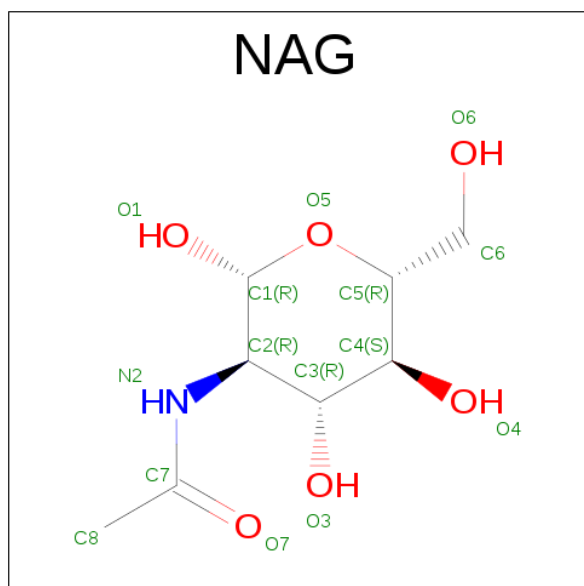
There are 5 unique types of molecules in this entry. The entry contains 5962 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Neprilysin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	696	5595	3538	957	1074	26	0	0	0

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

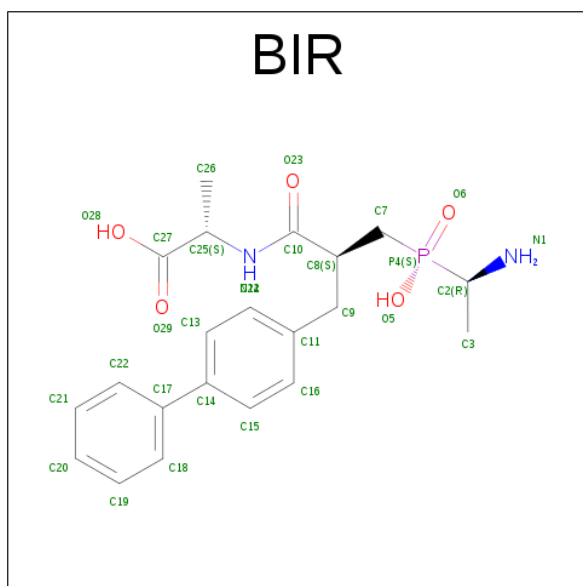


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	14	8	1	5	0	0
2	A	1	14	8	1	5	0	0
2	A	1	14	8	1	5	0	0

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is N-[3-[(1-AMINOETHYL)(HYDROXY)PHOSPHORYL]-2-(1,1'-BIPHENYL-4-YLMETHYL)PROPANOYL]ALANINE (three-letter code: BIR) (formula: C<sub>21</sub>H<sub>27</sub>N<sub>2</sub>O<sub>5</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			29	21	2	5	1		

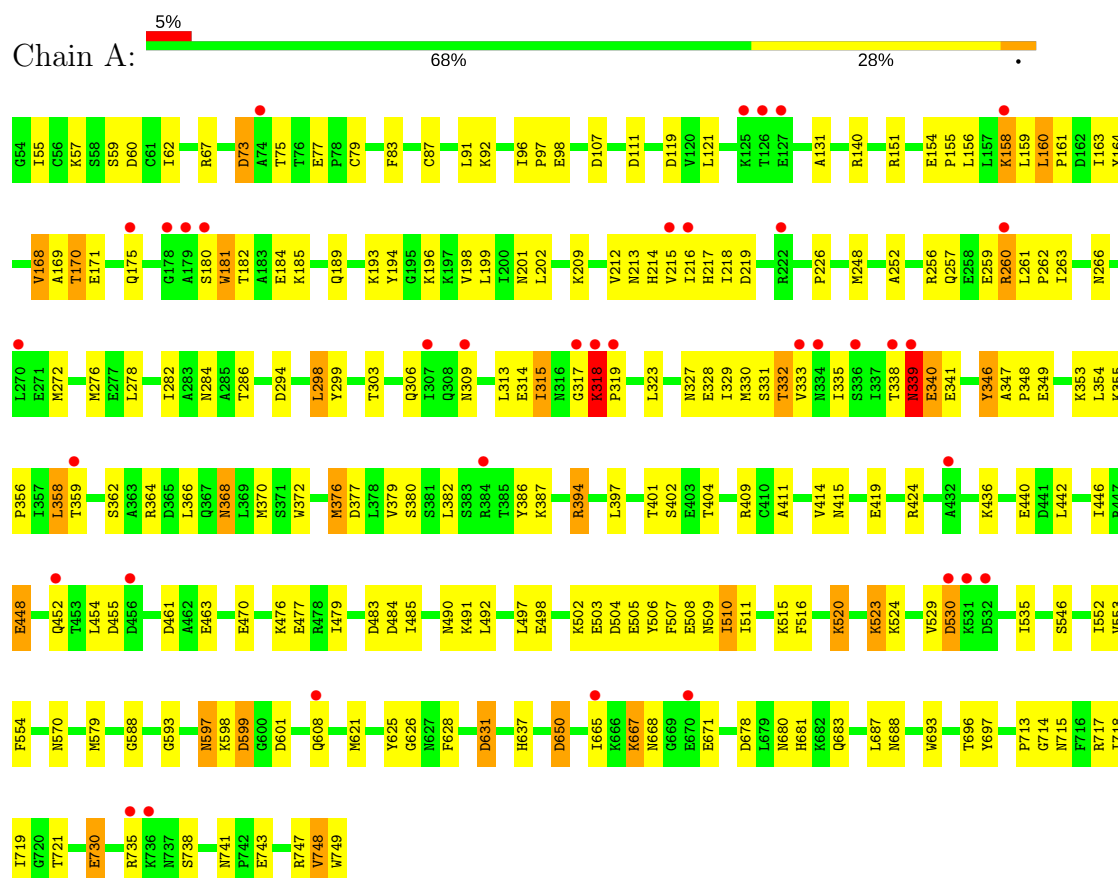
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	295	Total	O	0	0
			295	295		

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

These plots are drawn for all protein, RNA and DNA 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 ( $\text{RSRZ} > 2$ ). 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: Neprilysin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	107.79Å 107.79Å 113.09Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 1.95 17.92 – 1.95	Depositor EDS
% Data completeness (in resolution range)	96.0 (20.00-1.95) 96.0 (17.92-1.95)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.76 (at 1.96Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.209 , 0.260 0.216 , 0.265	Depositor DCC
$R_{free}$ test set	2707 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	25.2	Xtriage
Anisotropy	0.085	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.39 , 53.7	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.019 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	5962	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.01% 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: ZN, BIR, 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	0.36	0/5713	0.62	14/7727 (0.2%)

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	A	0	1

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	631	ASP	CB-CG-OD2	7.37	124.93	118.30
1	A	650	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	504	ASP	CB-CG-OD2	6.28	123.95	118.30
1	A	73	ASP	CB-CG-OD2	6.06	123.76	118.30
1	A	461	ASP	CB-CG-OD2	5.90	123.61	118.30
1	A	377	ASP	CB-CG-OD2	5.81	123.53	118.30
1	A	111	ASP	CB-CG-OD2	5.72	123.45	118.30
1	A	294	ASP	CB-CG-OD2	5.67	123.41	118.30
1	A	455	ASP	CB-CG-OD2	5.58	123.33	118.30
1	A	678	ASP	CB-CG-OD2	5.40	123.16	118.30
1	A	60	ASP	CB-CG-OD2	5.38	123.15	118.30
1	A	107	ASP	CB-CG-OD2	5.32	123.08	118.30
1	A	530	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	599	ASP	CB-CG-OD2	5.07	122.87	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	TRP	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	5595	0	5447	262	8
2	A	42	0	39	1	0
3	A	1	0	0	0	0
4	A	29	0	25	0	0
5	A	295	0	0	18	2
All	All	5962	0	5511	262	10

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 23.

All (262) 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:714:GLY:O	1:A:718:ILE:CD1	1.74	1.32
1:A:714:GLY:O	1:A:718:ILE:HD12	1.21	1.27
1:A:318:LYS:HB3	1:A:319:PRO:C	1.65	1.17
1:A:523:LYS:HZ2	1:A:523:LYS:CB	1.58	1.13
1:A:323:LEU:HD22	1:A:339:ASN:OD1	1.46	1.12
1:A:523:LYS:HZ2	1:A:523:LYS:HB2	1.14	1.12
1:A:523:LYS:NZ	1:A:523:LYS:CB	2.04	1.11
1:A:715:ASN:O	1:A:719:ILE:HD12	1.51	1.09
1:A:523:LYS:HB3	1:A:523:LYS:NZ	1.62	1.09
1:A:202:LEU:HD21	1:A:216:ILE:CG2	1.85	1.06
1:A:507:PHE:HA	1:A:510:ILE:HD13	1.37	1.06
1:A:284:ASN:OD1	5:A:2270:HOH:O	1.73	1.04
1:A:318:LYS:HB3	1:A:319:PRO:O	1.54	1.03
1:A:131:ALA:CB	1:A:492:LEU:CD1	2.37	1.01
1:A:131:ALA:CB	1:A:492:LEU:HD12	1.92	1.00
1:A:168:VAL:HG12	1:A:368:ASN:ND2	1.75	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:GLU:OE1	1:A:158:LYS:CE	2.11	0.99
1:A:168:VAL:H	1:A:368:ASN:HD21	1.13	0.96
1:A:156:LEU:O	1:A:156:LEU:HD23	1.66	0.95
1:A:318:LYS:HB3	1:A:319:PRO:CA	1.94	0.94
1:A:507:PHE:HA	1:A:510:ILE:CD1	1.98	0.94
1:A:523:LYS:HB3	1:A:523:LYS:HZ3	1.24	0.93
1:A:516:PHE:CE1	1:A:520:LYS:HE2	2.06	0.91
1:A:318:LYS:CB	1:A:319:PRO:CA	2.48	0.91
1:A:730:GLU:OE2	1:A:730:GLU:O	1.90	0.88
1:A:131:ALA:HB1	1:A:492:LEU:CD1	2.01	0.88
1:A:202:LEU:HD22	1:A:217:HIS:O	1.73	0.88
1:A:354:LEU:HG	1:A:358:LEU:HD22	1.56	0.88
1:A:355:LYS:O	1:A:359:THR:HG23	1.73	0.87
1:A:349:GLU:HG3	5:A:2158:HOH:O	1.74	0.86
1:A:404:THR:CG2	1:A:409:ARG:CG	2.53	0.86
1:A:154:GLU:OE1	1:A:158:LYS:HE3	1.73	0.86
1:A:199:LEU:CD1	1:A:370:MET:HE1	2.07	0.85
1:A:380:SER:O	1:A:387:LYS:NZ	2.11	0.84
1:A:404:THR:CG2	1:A:409:ARG:HG3	2.07	0.83
1:A:199:LEU:HD12	1:A:370:MET:HE1	1.61	0.83
1:A:96:ILE:HD11	1:A:696:THR:HG23	1.60	0.83
1:A:516:PHE:CE1	1:A:520:LYS:CE	2.61	0.83
1:A:318:LYS:CB	1:A:319:PRO:HA	2.08	0.82
1:A:404:THR:HG22	1:A:409:ARG:CG	2.10	0.82
1:A:505:GLU:HB3	1:A:508:GLU:OE1	1.79	0.82
1:A:193:LYS:CE	1:A:515:LYS:HZ3	1.93	0.80
1:A:546:SER:OG	5:A:2083:HOH:O	1.98	0.80
1:A:154:GLU:OE1	1:A:158:LYS:HE2	1.82	0.80
1:A:333:VAL:HG12	1:A:333:VAL:O	1.80	0.80
1:A:131:ALA:HB3	1:A:492:LEU:HD12	1.64	0.78
1:A:338:THR:O	1:A:341:GLU:N	2.17	0.77
1:A:156:LEU:HD22	1:A:160:LEU:HD22	1.65	0.77
1:A:484:ASP:OD1	1:A:491:LYS:NZ	2.13	0.77
1:A:184:GLU:OE2	1:A:318:LYS:HE2	1.85	0.76
1:A:193:LYS:HE2	1:A:515:LYS:NZ	1.99	0.76
1:A:440:GLU:HG3	1:A:479:ILE:HD13	1.66	0.75
1:A:318:LYS:CB	1:A:319:PRO:C	2.51	0.75
1:A:323:LEU:CD2	1:A:339:ASN:OD1	2.33	0.75
1:A:168:VAL:CG1	1:A:368:ASN:ND2	2.49	0.75
1:A:184:GLU:N	1:A:184:GLU:OE1	2.19	0.75
1:A:202:LEU:HD21	1:A:216:ILE:HG22	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:THR:HG22	1:A:340:GLU:CD	2.08	0.74
1:A:315:ILE:CD1	1:A:315:ILE:N	2.50	0.73
1:A:193:LYS:NZ	1:A:515:LYS:NZ	2.36	0.73
1:A:202:LEU:HD23	1:A:218:ILE:HD13	1.70	0.73
1:A:748:VAL:HG13	5:A:2140:HOH:O	1.89	0.73
1:A:202:LEU:HD23	1:A:218:ILE:CD1	2.19	0.73
1:A:199:LEU:HD11	1:A:370:MET:CE	2.19	0.73
1:A:131:ALA:HB1	1:A:492:LEU:HD11	1.71	0.73
1:A:338:THR:CG2	1:A:340:GLU:CD	2.57	0.72
1:A:404:THR:HG23	1:A:409:ARG:HG3	1.71	0.72
1:A:156:LEU:CD2	1:A:160:LEU:HD22	2.19	0.72
1:A:419:GLU:OE1	5:A:2056:HOH:O	2.07	0.72
1:A:209:LYS:HE2	1:A:299:TYR:CD1	2.25	0.72
1:A:119:ASP:OD2	5:A:2095:HOH:O	2.08	0.72
1:A:323:LEU:HD22	1:A:339:ASN:CG	2.10	0.72
1:A:338:THR:O	1:A:340:GLU:N	2.22	0.72
1:A:404:THR:CG2	1:A:409:ARG:HG2	2.20	0.71
1:A:193:LYS:CE	1:A:515:LYS:NZ	2.52	0.71
1:A:718:ILE:H	1:A:718:ILE:HD12	1.54	0.71
1:A:180:SER:O	1:A:185:LYS:NZ	2.21	0.71
1:A:570:ASN:ND2	1:A:671:GLU:OE2	2.22	0.71
1:A:338:THR:C	1:A:340:GLU:H	1.92	0.70
1:A:366:LEU:HB3	1:A:370:MET:HE3	1.73	0.70
1:A:667:LYS:HG2	1:A:668:ASN:ND2	2.06	0.70
1:A:631:ASP:OD1	5:A:2184:HOH:O	2.09	0.69
1:A:151:ARG:HD2	5:A:2043:HOH:O	1.92	0.69
1:A:198:VAL:HG21	1:A:370:MET:HG2	1.74	0.69
1:A:67:ARG:HH12	1:A:688:ASN:ND2	1.91	0.69
1:A:156:LEU:C	1:A:156:LEU:HD23	2.10	0.68
1:A:338:THR:C	1:A:340:GLU:N	2.46	0.68
1:A:597:ASN:HD22	1:A:597:ASN:C	1.95	0.68
1:A:507:PHE:O	1:A:510:ILE:HG12	1.95	0.67
1:A:693:TRP:HB2	1:A:718:ILE:HD11	1.75	0.67
1:A:159:LEU:HD11	1:A:194:TYR:OH	1.94	0.66
1:A:516:PHE:HE1	1:A:520:LYS:CE	2.08	0.66
1:A:193:LYS:NZ	1:A:515:LYS:HZ3	1.91	0.66
1:A:516:PHE:CZ	1:A:520:LYS:HE2	2.31	0.66
1:A:318:LYS:HB2	1:A:319:PRO:HA	1.76	0.65
1:A:338:THR:HG22	1:A:340:GLU:OE2	1.96	0.65
1:A:156:LEU:CD2	1:A:156:LEU:C	2.64	0.65
1:A:424:ARG:HD2	1:A:485:ILE:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:67:ARG:HH12	1:A:688:ASN:HD22	1.44	0.65
1:A:366:LEU:HB3	1:A:370:MET:CE	2.27	0.64
1:A:168:VAL:HG12	1:A:368:ASN:CG	2.18	0.64
1:A:516:PHE:HE1	1:A:520:LYS:HE3	1.62	0.64
1:A:248:MET:HB3	1:A:272:MET:SD	2.37	0.64
1:A:328:GLU:HG2	2:A:753:NAG:H82	1.80	0.64
1:A:338:THR:HG21	1:A:340:GLU:OE1	1.98	0.63
1:A:198:VAL:CG2	1:A:370:MET:HG2	2.29	0.63
1:A:202:LEU:HD21	1:A:216:ILE:HG23	1.79	0.63
1:A:516:PHE:CE1	1:A:520:LYS:HE3	2.34	0.63
1:A:314:GLU:C	1:A:315:ILE:HD12	2.20	0.62
1:A:184:GLU:H	1:A:184:GLU:CD	2.01	0.62
1:A:355:LYS:HB3	1:A:356:PRO:CD	2.29	0.62
1:A:199:LEU:CD1	1:A:370:MET:CE	2.75	0.62
1:A:714:GLY:O	1:A:718:ILE:HD13	1.91	0.61
1:A:411:ALA:O	1:A:414:VAL:HG22	1.99	0.61
1:A:394:ARG:HH21	1:A:401:THR:C	2.04	0.61
1:A:353:LYS:O	1:A:356:PRO:HG2	2.01	0.61
1:A:168:VAL:HG12	1:A:368:ASN:HD21	1.59	0.61
1:A:379:VAL:CG1	1:A:386:TYR:O	2.49	0.61
1:A:597:ASN:ND2	1:A:599:ASP:H	1.99	0.61
1:A:257:GLN:NE2	5:A:2039:HOH:O	2.34	0.60
1:A:588:GLY:O	1:A:593:GLY:O	2.18	0.60
1:A:96:ILE:CD1	1:A:696:THR:HG23	2.32	0.60
1:A:404:THR:HG22	1:A:409:ARG:HG2	1.83	0.59
1:A:697:TYR:OH	5:A:2078:HOH:O	1.97	0.59
1:A:151:ARG:HH11	1:A:151:ARG:HG2	1.68	0.59
1:A:338:THR:CG2	1:A:340:GLU:OE2	2.50	0.59
1:A:621:MET:CE	1:A:748:VAL:HG12	2.33	0.59
1:A:55:ILE:N	1:A:55:ILE:HD13	2.18	0.58
1:A:67:ARG:HH22	1:A:688:ASN:HD21	1.50	0.58
1:A:184:GLU:OE2	1:A:318:LYS:HG3	2.04	0.58
1:A:693:TRP:CB	1:A:718:ILE:HD11	2.34	0.58
1:A:202:LEU:CD2	1:A:217:HIS:O	2.51	0.58
1:A:329:ILE:O	1:A:332:THR:HB	2.03	0.58
1:A:96:ILE:C	5:A:2112:HOH:O	2.08	0.58
1:A:199:LEU:HD11	1:A:370:MET:HE2	1.85	0.57
1:A:193:LYS:HE2	1:A:515:LYS:HZ2	1.69	0.57
1:A:67:ARG:HH22	1:A:688:ASN:ND2	2.03	0.57
1:A:315:ILE:HD12	1:A:315:ILE:N	2.20	0.57
1:A:424:ARG:NH2	5:A:2200:HOH:O	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:715:ASN:HA	1:A:718:ILE:HD13	1.86	0.56
1:A:193:LYS:HZ3	1:A:515:LYS:HZ3	1.52	0.56
1:A:97:PRO:CD	5:A:2112:HOH:O	2.54	0.56
1:A:510:ILE:HG12	1:A:511:ILE:N	2.20	0.56
1:A:163:ILE:O	1:A:164:TYR:HB2	2.06	0.56
1:A:168:VAL:HG22	1:A:169:ALA:N	2.20	0.56
1:A:414:VAL:HG23	1:A:415:ASN:N	2.21	0.55
1:A:463:GLU:HG2	5:A:2196:HOH:O	2.04	0.55
1:A:202:LEU:CD2	1:A:216:ILE:CG2	2.74	0.55
1:A:621:MET:HE3	1:A:748:VAL:HG12	1.88	0.55
1:A:492:LEU:HD13	1:A:492:LEU:C	2.27	0.55
1:A:338:THR:HG21	1:A:340:GLU:CD	2.27	0.55
1:A:154:GLU:N	1:A:155:PRO:CD	2.70	0.54
1:A:315:ILE:HD13	1:A:315:ILE:N	2.21	0.54
1:A:355:LYS:N	1:A:356:PRO:HD2	2.22	0.54
1:A:354:LEU:HG	1:A:358:LEU:CD2	2.35	0.54
1:A:193:LYS:HZ3	1:A:515:LYS:NZ	2.03	0.54
1:A:440:GLU:CG	1:A:479:ILE:HD13	2.37	0.54
1:A:121:LEU:HD13	1:A:414:VAL:HG21	1.90	0.53
1:A:193:LYS:HE2	1:A:515:LYS:HZ3	1.63	0.53
1:A:714:GLY:O	1:A:718:ILE:HD11	1.98	0.53
1:A:333:VAL:O	1:A:335:ILE:HG13	2.09	0.53
1:A:168:VAL:HG11	1:A:272:MET:CE	2.40	0.52
1:A:209:LYS:HE2	1:A:299:TYR:CE1	2.44	0.52
1:A:597:ASN:ND2	1:A:597:ASN:C	2.61	0.52
1:A:180:SER:O	1:A:185:LYS:CE	2.58	0.52
1:A:448:GLU:O	1:A:452:GLN:HG3	2.09	0.52
1:A:530:ASP:OD1	1:A:530:ASP:C	2.49	0.52
1:A:355:LYS:HB3	1:A:356:PRO:HD3	1.92	0.51
1:A:523:LYS:NZ	1:A:523:LYS:HB2	1.85	0.51
1:A:507:PHE:HA	1:A:510:ILE:HD11	1.89	0.51
1:A:261:LEU:HB3	1:A:262:PRO:HD2	1.92	0.51
1:A:333:VAL:O	1:A:333:VAL:CG1	2.53	0.51
1:A:282:ILE:O	1:A:286:THR:HG23	2.11	0.51
1:A:151:ARG:HG2	1:A:151:ARG:NH1	2.25	0.51
1:A:160:LEU:N	1:A:161:PRO:CD	2.74	0.50
1:A:492:LEU:O	1:A:492:LEU:HD13	2.10	0.50
1:A:257:GLN:HG3	1:A:263:ILE:HD11	1.92	0.50
1:A:215:VAL:HG12	1:A:216:ILE:N	2.27	0.50
1:A:626:GLY:O	1:A:637:HIS:HD2	1.95	0.50
1:A:209:LYS:CE	1:A:299:TYR:CD1	2.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:730:GLU:C	1:A:730:GLU:OE2	2.49	0.50
1:A:303:THR:OG1	1:A:306:GLN:HG3	2.12	0.49
1:A:77:GLU:HG3	1:A:79:CYS:H	1.77	0.49
1:A:214:HIS:CE1	1:A:524:LYS:HD2	2.47	0.49
1:A:209:LYS:CE	1:A:299:TYR:CE1	2.96	0.49
1:A:131:ALA:HB2	1:A:492:LEU:CD1	2.37	0.49
1:A:502:LYS:H	1:A:509:ASN:HD21	1.60	0.49
1:A:579:MET:HE3	1:A:650:ASP:HA	1.96	0.48
1:A:156:LEU:CD2	1:A:160:LEU:CD2	2.90	0.48
1:A:156:LEU:O	1:A:156:LEU:CD2	2.50	0.48
1:A:170:THR:O	1:A:256:ARG:NH2	2.45	0.48
1:A:436:LYS:HE3	5:A:2060:HOH:O	2.11	0.48
1:A:201:ASN:HB3	1:A:219:ASP:O	2.13	0.48
1:A:570:ASN:HD22	1:A:671:GLU:CD	2.14	0.48
1:A:202:LEU:CD2	1:A:216:ILE:HG22	2.41	0.47
1:A:626:GLY:O	1:A:637:HIS:CD2	2.67	0.47
1:A:156:LEU:HB2	1:A:382:LEU:HD11	1.95	0.47
1:A:506:TYR:O	1:A:510:ILE:HG23	2.14	0.47
1:A:680:ASN:OD1	1:A:683:GLN:HG3	2.13	0.47
1:A:333:VAL:HG11	1:A:523:LYS:HZ2	1.79	0.47
1:A:156:LEU:HD22	1:A:160:LEU:CD2	2.42	0.47
1:A:158:LYS:HD3	1:A:158:LYS:HA	1.39	0.47
1:A:97:PRO:N	5:A:2112:HOH:O	2.39	0.47
1:A:535:ILE:HG12	1:A:553:VAL:HG21	1.95	0.47
1:A:314:GLU:C	1:A:315:ILE:CD1	2.82	0.46
1:A:160:LEU:HA	1:A:160:LEU:HD12	1.76	0.46
1:A:671:GLU:HB2	1:A:681:HIS:CD2	2.50	0.46
1:A:159:LEU:HD11	1:A:194:TYR:CZ	2.50	0.46
1:A:510:ILE:HG12	1:A:511:ILE:H	1.78	0.46
1:A:738:SER:OG	1:A:741:ASN:HB3	2.16	0.46
1:A:202:LEU:HD13	1:A:202:LEU:C	2.37	0.46
1:A:717:ARG:O	1:A:721:THR:HG23	2.17	0.45
1:A:718:ILE:HD12	1:A:718:ILE:N	2.27	0.45
1:A:333:VAL:HG11	1:A:523:LYS:HB2	1.99	0.45
1:A:168:VAL:CG1	1:A:368:ASN:HD21	2.25	0.45
1:A:131:ALA:HB2	1:A:492:LEU:HD12	1.92	0.45
1:A:394:ARG:NH2	1:A:401:THR:C	2.69	0.45
1:A:121:LEU:CD1	1:A:414:VAL:HG21	2.47	0.45
1:A:83:PHE:O	1:A:87:CYS:HB2	2.17	0.45
1:A:196:LYS:HD3	1:A:196:LYS:HA	1.81	0.45
1:A:257:GLN:HG3	1:A:263:ILE:CD1	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:ALA:N	1:A:348:PRO:CD	2.79	0.44
1:A:442:LEU:O	1:A:446:ILE:HD12	2.18	0.44
1:A:168:VAL:HG11	1:A:272:MET:HE1	1.99	0.44
1:A:199:LEU:HD11	1:A:370:MET:HE1	1.80	0.44
1:A:667:LYS:HB2	1:A:667:LYS:HE2	1.73	0.44
1:A:330:MET:C	1:A:332:THR:H	2.21	0.44
1:A:372:TRP:O	1:A:376:MET:HB2	2.17	0.44
1:A:714:GLY:C	1:A:718:ILE:CD1	2.72	0.44
1:A:362:SER:O	1:A:366:LEU:HG	2.18	0.44
1:A:552:ILE:HD12	1:A:554:PHE:HE2	1.83	0.44
1:A:625:TYR:HA	1:A:628:PHE:CD2	2.53	0.43
1:A:713:PRO:HG3	5:A:2015:HOH:O	2.17	0.43
1:A:168:VAL:HG11	1:A:272:MET:HE3	2.00	0.43
1:A:140:ARG:HH21	1:A:503:GLU:CD	2.20	0.43
1:A:298:LEU:HD22	1:A:346:TYR:O	2.19	0.43
1:A:748:VAL:HG22	1:A:749:TRP:CD1	2.54	0.43
1:A:404:THR:HG21	1:A:409:ARG:HG2	1.98	0.43
1:A:259:GLU:HA	1:A:259:GLU:OE2	2.18	0.42
1:A:454:LEU:HD23	1:A:454:LEU:HA	1.81	0.42
1:A:97:PRO:HD2	5:A:2112:HOH:O	2.17	0.42
1:A:404:THR:HG22	1:A:409:ARG:CD	2.48	0.42
1:A:298:LEU:HD23	1:A:298:LEU:HA	1.79	0.42
1:A:379:VAL:HG13	1:A:386:TYR:HB3	2.01	0.42
1:A:181:TRP:CE3	1:A:182:THR:HA	2.55	0.42
1:A:168:VAL:CG2	1:A:252:ALA:HB1	2.50	0.42
1:A:366:LEU:CB	1:A:370:MET:HE3	2.48	0.42
1:A:212:VAL:HG23	1:A:213:ASN:OD1	2.20	0.42
1:A:414:VAL:HG23	1:A:415:ASN:H	1.85	0.42
1:A:315:ILE:C	1:A:317:GLY:N	2.73	0.41
1:A:98:GLU:HB3	1:A:401:THR:OG1	2.20	0.41
1:A:214:HIS:ND1	1:A:524:LYS:O	2.51	0.41
1:A:597:ASN:ND2	1:A:601:ASP:H	2.19	0.41
1:A:202:LEU:HD21	1:A:216:ILE:HG21	1.88	0.41
1:A:226:PRO:HG3	1:A:397:LEU:HD13	2.03	0.41
1:A:414:VAL:CG2	1:A:415:ASN:N	2.84	0.41
1:A:394:ARG:HH21	1:A:402:SER:N	2.19	0.40
1:A:73:ASP:OD1	1:A:75:THR:OG1	2.37	0.40
1:A:313:LEU:HD23	1:A:355:LYS:HA	2.02	0.40
1:A:327:ASN:O	1:A:331:SER:HB3	2.22	0.40
1:A:214:HIS:NE2	1:A:529:VAL:HG22	2.36	0.40
1:A:330:MET:C	1:A:332:THR:N	2.72	0.40

All (10) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:2109:HOH:O	5:A:2137:HOH:O[4_556]	1.04	1.16
1:A:175:GLN:OE1	1:A:260:ARG:O[6_555]	1.05	1.15
1:A:175:GLN:OE1	1:A:260:ARG:C[6_555]	1.55	0.65
5:A:2283:HOH:O	5:A:2283:HOH:O[4_556]	1.59	0.61
1:A:175:GLN:CD	1:A:260:ARG:O[6_555]	1.92	0.28
1:A:175:GLN:OE1	1:A:261:LEU:N[6_555]	2.00	0.20
1:A:175:GLN:OE1	1:A:261:LEU:CA[6_555]	2.09	0.11
1:A:171:GLU:CD	1:A:171:GLU:CD[6_555]	2.11	0.09
1:A:175:GLN:CD	1:A:260:ARG:C[6_555]	2.13	0.07
1:A:171:GLU:OE1	1:A:171:GLU:OE1[6_555]	2.19	0.01

### 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	694/696 (100%)	670 (96%)	22 (3%)	2 (0%)	44 33

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	339	ASN
1	A	318	LYS

#### 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	605/605 (100%)	556 (92%)	49 (8%)	14 4

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	LYS
1	A	59	SER
1	A	62	ILE
1	A	91	LEU
1	A	92	LYS
1	A	158	LYS
1	A	160	LEU
1	A	168	VAL
1	A	170	THR
1	A	189	GLN
1	A	260	ARG
1	A	266	ASN
1	A	276	MET
1	A	278	LEU
1	A	298	LEU
1	A	309	ASN
1	A	315	ILE
1	A	318	LYS
1	A	332	THR
1	A	339	ASN
1	A	340	GLU
1	A	346	TYR
1	A	358	LEU
1	A	364	ARG
1	A	368	ASN
1	A	376	MET
1	A	394	ARG
1	A	448	GLU
1	A	470	GLU
1	A	476	LYS
1	A	477	GLU
1	A	483	ASP
1	A	490	ASN
1	A	497	LEU
1	A	498	GLU
1	A	510	ILE
1	A	520	LYS
1	A	523	LYS

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Mol	Chain	Res	Type
1	A	597	ASN
1	A	598	LYS
1	A	608	GLN
1	A	665	ILE
1	A	667	LYS
1	A	687	LEU
1	A	730	GLU
1	A	735	ARG
1	A	743	GLU
1	A	747	ARG
1	A	748	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	ASN
1	A	257	GLN
1	A	267	GLN
1	A	306	GLN
1	A	316	ASN
1	A	368	ASN
1	A	490	ASN
1	A	500	ASN
1	A	509	ASN
1	A	550	ASN
1	A	551	GLN
1	A	570	ASN
1	A	597	ASN
1	A	619	GLN
1	A	637	HIS
1	A	656	GLN
1	A	668	ASN
1	A	688	ASN

### 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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 1 is monoatomic - leaving 4 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	$\# Z  > 2$
4	BIR	A	2001	3	23,30,30	1.41	1 (4%)	28,42,42	1.10	2 (7%)
2	NAG	A	752	1	14,14,15	0.63	0	15,19,21	1.19	1 (6%)
2	NAG	A	753	1	14,14,15	0.70	0	15,19,21	0.78	0
2	NAG	A	754	1	14,14,15	0.58	0	15,19,21	1.05	2 (13%)

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
4	BIR	A	2001	3	-	0/20/31/31	0/2/2/2
2	NAG	A	752	1	-	0/6/23/26	0/1/1/1
2	NAG	A	753	1	-	0/6/23/26	0/1/1/1
2	NAG	A	754	1	-	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)
4	A	2001	BIR	P4-C7	-6.38	1.73	1.79

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	752	NAG	O5-C1-C2	-3.83	106.14	111.47
4	A	2001	BIR	C25-N24-C10	-3.60	117.96	123.00
4	A	2001	BIR	O6-P4-C2	-3.11	103.44	111.11
2	A	754	NAG	O5-C1-C2	-2.30	108.27	111.47
2	A	754	NAG	C2-N2-C7	-2.06	119.93	122.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	753	NAG	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	696/696 (100%)	0.35	37 (5%) 27 37	14, 27, 44, 58	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	432	ALA	4.8
1	A	735	ARG	4.1
1	A	309	ASN	4.0
1	A	175	GLN	3.7
1	A	127	GLU	3.7
1	A	531	LYS	3.6
1	A	180	SER	3.5
1	A	333	VAL	3.3
1	A	318	LYS	3.2
1	A	319	PRO	3.1
1	A	270	LEU	2.9
1	A	334	ASN	2.8
1	A	338	THR	2.8
1	A	336	SER	2.6
1	A	736	LYS	2.6
1	A	452	GLN	2.5
1	A	317	GLY	2.5
1	A	178	GLY	2.5
1	A	530	ASP	2.5
1	A	532	ASP	2.5
1	A	216	ILE	2.5
1	A	384	ARG	2.5
1	A	260	ARG	2.5
1	A	74	ALA	2.4
1	A	125	LYS	2.4
1	A	222	ARG	2.4
1	A	339	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	126	THR	2.3
1	A	608	GLN	2.3
1	A	670	GLU	2.2
1	A	158	LYS	2.2
1	A	665	ILE	2.2
1	A	215	VAL	2.2
1	A	307	ILE	2.2
1	A	179	ALA	2.1
1	A	456	ASP	2.1
1	A	359	THR	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
2	NAG	A	754	14/15	0.87	0.25	1.37	40,42,46,48	0
4	BIR	A	2001	29/29	0.96	0.10	-0.20	12,18,29,29	0
3	ZN	A	1001	1/1	1.00	0.05	-3.39	20,20,20,20	0
2	NAG	A	752	14/15	0.80	0.28	-	37,41,45,45	0
2	NAG	A	753	14/15	0.87	0.23	-	42,45,47,49	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.