



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2024 – 01:49 PM EST

PDB ID : 3P40  
Title : Crystal structure of neurofascin adhesion complex in space group p3221  
Authors : Liu, H.; He, X.  
Deposited on : 2010-10-05  
Resolution : 3.20 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

<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>.

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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

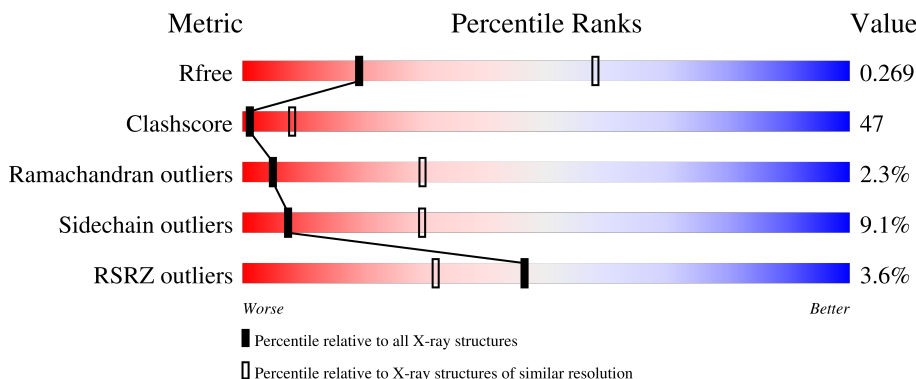
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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	404	

## 2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3337 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 Neurofascin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	390	3068	1928	547	575	18	0	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (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

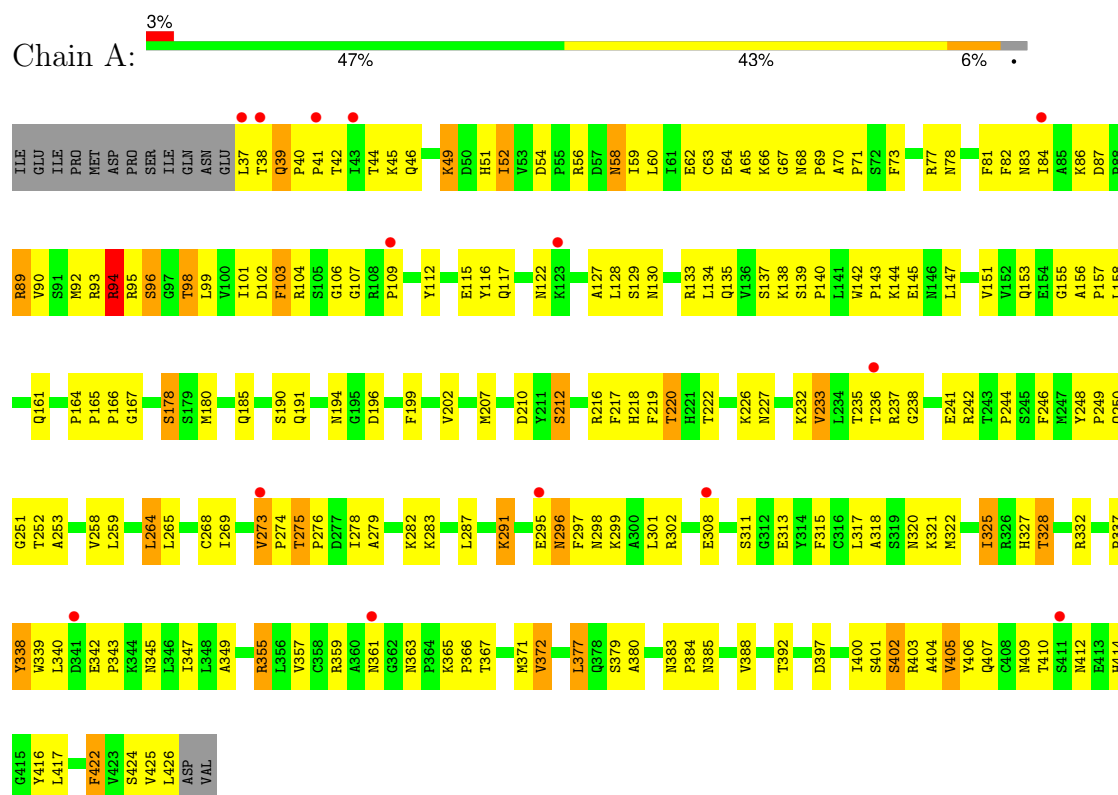
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	255	Total 255 O 255	0	0

### 3 Residue-property plots

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: Neurofascin



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.51Å 94.51Å 126.72Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	40.92 – 3.20 40.92 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.6 (40.92-3.20) 99.5 (40.92-3.20)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.98 (at 3.12Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.273 , 0.316 0.264 , 0.269	Depositor DCC
$R_{free}$ test set	526 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	77.1	Xtriage
Anisotropy	0.295	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 67.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.029 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	3337	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	63.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.14% 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: 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	0.50	0/3145	0.72	0/4273

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	3068	0	3010	286	0
2	A	14	0	13	1	0
3	A	255	0	0	130	0
All	All	3337	0	3023	286	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 47.

All (286) 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:273:VAL:HG23	1:A:274:PRO:HD3	1.36	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:371:MET:HA	3:A:550:HOH:O	1.58	1.01
1:A:372:VAL:HA	3:A:509:HOH:O	1.63	0.96
1:A:52:ILE:HD13	1:A:52:ILE:H	1.30	0.94
1:A:69:PRO:HD3	3:A:647:HOH:O	1.65	0.93
1:A:40:PRO:HG2	3:A:13:HOH:O	1.68	0.93
1:A:222:THR:HB	3:A:622:HOH:O	1.69	0.92
1:A:92:MET:HG2	1:A:93:ARG:H	1.39	0.87
1:A:66:LYS:O	3:A:437:HOH:O	1.94	0.85
1:A:273:VAL:CG2	1:A:274:PRO:HD3	2.07	0.85
1:A:372:VAL:HG22	1:A:377:LEU:HD12	1.60	0.83
1:A:101:ILE:HG21	1:A:112:TYR:HE2	1.43	0.82
1:A:68:ASN:HB2	3:A:647:HOH:O	1.79	0.82
1:A:402:SER:HB3	3:A:542:HOH:O	1.81	0.81
1:A:252:THR:HA	3:A:632:HOH:O	1.80	0.81
1:A:185:GLN:HE21	1:A:190:SER:HA	1.45	0.79
1:A:296:ASN:N	3:A:15:HOH:O	2.16	0.79
1:A:90:VAL:HG23	3:A:532:HOH:O	1.83	0.78
1:A:217:PHE:HB2	3:A:622:HOH:O	1.83	0.78
1:A:241:GLU:HA	1:A:273:VAL:HG11	1.66	0.78
1:A:283:LYS:N	3:A:592:HOH:O	2.18	0.77
1:A:345:ASN:HB3	1:A:422:PHE:CE1	2.21	0.76
1:A:274:PRO:HD2	1:A:320:ASN:OD1	1.86	0.75
1:A:242:ARG:H	1:A:273:VAL:CG2	2.00	0.75
1:A:424:SER:HB2	3:A:538:HOH:O	1.86	0.75
1:A:377:LEU:N	3:A:550:HOH:O	2.19	0.74
1:A:122:ASN:ND2	3:A:620:HOH:O	2.21	0.73
1:A:101:ILE:HG21	1:A:112:TYR:CE2	2.23	0.73
1:A:98:THR:O	1:A:99:LEU:HD23	1.89	0.72
1:A:89:ARG:HB2	3:A:544:HOH:O	1.87	0.72
1:A:337:PRO:HD3	1:A:412:ASN:HD22	1.53	0.71
1:A:400:ILE:HD12	1:A:400:ILE:H	1.57	0.69
1:A:56:ARG:HH11	1:A:56:ARG:HB3	1.57	0.69
1:A:151:VAL:HG22	1:A:232:LYS:HB2	1.75	0.69
1:A:424:SER:N	3:A:660:HOH:O	2.25	0.68
1:A:248:TYR:HB3	3:A:446:HOH:O	1.94	0.67
1:A:103:PHE:CE2	1:A:109:PRO:HG3	2.30	0.67
1:A:156:ALA:N	3:A:588:HOH:O	2.28	0.67
1:A:46:GLN:HE22	1:A:130:ASN:H	1.43	0.66
1:A:144:LYS:HA	3:A:431:HOH:O	1.94	0.66
1:A:320:ASN:HB3	3:A:578:HOH:O	1.95	0.65
1:A:259:LEU:HD21	1:A:414:HIS:CD2	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:ARG:H	1:A:273:VAL:HG22	1.61	0.65
1:A:283:LYS:HG3	3:A:592:HOH:O	1.96	0.65
1:A:372:VAL:CG2	1:A:377:LEU:HD12	2.26	0.65
1:A:39:GLN:NE2	3:A:437:HOH:O	2.29	0.65
1:A:52:ILE:HD13	1:A:52:ILE:N	2.10	0.65
1:A:207:MET:HG3	1:A:233:VAL:CG2	2.27	0.64
1:A:406:TYR:HA	3:A:509:HOH:O	1.96	0.64
1:A:59:ILE:HG12	1:A:103:PHE:HZ	1.62	0.64
1:A:142:TRP:HB3	3:A:524:HOH:O	1.97	0.64
1:A:127:ALA:O	1:A:128:LEU:HD23	1.96	0.64
1:A:238:GLY:HA2	3:A:483:HOH:O	1.98	0.64
1:A:422:PHE:CD1	3:A:660:HOH:O	2.49	0.64
1:A:424:SER:HB3	3:A:660:HOH:O	1.97	0.64
1:A:249:PRO:CD	3:A:446:HOH:O	2.45	0.64
1:A:185:GLN:NE2	1:A:191:GLN:H	1.96	0.64
1:A:207:MET:SD	1:A:233:VAL:HG23	2.38	0.63
1:A:60:LEU:HD22	1:A:99:LEU:O	1.98	0.63
1:A:219:PHE:N	3:A:625:HOH:O	2.32	0.63
1:A:338:TYR:HB2	3:A:476:HOH:O	1.97	0.63
1:A:405:VAL:HG13	1:A:422:PHE:HB3	1.80	0.62
1:A:349:ALA:HA	1:A:426:LEU:HD12	1.80	0.62
1:A:275:THR:N	3:A:460:HOH:O	2.32	0.62
1:A:98:THR:HG22	1:A:99:LEU:N	2.15	0.62
1:A:151:VAL:HB	3:A:511:HOH:O	1.99	0.61
1:A:52:ILE:H	1:A:52:ILE:CD1	2.10	0.61
1:A:422:PHE:O	1:A:422:PHE:HD1	1.82	0.61
1:A:151:VAL:HG22	1:A:232:LYS:CB	2.31	0.61
1:A:249:PRO:HD3	3:A:446:HOH:O	1.99	0.61
1:A:317:LEU:N	3:A:525:HOH:O	2.31	0.61
1:A:322:MET:N	3:A:578:HOH:O	2.25	0.61
1:A:117:GLN:NE2	1:A:128:LEU:HD13	2.15	0.60
1:A:137:SER:HB3	3:A:612:HOH:O	2.01	0.60
1:A:397:ASP:OD1	1:A:397:ASP:O	2.18	0.60
1:A:405:VAL:O	3:A:509:HOH:O	2.17	0.60
1:A:194:ASN:ND2	1:A:196:ASP:CG	2.55	0.60
1:A:241:GLU:HB3	1:A:322:MET:CE	2.32	0.59
1:A:37:LEU:N	3:A:631:HOH:O	2.35	0.59
1:A:377:LEU:CD2	1:A:388:VAL:HG11	2.33	0.59
1:A:273:VAL:CB	1:A:274:PRO:HD3	2.32	0.58
1:A:325:ILE:HD13	1:A:325:ILE:H	1.68	0.58
1:A:207:MET:HG3	1:A:233:VAL:HG23	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:ILE:HD12	1:A:400:ILE:N	2.18	0.58
1:A:359:ARG:HB3	3:A:470:HOH:O	2.04	0.58
1:A:44:THR:HB	3:A:456:HOH:O	2.03	0.58
1:A:178:SER:OG	1:A:210:ASP:OD1	2.22	0.58
1:A:185:GLN:HE21	1:A:190:SER:CA	2.17	0.58
1:A:56:ARG:HH11	1:A:56:ARG:CB	2.17	0.57
1:A:242:ARG:H	1:A:273:VAL:HG21	1.68	0.57
1:A:46:GLN:NE2	1:A:129:SER:HB2	2.20	0.57
1:A:342:GLU:HG3	1:A:343:PRO:HD2	1.87	0.57
1:A:273:VAL:HG23	1:A:274:PRO:CD	2.23	0.56
1:A:70:ALA:HA	3:A:633:HOH:O	2.04	0.56
1:A:147:LEU:HD12	1:A:227:ASN:HB2	1.88	0.56
1:A:41:PRO:HA	3:A:437:HOH:O	2.04	0.56
1:A:84:ILE:HG22	3:A:2:HOH:O	2.05	0.56
1:A:51:HIS:HD2	1:A:134:LEU:HD13	1.71	0.55
1:A:96:SER:HB2	3:A:624:HOH:O	2.05	0.55
1:A:212:SER:HA	3:A:445:HOH:O	2.06	0.55
1:A:71:PRO:HA	3:A:620:HOH:O	2.06	0.55
1:A:405:VAL:CG1	1:A:422:PHE:HB3	2.37	0.55
1:A:380:ALA:N	3:A:613:HOH:O	2.39	0.55
1:A:365:LYS:HD2	1:A:366:PRO:HD2	1.87	0.55
1:A:151:VAL:CG2	1:A:232:LYS:HD2	2.37	0.55
1:A:216:ARG:NH1	3:A:3:HOH:O	2.39	0.54
1:A:347:ILE:HD12	1:A:347:ILE:N	2.22	0.54
1:A:355:ARG:H	1:A:355:ARG:HD3	1.71	0.54
1:A:39:GLN:HG2	1:A:40:PRO:N	2.22	0.54
1:A:338:TYR:CE2	1:A:361:ASN:HB3	2.42	0.54
1:A:164:PRO:HD3	3:A:493:HOH:O	2.06	0.54
1:A:202:VAL:N	3:A:588:HOH:O	2.18	0.54
1:A:400:ILE:HG23	1:A:403:ARG:HD2	1.89	0.54
1:A:264:LEU:C	1:A:264:LEU:HD22	2.29	0.53
1:A:83:ASN:HB2	3:A:22:HOH:O	2.07	0.53
1:A:241:GLU:HA	1:A:273:VAL:HG21	1.90	0.53
1:A:385:ASN:HB2	3:A:542:HOH:O	2.08	0.53
1:A:56:ARG:CB	1:A:56:ARG:NH1	2.72	0.53
1:A:220:THR:N	3:A:625:HOH:O	2.41	0.53
1:A:278:ILE:HG22	3:A:525:HOH:O	2.09	0.52
1:A:338:TYR:HA	3:A:611:HOH:O	2.09	0.52
1:A:246:PHE:CE1	1:A:325:ILE:HG12	2.45	0.52
1:A:242:ARG:NH2	3:A:659:HOH:O	2.42	0.52
1:A:217:PHE:C	3:A:625:HOH:O	2.48	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:TYR:N	3:A:446:HOH:O	2.36	0.51
1:A:372:VAL:HG13	3:A:509:HOH:O	2.10	0.51
1:A:145:GLU:OE1	1:A:226:LYS:HE3	2.09	0.51
1:A:153:GLN:NE2	3:A:508:HOH:O	2.44	0.51
1:A:157:PRO:HG3	3:A:636:HOH:O	2.09	0.51
1:A:59:ILE:HG12	1:A:103:PHE:CZ	2.44	0.51
1:A:269:ILE:HB	3:A:446:HOH:O	2.11	0.51
1:A:241:GLU:CA	1:A:273:VAL:HG21	2.40	0.51
1:A:250:GLN:HA	3:A:549:HOH:O	2.10	0.51
1:A:71:PRO:CA	3:A:620:HOH:O	2.58	0.50
1:A:337:PRO:HD3	1:A:412:ASN:ND2	2.25	0.50
1:A:248:TYR:HB3	1:A:249:PRO:HD3	1.93	0.50
1:A:77:ARG:H	1:A:82:PHE:HB2	1.77	0.50
1:A:422:PHE:HD1	1:A:422:PHE:C	2.15	0.50
1:A:66:LYS:HD3	3:A:526:HOH:O	2.12	0.50
1:A:242:ARG:N	1:A:273:VAL:HG21	2.26	0.50
1:A:282:LYS:NZ	3:A:20:HOH:O	2.43	0.50
1:A:299:LYS:HE3	3:A:608:HOH:O	2.11	0.50
1:A:367:THR:HB	3:A:515:HOH:O	2.11	0.49
1:A:422:PHE:CD1	1:A:422:PHE:C	2.86	0.49
1:A:156:ALA:O	1:A:202:VAL:HG23	2.12	0.49
1:A:367:THR:O	1:A:410:THR:HA	2.13	0.49
1:A:143:PRO:O	3:A:524:HOH:O	2.19	0.49
1:A:220:THR:HG23	3:A:622:HOH:O	2.13	0.49
1:A:241:GLU:HB3	1:A:322:MET:HE1	1.94	0.49
1:A:273:VAL:C	1:A:275:THR:H	2.16	0.49
1:A:279:ALA:N	3:A:525:HOH:O	2.27	0.49
1:A:62:GLU:HA	1:A:98:THR:HG23	1.94	0.49
1:A:45:LYS:HB2	3:A:529:HOH:O	2.12	0.49
1:A:156:ALA:O	3:A:588:HOH:O	2.20	0.49
1:A:77:ARG:HB2	1:A:82:PHE:CD2	2.48	0.48
1:A:103:PHE:HB3	1:A:106:GLY:O	2.13	0.48
1:A:235:THR:HG22	3:A:8:HOH:O	2.13	0.48
1:A:345:ASN:ND2	1:A:422:PHE:H	2.11	0.48
1:A:246:PHE:CE1	1:A:327:HIS:HB2	2.48	0.48
1:A:416:TYR:CD1	1:A:416:TYR:C	2.86	0.48
1:A:308:GLU:N	1:A:308:GLU:OE2	2.46	0.48
1:A:227:ASN:N	3:A:540:HOH:O	2.46	0.48
1:A:37:LEU:HD12	1:A:68:ASN:OD1	2.13	0.48
1:A:185:GLN:NE2	1:A:191:GLN:N	2.61	0.48
1:A:207:MET:CG	1:A:233:VAL:HG23	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:VAL:N	3:A:460:HOH:O	2.46	0.48
1:A:299:LYS:HG3	3:A:614:HOH:O	2.14	0.48
1:A:64:GLU:HA	3:A:624:HOH:O	2.14	0.48
1:A:138:LYS:NZ	1:A:138:LYS:HB3	2.29	0.48
1:A:158:LEU:HB3	1:A:199:PHE:HB2	1.95	0.48
1:A:54:ASP:OD2	1:A:56:ARG:NH1	2.47	0.47
1:A:67:GLY:HA3	3:A:429:HOH:O	2.14	0.47
1:A:253:ALA:HA	1:A:327:HIS:CE1	2.49	0.47
1:A:332:ARG:NH2	3:A:486:HOH:O	2.36	0.47
1:A:65:ALA:HB2	1:A:73:PHE:HE2	1.79	0.47
1:A:92:MET:HG2	1:A:93:ARG:N	2.18	0.47
1:A:241:GLU:HB3	1:A:322:MET:HE3	1.96	0.47
1:A:138:LYS:HB2	1:A:167:GLY:HA2	1.97	0.47
1:A:216:ARG:NE	3:A:6:HOH:O	2.39	0.47
1:A:147:LEU:HB3	3:A:537:HOH:O	2.14	0.47
1:A:355:ARG:HD3	1:A:355:ARG:N	2.30	0.47
1:A:39:GLN:HA	1:A:40:PRO:HD3	1.77	0.47
1:A:49:LYS:HD2	3:A:442:HOH:O	2.15	0.47
1:A:295:GLU:OE2	1:A:302:ARG:NE	2.47	0.47
1:A:338:TYR:N	1:A:338:TYR:CD2	2.82	0.47
1:A:143:PRO:HD3	3:A:644:HOH:O	2.15	0.46
1:A:282:LYS:HB2	1:A:287:LEU:HD23	1.96	0.46
1:A:51:HIS:CD2	1:A:134:LEU:HD13	2.49	0.46
1:A:96:SER:HA	3:A:624:HOH:O	2.14	0.46
1:A:291:LYS:O	1:A:291:LYS:HG3	2.15	0.46
1:A:409:ASN:HA	3:A:450:HOH:O	2.16	0.46
1:A:81:PHE:HB2	3:A:643:HOH:O	2.16	0.46
1:A:94:ARG:O	3:A:599:HOH:O	2.20	0.46
1:A:318:ALA:HB3	1:A:325:ILE:CD1	2.46	0.46
1:A:180:MET:HE2	3:A:556:HOH:O	2.17	0.45
1:A:383:ASN:ND2	3:A:542:HOH:O	2.42	0.45
1:A:98:THR:CG2	1:A:99:LEU:N	2.79	0.45
1:A:236:THR:HG22	1:A:237:ARG:HG3	1.98	0.45
1:A:276:PRO:HB3	3:A:650:HOH:O	2.17	0.45
1:A:250:GLN:HG2	3:A:443:HOH:O	2.16	0.45
1:A:371:MET:HB2	1:A:407:GLN:HB2	1.99	0.45
1:A:58:ASN:C	1:A:58:ASN:HD22	2.20	0.45
1:A:216:ARG:NH2	3:A:479:HOH:O	2.50	0.45
1:A:338:TYR:H	1:A:338:TYR:HD2	1.65	0.45
1:A:115:GLU:C	1:A:116:TYR:HD1	2.20	0.45
1:A:403:ARG:NH2	1:A:425:VAL:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:TYR:N	1:A:338:TYR:HD2	2.15	0.45
1:A:109:PRO:HD2	3:A:545:HOH:O	2.16	0.45
1:A:404:ALA:N	3:A:13:HOH:O	2.50	0.45
1:A:328:THR:O	1:A:328:THR:HG22	2.17	0.44
1:A:77:ARG:O	1:A:78:ASN:HB2	2.16	0.44
1:A:44:THR:CB	3:A:456:HOH:O	2.62	0.44
1:A:216:ARG:NH1	1:A:216:ARG:HG2	2.32	0.44
1:A:315:PHE:CE2	3:A:592:HOH:O	2.69	0.44
1:A:388:VAL:HG22	3:A:433:HOH:O	2.16	0.44
1:A:39:GLN:HG2	1:A:40:PRO:O	2.17	0.44
1:A:138:LYS:NZ	3:A:543:HOH:O	2.51	0.44
1:A:139:SER:N	1:A:140:PRO:HD3	2.32	0.44
1:A:226:LYS:C	3:A:540:HOH:O	2.55	0.44
1:A:151:VAL:HG22	1:A:232:LYS:HD2	2.00	0.44
1:A:251:GLY:HA3	3:A:528:HOH:O	2.18	0.44
1:A:388:VAL:O	1:A:388:VAL:HG23	2.18	0.44
1:A:320:ASN:ND2	3:A:578:HOH:O	2.50	0.44
1:A:377:LEU:HD21	1:A:388:VAL:HG11	1.99	0.44
1:A:409:ASN:OD1	2:A:1:NAG:N2	2.49	0.44
1:A:248:TYR:CB	1:A:249:PRO:HD3	2.48	0.43
1:A:265:LEU:HA	1:A:265:LEU:HD23	1.75	0.43
1:A:278:ILE:CG2	3:A:525:HOH:O	2.65	0.43
1:A:95:ARG:N	3:A:616:HOH:O	2.50	0.43
1:A:297:PHE:HB2	3:A:614:HOH:O	2.18	0.43
1:A:298:ASN:N	1:A:298:ASN:HD22	2.17	0.43
1:A:117:GLN:N	3:A:435:HOH:O	2.52	0.43
1:A:56:ARG:HD2	3:A:436:HOH:O	2.19	0.43
1:A:295:GLU:CD	1:A:302:ARG:HE	2.22	0.43
1:A:104:ARG:C	3:A:651:HOH:O	2.57	0.43
1:A:383:ASN:OD1	1:A:385:ASN:N	2.51	0.42
1:A:41:PRO:CG	1:A:122:ASN:HB2	2.48	0.42
1:A:77:ARG:NH2	3:A:517:HOH:O	2.52	0.42
1:A:155:GLY:C	3:A:588:HOH:O	2.57	0.42
1:A:103:PHE:N	3:A:505:HOH:O	2.38	0.42
1:A:265:LEU:HD23	1:A:301:LEU:O	2.18	0.42
1:A:89:ARG:CG	3:A:532:HOH:O	2.67	0.42
1:A:311:SER:O	3:A:20:HOH:O	2.20	0.42
1:A:56:ARG:NH1	1:A:56:ARG:HB2	2.34	0.42
1:A:89:ARG:H	1:A:89:ARG:HG2	1.51	0.42
1:A:315:PHE:HA	1:A:327:HIS:O	2.19	0.42
1:A:311:SER:C	3:A:20:HOH:O	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:64:GLU:CB	3:A:456:HOH:O	2.68	0.42
1:A:283:LYS:HD2	1:A:313:GLU:HB2	2.02	0.42
1:A:404:ALA:O	3:A:13:HOH:O	2.21	0.42
1:A:363:ASN:ND2	3:A:534:HOH:O	2.43	0.42
1:A:103:PHE:CZ	1:A:109:PRO:HG3	2.55	0.42
1:A:216:ARG:HG2	1:A:216:ARG:HH11	1.85	0.42
1:A:248:TYR:CD1	1:A:248:TYR:C	2.91	0.42
1:A:345:ASN:HD22	1:A:422:PHE:H	1.66	0.42
1:A:155:GLY:HA2	3:A:463:HOH:O	2.19	0.41
1:A:38:THR:HG23	1:A:38:THR:O	2.20	0.41
1:A:94:ARG:N	3:A:616:HOH:O	2.53	0.41
1:A:158:LEU:HD23	1:A:199:PHE:CD1	2.55	0.41
1:A:275:THR:HA	1:A:276:PRO:HD3	1.84	0.41
1:A:138:LYS:C	1:A:140:PRO:HD3	2.41	0.41
1:A:41:PRO:HG3	1:A:122:ASN:HB2	2.03	0.41
1:A:92:MET:CG	1:A:93:ARG:H	2.19	0.41
1:A:117:GLN:N	3:A:547:HOH:O	2.40	0.41
1:A:320:ASN:HB2	3:A:650:HOH:O	2.21	0.41
1:A:52:ILE:N	1:A:52:ILE:CD1	2.77	0.41
1:A:218:HIS:HB2	3:A:471:HOH:O	2.20	0.41
1:A:165:PRO:HB3	3:A:644:HOH:O	2.19	0.41
1:A:71:PRO:HD3	3:A:633:HOH:O	2.20	0.41
1:A:86:LYS:HD2	3:A:10:HOH:O	2.19	0.41
1:A:94:ARG:HB2	3:A:9:HOH:O	2.20	0.41
1:A:40:PRO:HA	1:A:41:PRO:HD3	1.88	0.41
1:A:70:ALA:HA	1:A:71:PRO:HD3	1.91	0.41
1:A:357:VAL:HG13	1:A:392:THR:OG1	2.21	0.41
1:A:338:TYR:CD2	1:A:361:ASN:O	2.73	0.41
1:A:340:LEU:HD13	1:A:361:ASN:HB2	2.03	0.41
1:A:383:ASN:HA	1:A:384:PRO:HD3	1.87	0.41
1:A:185:GLN:HE21	1:A:191:GLN:N	2.19	0.40
1:A:64:GLU:C	3:A:456:HOH:O	2.59	0.40
1:A:244:PRO:HD3	1:A:320:ASN:CB	2.52	0.40
1:A:410:THR:N	3:A:450:HOH:O	2.55	0.40
1:A:258:VAL:HG21	1:A:264:LEU:HD23	2.03	0.40
1:A:52:ILE:HA	1:A:135:GLN:O	2.22	0.40
1:A:339:TRP:CE2	1:A:417:LEU:HD13	2.57	0.40
1:A:241:GLU:HA	1:A:273:VAL:CG1	2.45	0.40
1:A:377:LEU:HD22	1:A:388:VAL:HG11	2.03	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	388/404 (96%)	336 (87%)	43 (11%)	9 (2%)	5 29

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	ARG
1	A	166	PRO
1	A	107	GLY
1	A	296	ASN
1	A	63	CYS
1	A	98	THR
1	A	401	SER
1	A	275	THR
1	A	321	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	342/356 (96%)	311 (91%)	31 (9%)	7 29

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	42	THR

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Mol	Chain	Res	Type
1	A	49	LYS
1	A	52	ILE
1	A	58	ASN
1	A	87	ASP
1	A	89	ARG
1	A	94	ARG
1	A	96	SER
1	A	102	ASP
1	A	103	PHE
1	A	133	ARG
1	A	161	GLN
1	A	178	SER
1	A	212	SER
1	A	220	THR
1	A	233	VAL
1	A	264	LEU
1	A	268	CYS
1	A	273	VAL
1	A	291	LYS
1	A	325	ILE
1	A	328	THR
1	A	338	TYR
1	A	355	ARG
1	A	372	VAL
1	A	377	LEU
1	A	379	SER
1	A	402	SER
1	A	405	VAL
1	A	422	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	51	HIS
1	A	58	ASN
1	A	117	GLN
1	A	153	GLN
1	A	185	GLN
1	A	298	ASN
1	A	305	ASN
1	A	327	HIS

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Mol	Chain	Res	Type
1	A	345	ASN
1	A	407	GLN
1	A	412	ASN
1	A	414	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

1 ligand is 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	1	1	14,14,15	0.64	0	17,19,21	0.70	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
2	NAG	A	1	1	-	2/6/23/26	0/1/1/1



There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1	NAG	C8-C7-N2-C2
2	A	1	NAG	O7-C7-N2-C2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	390/404 (96%)	0.28	14 (3%) 46 32	26, 59, 106, 124	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	411	SER	4.1
1	A	295	GLU	3.7
1	A	236	THR	3.6
1	A	109	PRO	3.4
1	A	308	GLU	3.4
1	A	341	ASP	3.0
1	A	43	ILE	2.6
1	A	273	VAL	2.5
1	A	38	THR	2.4
1	A	84	ILE	2.3
1	A	123	LYS	2.3
1	A	361	ASN	2.2
1	A	37	LEU	2.2
1	A	41	PRO	2.1

### 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
2	NAG	A	1	14/15	0.94	0.07	60,62,63,64	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.