



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 08:11 PM UTC

PDB ID : 7CEG / pdb_00007ceg
Title : Crystal structure of the complex between mouse PTP delta and neuroligin-3
Authors : Yamagata, A.; Yoshida, T.; Shiroshima, T.; Maeda, A.; Fukai, S.
Deposited on : 2020-06-23
Resolution : 3.85 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

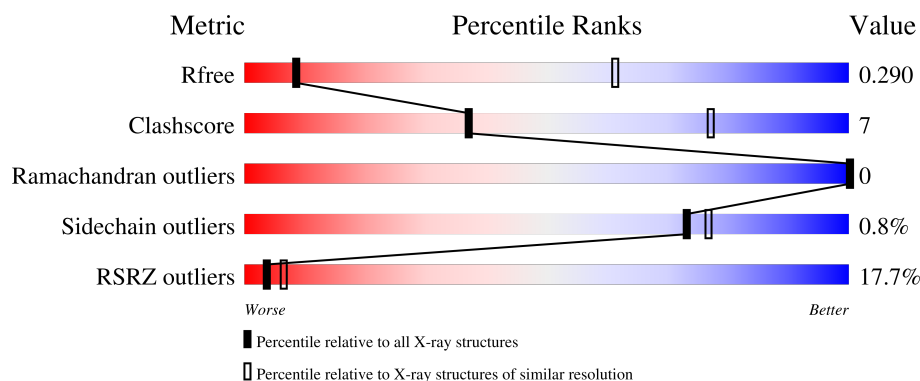
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.85 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}	180053	1165 (4.02-3.70)
Clashscore	190562	1207 (4.02-3.70)
Ramachandran outliers	187476	1149 (4.02-3.70)
Sidechain outliers	187428	1142 (4.02-3.70)
RSRZ outliers	180081	1164 (4.02-3.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	386	12% 79% 21% .
2	B	579	20% 79% 14% 7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7273 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 Isoform C of Receptor-type tyrosine-protein phosphatase delta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	386	2975	1859	523	580	13	0	0	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	409	LYS	-	expression tag	UNP Q64487
A	410	HIS	-	expression tag	UNP Q64487
A	411	HIS	-	expression tag	UNP Q64487
A	412	HIS	-	expression tag	UNP Q64487
A	413	HIS	-	expression tag	UNP Q64487

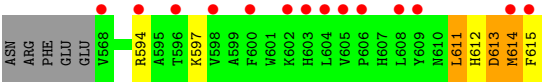
- Molecule 2 is a protein called Neuroligin-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	540	4242	2730	706	786	20	0	0	0

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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		



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 1 2	Depositor
Cell constants a, b, c, α , β , γ	96.11Å 96.11Å 371.61Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.69 – 3.85 49.69 – 3.85	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.69-3.85) 99.9 (49.69-3.85)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.53 (at 3.88Å)	Xtriage
Refinement program	PHENIX (1.17.1_3660: ???)	Depositor
R, R_{free}	0.253 , 0.289 0.253 , 0.290	Depositor DCC
R_{free} test set	928 reflections (3.35%)	wwPDB-VP
Wilson B-factor (Å ²)	153.6	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 112.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.079 for -h,-k,l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	7273	wwPDB-VP
Average B, all atoms (Å ²)	189.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.10% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

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	0.12	0/3043	0.33	0/4151
2	B	0.10	0/4371	0.27	0/5973
All	All	0.11	0/7414	0.30	0/10124

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	2975	0	2934	55	0
2	B	4242	0	4091	54	0
3	A	28	0	26	0	0
3	B	28	0	26	0	0
All	All	7273	0	7077	102	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 (102) 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:145:GLU:HG3	1:A:228:VAL:HG11	1.58	0.84
1:A:317:LYS:HB3	1:A:396:ILE:HD12	1.71	0.70
2:B:613:ASP:OD1	2:B:613:ASP:N	2.26	0.68
1:A:323:PRO:HG3	1:A:392:ALA:HB2	1.77	0.66
1:A:247:GLY:N	1:A:291:VAL:O	2.28	0.66
1:A:228:VAL:HG22	1:A:229:ARG:H	1.60	0.65
2:B:295:LEU:HB2	2:B:463:PRO:HB3	1.78	0.65
1:A:77:GLU:HB3	2:B:320:LEU:HD23	1.79	0.65
1:A:229:ARG:NH1	2:B:369:GLU:OE1	2.31	0.64
1:A:354:GLN:HG2	1:A:366:GLU:HG2	1.81	0.63
2:B:489:SER:HB3	2:B:521:CYS:HA	1.81	0.63
1:A:233:PRO:HB3	1:A:262:PRO:HG3	1.85	0.58
2:B:205:GLY:HA3	2:B:539:THR:HG21	1.86	0.57
2:B:181:VAL:HB	2:B:261:VAL:HG12	1.86	0.57
1:A:262:PRO:HB3	1:A:303:SER:HB2	1.86	0.57
2:B:344:PRO:HB3	2:B:350:ALA:HB2	1.87	0.56
1:A:40:GLN:NE2	1:A:49:SER:O	2.37	0.56
2:B:123:ASN:HB3	2:B:126:ILE:HD13	1.88	0.55
2:B:612:HIS:HB3	2:B:615:PHE:CE2	2.43	0.54
1:A:321:LYS:N	1:A:344:ASN:OD1	2.40	0.54
1:A:350:TYR:HE1	1:A:393:VAL:HB	1.72	0.53
1:A:108:SER:HB3	1:A:113:GLU:HG3	1.91	0.53
1:A:354:GLN:HB3	1:A:364:TYR:HB3	1.90	0.53
2:B:422:GLU:HB2	2:B:611:LEU:HD13	1.90	0.53
1:A:245:MET:SD	1:A:245:MET:N	2.81	0.53
1:A:58:PRO:HD2	1:A:109:ASN:HD22	1.73	0.52
1:A:99:ASP:O	1:A:103:TYR:OH	2.26	0.52
2:B:81:PHE:HE1	2:B:219:LEU:HA	1.74	0.52
1:A:162:PRO:HB2	1:A:210:ALA:HB1	1.91	0.52
1:A:324:GLY:HA3	1:A:341:ASP:HB3	1.91	0.52
2:B:471:HIS:O	2:B:476:SER:OG	2.27	0.52
1:A:83:ASP:OD1	1:A:85:SER:OG	2.23	0.52
2:B:319:VAL:HG22	2:B:325:MET:HB3	1.92	0.52
1:A:144:VAL:HG11	1:A:150:ALA:HB2	1.91	0.52
2:B:361:PRO:HG2	2:B:367:LEU:HD21	1.91	0.52
2:B:43:THR:OG1	2:B:46:GLY:O	2.27	0.52
1:A:104:GLU:HA	1:A:117:SER:HA	1.93	0.51
1:A:203:GLN:HE21	1:A:225:TYR:HD1	1.58	0.51
1:A:223:ASN:ND2	2:B:225:GLY:O	2.43	0.51
1:A:92:GLN:HB3	2:B:320:LEU:HD13	1.93	0.51
1:A:339:THR:HG22	1:A:374:ARG:HB2	1.92	0.51
2:B:296:SER:HG	2:B:298:TRP:CD1	2.29	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:457:ASP:HA	2:B:461:VAL:HB	1.92	0.51
2:B:68:GLY:HA2	2:B:100:PRO:HG3	1.91	0.51
1:A:183:LYS:NZ	1:A:196:GLU:OE2	2.33	0.50
1:A:326:PRO:HB3	1:A:340:TRP:HB3	1.94	0.50
1:A:229:ARG:HD3	2:B:366:ILE:HG23	1.93	0.50
1:A:123:LEU:HD13	1:A:127:GLN:HB2	1.94	0.49
1:A:70:LYS:HD2	1:A:98:ARG:HG2	1.92	0.49
1:A:150:ALA:HB3	1:A:195:ILE:HB	1.95	0.49
1:A:393:VAL:HG22	1:A:398:ARG:HA	1.94	0.48
2:B:48:LEU:HD23	2:B:94:ARG:HB3	1.94	0.48
2:B:614:MET:H	2:B:614:MET:HG3	1.43	0.48
2:B:182:TYR:HA	2:B:262:PHE:O	2.13	0.48
2:B:421:PRO:HD2	2:B:424:LYS:HD2	1.95	0.48
2:B:239:ILE:HD11	2:B:274:LEU:HD22	1.96	0.47
1:A:241:ASN:HB3	1:A:313:GLN:H	1.79	0.47
2:B:288:ILE:HG12	2:B:379:MET:HB3	1.96	0.47
1:A:350:TYR:CE1	1:A:393:VAL:HB	2.49	0.47
2:B:399:ASP:O	2:B:448:ARG:NH1	2.46	0.47
1:A:203:GLN:HG3	1:A:225:TYR:HA	1.96	0.47
2:B:80:ARG:NE	2:B:136:GLU:OE1	2.45	0.47
2:B:265:GLY:HA2	2:B:500:HIS:CE1	2.50	0.47
2:B:63:VAL:HG12	2:B:146:PRO:HA	1.97	0.46
2:B:266:ILE:HD13	2:B:266:ILE:HA	1.80	0.46
2:B:361:PRO:HD2	2:B:367:LEU:HD11	1.97	0.46
2:B:594:ARG:HE	2:B:597:LYS:HG3	1.80	0.46
1:A:247:GLY:H	1:A:291:VAL:HB	1.79	0.45
1:A:352:ILE:HB	1:A:391:VAL:HB	1.98	0.45
1:A:41:THR:HG23	1:A:121:THR:HB	1.98	0.45
1:A:383:TYR:HB3	1:A:411:HIS:ND1	2.32	0.45
2:B:118:VAL:HG22	2:B:389:LYS:HE3	1.99	0.45
2:B:414:VAL:HG12	2:B:424:LYS:HE2	1.99	0.44
2:B:198:GLY:HA3	2:B:209:VAL:HG11	1.99	0.44
1:A:47:VAL:HG11	1:A:90:ARG:CZ	2.47	0.43
2:B:492:LYS:HZ2	2:B:499:ALA:HB3	1.83	0.43
2:B:432:LYS:O	2:B:436:THR:OG1	2.25	0.43
2:B:443:ASN:HB3	2:B:446:THR:HB	2.00	0.43
1:A:266:TRP:CD1	1:A:286:LEU:HB2	2.53	0.43
2:B:420:TYR:HA	2:B:424:LYS:HD2	2.00	0.43
1:A:253:THR:HA	1:A:285:VAL:HG12	2.01	0.42
2:B:182:TYR:CE2	2:B:196:ILE:HD12	2.54	0.42
2:B:440:ASP:CG	2:B:443:ASN:HB2	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:492:LYS:NZ	2:B:499:ALA:HB3	2.33	0.42
2:B:113:GLU:O	2:B:389:LYS:NZ	2.49	0.42
1:A:30:PRO:HB2	1:A:32:ARG:HH12	1.85	0.42
1:A:241:ASN:O	1:A:242:HIS:ND1	2.52	0.42
2:B:276:LEU:HD21	2:B:368:MET:HG2	2.01	0.42
2:B:382:VAL:HG21	2:B:461:VAL:HG22	2.02	0.42
2:B:396:ASP:HB2	2:B:397:PRO:HD2	2.02	0.41
2:B:401:VAL:O	2:B:447:ARG:HD2	2.20	0.41
1:A:96:THR:HB	1:A:122:VAL:HG12	2.01	0.41
1:A:28:GLU:HB3	1:A:111:VAL:HG21	2.02	0.41
2:B:335:LYS:HA	2:B:335:LYS:HD2	1.76	0.41
1:A:90:ARG:HE	2:B:320:LEU:HD11	1.85	0.41
1:A:381:SER:HA	1:A:382:PRO:HD3	1.93	0.41
1:A:181:ARG:HD2	1:A:197:GLN:O	2.20	0.41
1:A:141:LEU:HD12	2:B:302:TYR:HA	2.03	0.41
1:A:323:PRO:HD2	1:A:402:SER:HB3	2.03	0.41
1:A:32:ARG:HD3	1:A:32:ARG:HA	1.89	0.40
1:A:145:GLU:HA	1:A:228:VAL:HB	2.04	0.40
2:B:364:PRO:O	2:B:368:MET:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	384/386 (100%)	363 (94%)	21 (6%)	0	100	100
2	B	534/579 (92%)	508 (95%)	26 (5%)	0	100	100
All	All	918/965 (95%)	871 (95%)	47 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	335/335 (100%)	333 (99%)	2 (1%)	78	80
2	B	462/494 (94%)	458 (99%)	4 (1%)	70	75
All	All	797/829 (96%)	791 (99%)	6 (1%)	73	77

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	291	VAL
1	A	350	TYR
2	B	266	ILE
2	B	611	LEU
2	B	613	ASP
2	B	614	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	ASN
1	A	355	HIS
1	A	410	HIS
2	B	348	HIS
2	B	384	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
3	NAG	A	501	1	14,14,15	0.40	0	17,19,21	0.52	0
3	NAG	B	702	2	14,14,15	0.31	0	17,19,21	0.33	0
3	NAG	A	502	1	14,14,15	0.25	0	17,19,21	0.36	0
3	NAG	B	701	2	14,14,15	0.23	0	17,19,21	0.46	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	501	1	-	2/6/23/26	0/1/1/1
3	NAG	B	702	2	-	2/6/23/26	0/1/1/1
3	NAG	A	502	1	-	1/6/23/26	0/1/1/1
3	NAG	B	701	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	NAG	O5-C5-C6-O6
3	B	702	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
3	A	501	NAG	C4-C5-C6-O6
3	B	702	NAG	O5-C5-C6-O6
3	A	502	NAG	O5-C5-C6-O6
3	B	701	NAG	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	386/386 (100%)	0.66	48 (12%) 8 12	135, 182, 255, 355	0
2	B	540/579 (93%)	1.08	116 (21%) 2 4	105, 184, 259, 333	0
All	All	926/965 (95%)	0.91	164 (17%) 4 6	105, 183, 259, 355	0

All (164) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	426	THR	8.3
2	B	604	LEU	8.2
2	B	427	LEU	8.2
2	B	608	LEU	8.2
2	B	191	GLY	7.8
2	B	105	GLN	6.4
2	B	334	ALA	6.3
2	B	298	TRP	6.2
2	B	186	GLY	5.9
2	B	190	GLU	5.4
1	A	406	LEU	5.4
2	B	196	ILE	5.1
2	B	187	SER	5.0
2	B	430	THR	5.0
1	A	357	PRO	4.9
1	A	60	PRO	4.8
1	A	89	LEU	4.8
1	A	363	PRO	4.8
2	B	143	VAL	4.7
2	B	337	LEU	4.6
2	B	266	ILE	4.6
1	A	246	PRO	4.4
1	A	92	GLN	4.3
1	A	407	THR	4.1

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Mol	Chain	Res	Type	RSRZ
2	B	115	MET	4.1
2	B	37	PRO	4.1
2	B	278	HIS	4.0
2	B	606	PRO	4.0
2	B	605	VAL	4.0
2	B	188	TYR	4.0
2	B	270	CYS	4.0
1	A	85	SER	3.9
1	A	387	GLU	3.8
2	B	110	ALA	3.8
2	B	600	PHE	3.8
2	B	431	ILE	3.7
1	A	47	VAL	3.7
2	B	609	TYR	3.7
1	A	360	SER	3.6
2	B	423	GLY	3.6
2	B	351	PHE	3.6
1	A	349	SER	3.6
2	B	603	HIS	3.6
1	A	411	HIS	3.5
2	B	114	VAL	3.5
1	A	350	TYR	3.4
2	B	66	TYR	3.4
2	B	174	SER	3.4
2	B	305	VAL	3.4
2	B	175	GLY	3.3
2	B	195	MET	3.3
1	A	413	HIS	3.3
2	B	455	PHE	3.3
2	B	209	VAL	3.3
2	B	273	LEU	3.2
1	A	359	ASN	3.2
2	B	602	LYS	3.2
1	A	81	PHE	3.2
2	B	373	PHE	3.2
2	B	433	PHE	3.2
1	A	346	GLU	3.2
2	B	112	PRO	3.2
1	A	227	ARG	3.1
2	B	284	PHE	3.1
1	A	91	ILE	3.0
2	B	349	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	297	TYR	3.0
2	B	347	TYR	3.0
1	A	54	ALA	3.0
2	B	281	GLU	2.9
2	B	252	PHE	2.9
2	B	219	LEU	2.9
2	B	490	LEU	2.9
2	B	518	LEU	2.9
2	B	120	PHE	2.9
1	A	355	HIS	2.9
2	B	116	LEU	2.8
2	B	223	SER	2.8
1	A	53	GLN	2.8
2	B	615	PHE	2.8
2	B	276	LEU	2.8
1	A	231	VAL	2.8
2	B	144	TYR	2.8
2	B	418	TYR	2.7
2	B	282	GLY	2.7
2	B	459	GLN	2.7
2	B	543	LYS	2.7
1	A	84	GLY	2.7
2	B	216	VAL	2.7
2	B	131	ILE	2.7
2	B	429	GLU	2.7
2	B	317	CYS	2.7
2	B	419	GLY	2.6
1	A	50	PHE	2.6
1	A	153	LEU	2.6
2	B	568	VAL	2.6
2	B	225	GLY	2.6
2	B	230	LYS	2.6
2	B	438	TRP	2.6
2	B	231	GLY	2.6
2	B	356	ASP	2.6
2	B	324	ASP	2.5
1	A	334	THR	2.5
1	A	229	ARG	2.5
2	B	274	LEU	2.5
2	B	614	MET	2.5
2	B	210	ILE	2.5
2	B	212	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	228	VAL	2.5
2	B	596	THR	2.4
1	A	201	SER	2.4
2	B	78	GLU	2.4
1	A	333	ALA	2.4
2	B	413	PHE	2.4
2	B	300	VAL	2.4
2	B	358	ASP	2.4
2	B	441	ARG	2.4
2	B	222	LEU	2.3
2	B	329	LEU	2.3
2	B	421	PRO	2.3
2	B	227	GLN	2.3
2	B	378	ILE	2.3
1	A	293	GLN	2.3
1	A	395	ASN	2.3
1	A	82	ASP	2.3
2	B	594	ARG	2.3
2	B	185	GLY	2.3
2	B	221	PHE	2.2
1	A	137	MET	2.2
1	A	80	GLU	2.2
1	A	141	LEU	2.2
2	B	420	TYR	2.2
2	B	336	GLU	2.2
1	A	48	ALA	2.2
1	A	174	ASP	2.2
2	B	294	ALA	2.2
2	B	311	LEU	2.2
2	B	145	VAL	2.2
2	B	598	VAL	2.1
2	B	332	LYS	2.1
2	B	104	PRO	2.1
2	B	198	GLY	2.1
1	A	185	LEU	2.1
1	A	412	HIS	2.1
2	B	371	GLY	2.1
2	B	295	LEU	2.1
2	B	492	LYS	2.1
2	B	488	GLN	2.1
2	B	391	VAL	2.1
1	A	90	ARG	2.0

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Mol	Chain	Res	Type	RSRZ
2	B	517	ASP	2.0
1	A	314	ILE	2.0
2	B	113	GLU	2.0
2	B	355	ILE	2.0
2	B	299	ALA	2.0
1	A	76	PHE	2.0
2	B	480	PHE	2.0
1	A	79	ILE	2.0
2	B	260	THR	2.0
2	B	81	PHE	2.0
2	B	242	LEU	2.0
2	B	184	HIS	2.0
2	B	99	PHE	2.0
2	B	327	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	NAG	B	701	14/15	0.31	0.11	259,300,346,347	0
3	NAG	A	501	14/15	0.35	0.15	146,190,208,211	0
3	NAG	A	502	14/15	0.62	0.19	100,184,206,208	0
3	NAG	B	702	14/15	0.88	0.09	223,282,370,389	0

6.5 Other polymers [i](#)

There are no such residues in this entry.