



# Full wwPDB X-ray Structure Validation Report i

Aug 7, 2020 – 10:08 PM BST

PDB ID : 2GY5  
Title : Tie2 Ligand-Binding Domain Crystal Structure  
Authors : Barton, W.A.; Nikolov, D.B.  
Deposited on : 2006-05-09  
Resolution : 2.90 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 i symbol.

---

The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.13.1  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.13.1

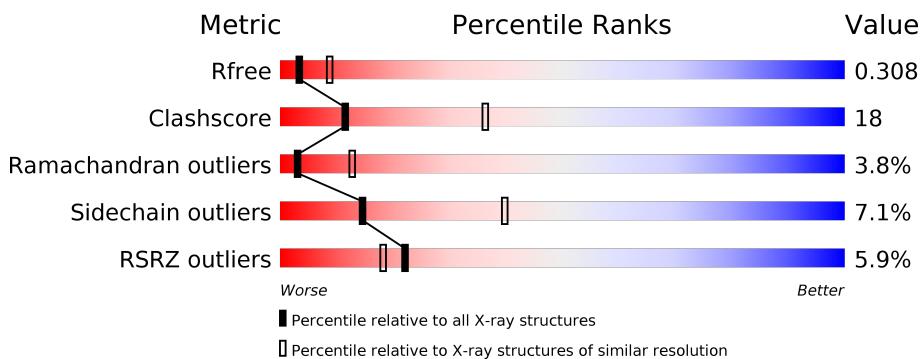
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

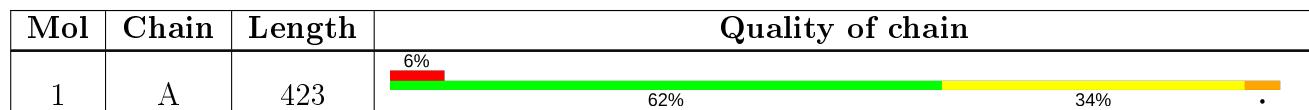
The reported resolution of this entry is 2.90 Å.

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))
$R_{free}$	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 >=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 <=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.



The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	NDG	A	1399	-	-	-	X
3	NDG	A	1438	-	-	X	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SO4	A	5	-	-	-	X

## 2 Entry composition (i)

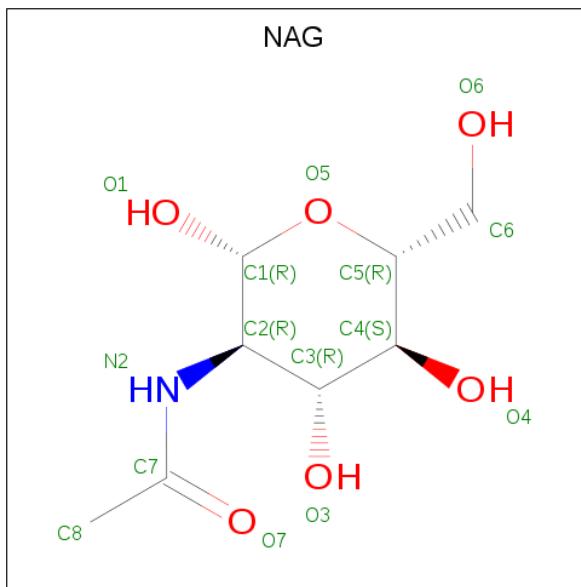
There are 4 unique types of molecules in this entry. The entry contains 3383 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Angiopoietin-1 receptor.

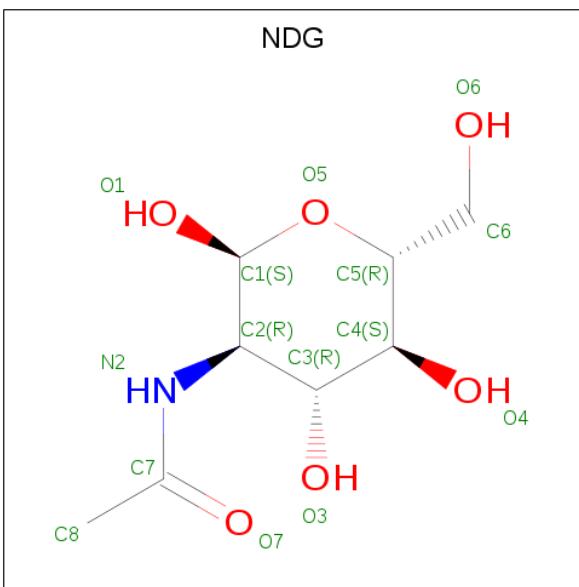
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	423	3289	2063	583	604	39	0	0	0

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



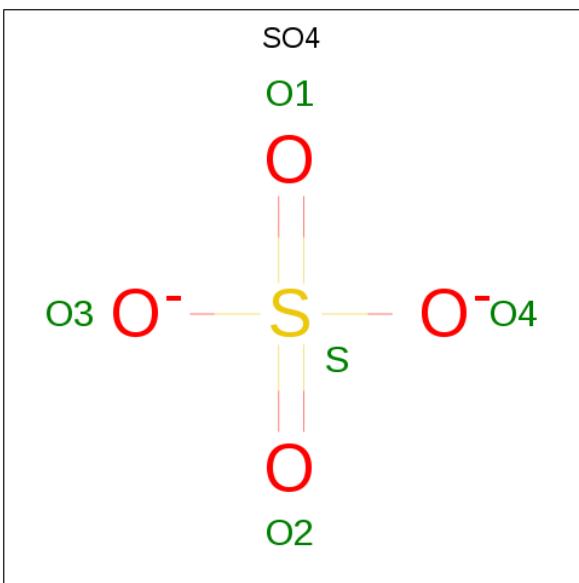
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O			
2	A	1	14	8	1	5		0	0

- Molecule 3 is 2-acetamido-2-deoxy-alpha-D-glucopyranose (three-letter code: NDG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O 15 8 1 6	0	0
3	A	1	Total C N O 15 8 1 6	0	0
3	A	1	Total C N O 15 8 1 6	0	0
3	A	1	Total C N O 15 8 1 6	0	0

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).

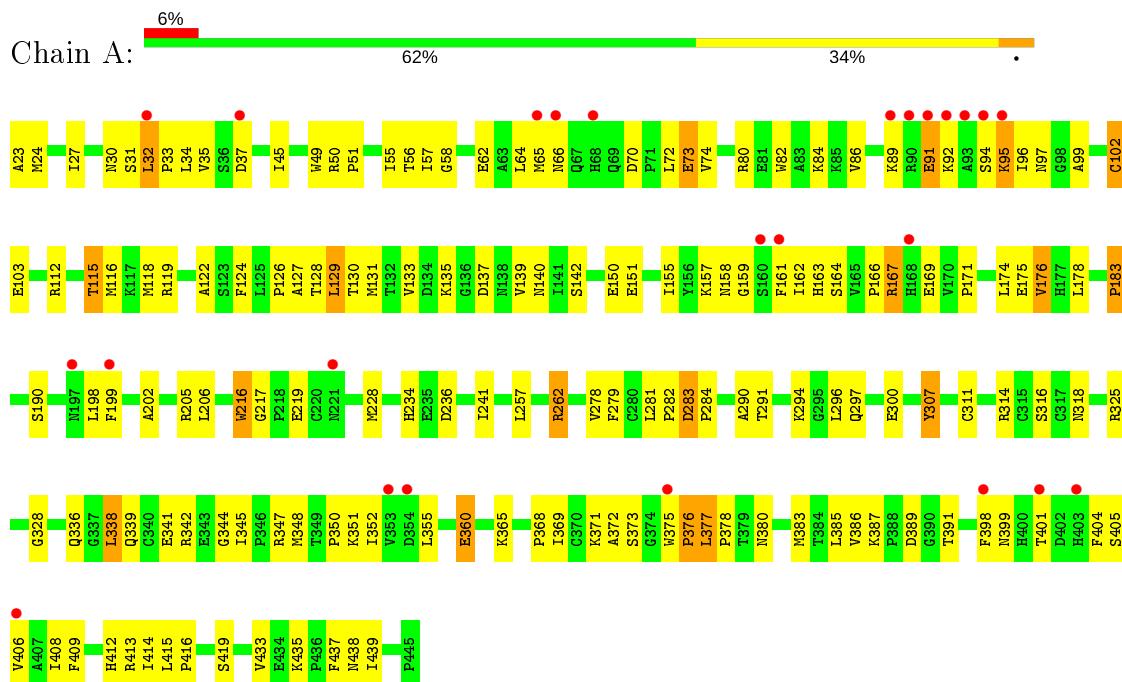


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0
4	A	1	Total O S 5 4 1	0	0

### 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: Angiopoietin-1 receptor



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.65 Å    114.65 Å    113.77 Å 90.00°    90.00°    90.00°	Depositor
Resolution (Å)	8.00 – 2.90 46.75 – 2.80	Depositor EDS
% Data completeness (in resolution range)	94.9 (8.00-2.90) 94.9 (46.75-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	2.84 (at 2.81 Å)	Xtriage
Refinement program	CNS 1.0	Depositor
$R$ , $R_{free}$	0.240 , 0.294 0.259 , 0.308	Depositor DCC
$R_{free}$ test set	3352 reflections (9.69%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	39.3	Xtriage
Anisotropy	0.214	Xtriage
Bulk solvent $k_{sol}(e/\text{\AA}^3)$ , $B_{sol}(\text{\AA}^2)$	0.33 , 37.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.020 for -h,-l,-k 0.014 for l,-k,h	Xtriage
$F_o, F_c$ correlation	0.83	EDS
Total number of atoms	3383	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.28% 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 [\(i\)](#)

### 5.1 Standard geometry [\(i\)](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, NDG, SO4

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	0.41	0/3372	0.75	3/4571 (0.1%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	283	ASP	N-CA-C	6.71	129.11	111.00
1	A	311	CYS	CA-CB-SG	-5.45	104.20	114.00
1	A	307	TYR	N-CA-C	5.03	124.59	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [\(i\)](#)

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	3289	0	3187	114	0
2	A	14	0	13	0	0
3	A	60	0	48	15	0
4	A	20	0	0	0	0
All	All	3383	0	3248	117	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 18.

All (117) 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:399:ASN:HD21	3:A:1399:NDG:C1	1.82	0.92
1:A:30:ASN:HD22	1:A:115:THR:HG21	1.33	0.92
1:A:142:SER:HB3	1:A:175:GLU:HG2	1.63	0.78
1:A:166:PRO:HG2	1:A:169:GLU:HB2	1.66	0.77
1:A:155:ILE:HD13	1:A:176:VAL:HG22	1.69	0.74
1:A:30:ASN:HD22	1:A:115:THR:CG2	2.01	0.74
1:A:151:GLU:HA	1:A:167:ARG:HG3	1.70	0.74
1:A:45:ILE:HD13	1:A:80:ARG:HD3	1.72	0.72
1:A:401:THR:HG21	3:A:1399:NDG:H8C3	1.70	0.72
1:A:375:TRP:C	1:A:377:LEU:H	1.94	0.71
1:A:62:GLU:OE1	3:A:1158:NDG:H4	1.91	0.71
3:A:1438:NDG:O4	3:A:1439:NDG:C1	2.39	0.71
1:A:95:LYS:H	1:A:95:LYS:HD3	1.54	0.70
1:A:438:ASN:ND2	3:A:1438:NDG:C1	2.58	0.67
1:A:64:LEU:HD12	1:A:158:ASN:HA	1.77	0.67
1:A:130:THR:HG22	1:A:205:ARG:HB3	1.78	0.66
1:A:345:ILE:HD12	1:A:345:ILE:H	1.59	0.66
1:A:399:ASN:ND2	3:A:1399:NDG:C1	2.58	0.66
1:A:118:MET:HE1	1:A:126:PRO:HD3	1.78	0.66
1:A:55:ILE:HB	1:A:84:LYS:HD2	1.78	0.66
1:A:133:VAL:HG11	1:A:139:VAL:HG22	1.78	0.66
1:A:369:ILE:HG12	1:A:408:ILE:HG12	1.77	0.66
1:A:296:LEU:O	1:A:297:GLN:HB2	1.97	0.65
1:A:34:LEU:H	1:A:297:GLN:HE22	1.45	0.63
1:A:161:PHE:HZ	1:A:164:SER:HB2	1.64	0.62
1:A:375:TRP:HB3	1:A:376:PRO:HD3	1.81	0.62
1:A:118:MET:CE	1:A:126:PRO:HD3	2.31	0.61
1:A:65:MET:HG3	1:A:66:ASN:ND2	2.15	0.61
1:A:23:ALA:HB2	1:A:386:VAL:HG11	1.82	0.61
1:A:296:LEU:O	1:A:297:GLN:CB	2.49	0.61
1:A:56:THR:O	1:A:102:CYS:HA	2.00	0.61
3:A:1158:NDG:O3	3:A:1158:NDG:H8C1	2.02	0.59
1:A:131:MET:CE	1:A:139:VAL:HG13	2.32	0.59
1:A:438:ASN:HD21	3:A:1438:NDG:C1	2.16	0.58
1:A:438:ASN:HD21	3:A:1438:NDG:C7	2.17	0.57
1:A:352:ILE:HB	1:A:435:LYS:HD3	1.86	0.57
1:A:371:LYS:HG3	1:A:406:VAL:HG22	1.86	0.56
1:A:155:ILE:CD1	1:A:176:VAL:HG22	2.34	0.56
1:A:50:ARG:HB2	1:A:82:TRP:CZ2	2.40	0.56
1:A:234:HIS:CD2	1:A:236:ASP:H	2.25	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:TRP:C	1:A:377:LEU:N	2.60	0.55
1:A:375:TRP:O	1:A:377:LEU:N	2.39	0.55
1:A:241:ILE:HD12	1:A:284:PRO:HG2	1.89	0.55
1:A:352:ILE:HG13	1:A:435:LYS:HB2	1.88	0.55
1:A:348:MET:HB2	1:A:375:TRP:H	1.72	0.55
1:A:74:VAL:HG22	1:A:86:VAL:HG22	1.88	0.54
1:A:155:ILE:HD13	1:A:176:VAL:CG2	2.36	0.54
1:A:387:LYS:HD3	1:A:391:THR:HB	1.90	0.54
1:A:161:PHE:CZ	1:A:164:SER:HB2	2.42	0.54
1:A:413:ARG:HG3	1:A:413:ARG:O	2.07	0.53
1:A:380:ASN:HD22	1:A:398:PHE:HB2	1.75	0.52
1:A:131:MET:HE1	1:A:139:VAL:HG13	1.92	0.52
1:A:373:SER:HB3	1:A:404:PHE:CE2	2.45	0.52
1:A:216:TRP:CD1	1:A:217:GLY:N	2.78	0.51
1:A:126:PRO:O	1:A:127:ALA:HB3	2.10	0.51
1:A:89:LYS:HB2	1:A:92:LYS:HB3	1.92	0.51
1:A:97:ASN:HD21	1:A:119:ARG:H	1.58	0.50
1:A:65:MET:HG2	1:A:158:ASN:O	2.12	0.49
1:A:376:PRO:O	1:A:377:LEU:O	2.31	0.49
1:A:139:VAL:HB	1:A:178:LEU:HB2	1.95	0.48
1:A:27:ILE:HG23	1:A:281:LEU:HD23	1.96	0.48
1:A:157:LYS:HB2	1:A:162:ILE:HG13	1.95	0.48
1:A:383:MET:SD	1:A:398:PHE:HE1	2.37	0.47
1:A:131:MET:HE2	1:A:139:VAL:HG13	1.95	0.47
1:A:438:ASN:HD21	3:A:1438:NDG:H8C3	1.79	0.47
1:A:198:LEU:HD23	1:A:198:LEU:C	2.35	0.47
1:A:118:MET:CE	1:A:202:ALA:HA	2.44	0.47
1:A:279:PHE:CE1	1:A:290:ALA:HB2	2.49	0.47
1:A:129:LEU:HD22	1:A:129:LEU:HA	1.80	0.47
1:A:158:ASN:ND2	3:A:1158:NDG:C1	2.77	0.47
1:A:27:ILE:HG23	1:A:281:LEU:CD2	2.45	0.46
1:A:57:ILE:HG12	1:A:102:CYS:HB2	1.97	0.46
1:A:291:THR:HG23	1:A:291:THR:O	2.15	0.46
1:A:58:GLY:HA2	1:A:72:LEU:HD12	1.98	0.46
1:A:438:ASN:HD21	3:A:1438:NDG:C8	2.29	0.46
1:A:163:HIS:CD2	1:A:164:SER:H	2.33	0.46
1:A:157:LYS:O	1:A:158:ASN:HB3	2.16	0.46
1:A:199:PHE:CD2	1:A:199:PHE:N	2.82	0.46
1:A:307:TYR:O	1:A:325:ARG:O	2.35	0.46
1:A:118:MET:HE1	1:A:202:ALA:HA	1.97	0.45
1:A:135:LYS:HG3	1:A:183:PRO:HD3	1.99	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:THR:HG22	3:A:1399:NDG:O7	2.17	0.45
1:A:80:ARG:HG2	1:A:80:ARG:HH11	1.81	0.45
1:A:351:LYS:O	1:A:372:ALA:HA	2.16	0.45
3:A:1438:NDG:O3	3:A:1439:NDG:O5	2.32	0.44
1:A:155:ILE:O	1:A:162:ILE:HB	2.18	0.44
1:A:142:SER:CB	1:A:175:GLU:HG2	2.42	0.44
1:A:35:VAL:HG21	1:A:96:ILE:HD11	1.99	0.44
1:A:169:GLU:O	1:A:171:PRO:HD3	2.17	0.44
1:A:378:PRO:HG2	1:A:405:SER:HB2	2.00	0.43
1:A:401:THR:CG2	3:A:1399:NDG:H8C3	2.43	0.43
1:A:139:VAL:HG12	1:A:140:ASN:N	2.33	0.43
1:A:37:ASP:OD2	1:A:91:GLU:HG2	2.18	0.43
1:A:155:ILE:HG21	1:A:176:VAL:HG21	1.99	0.43
1:A:33:PRO:HD3	1:A:278:VAL:HG21	1.99	0.43
1:A:376:PRO:O	1:A:377:LEU:C	2.57	0.43
1:A:115:THR:HG22	1:A:116:MET:H	1.84	0.42
1:A:49:TRP:O	1:A:51:PRO:HD3	2.19	0.42
1:A:73:GLU:OE1	1:A:73:GLU:HA	2.18	0.42
1:A:103:GLU:OE2	1:A:112:ARG:HD2	2.19	0.42
1:A:414:ILE:HG23	1:A:414:ILE:O	2.19	0.42
1:A:130:THR:HA	1:A:205:ARG:O	2.20	0.42
1:A:342:ARG:HH12	1:A:347:ARG:NH2	2.16	0.42
1:A:419:SER:HB2	1:A:439:ILE:O	2.20	0.42
1:A:23:ALA:HB2	1:A:386:VAL:CG1	2.50	0.41
1:A:30:ASN:O	1:A:32:LEU:N	2.54	0.41
1:A:415:LEU:HB3	1:A:416:PRO:HD2	2.03	0.41
1:A:307:TYR:CG	1:A:328:GLY:HA2	2.55	0.41
1:A:350:PRO:O	1:A:433:VAL:HG11	2.20	0.41
1:A:99:ALA:HA	1:A:116:MET:HG3	2.02	0.41
1:A:24:MET:HG3	1:A:262:ARG:HH21	1.85	0.41
1:A:124:PHE:O	1:A:202:ALA:HB2	2.21	0.40
1:A:368:PRO:HG2	1:A:409:PHE:HB2	2.02	0.40
1:A:228:MET:HB3	1:A:338:LEU:HD21	2.02	0.40
1:A:316:SER:O	1:A:339:GLN:HB3	2.21	0.40
1:A:126:PRO:O	1:A:128:THR:N	2.48	0.40
1:A:294:LYS:NZ	1:A:300:GLU:OE1	2.55	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	421/423 (100%)	372 (88%)	33 (8%)	16 (4%)	3 13

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	94	SER
1	A	122	ALA
1	A	137	ASP
1	A	377	LEU
1	A	257	LEU
1	A	167	ARG
1	A	360	GLU
1	A	32	LEU
1	A	159	GLY
1	A	318	ASN
1	A	412	HIS
1	A	31	SER
1	A	91	GLU
1	A	283	ASP
1	A	344	GLY
1	A	376	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.

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
-----	-------	----------	-----------	----------	-------------

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	366/367 (100%)	340 (93%)	26 (7%)	14 40

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	70	ASP
1	A	73	GLU
1	A	95	LYS
1	A	102	CYS
1	A	115	THR
1	A	129	LEU
1	A	150	GLU
1	A	174	LEU
1	A	176	VAL
1	A	183	PRO
1	A	190	SER
1	A	206	LEU
1	A	216	TRP
1	A	219	GLU
1	A	262	ARG
1	A	282	PRO
1	A	314	ARG
1	A	336	GLN
1	A	338	LEU
1	A	341	GLU
1	A	355	LEU
1	A	360	GLU
1	A	365	LYS
1	A	385	LEU
1	A	389	ASP
1	A	437	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	GLN
1	A	97	ASN
1	A	138	ASN
1	A	163	HIS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	221	ASN
1	A	234	HIS
1	A	297	GLN
1	A	319	ASN
1	A	380	ASN
1	A	399	ASN
1	A	438	ASN

### 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 monosaccharides in this entry.

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

9 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	NDG	A	1439	-	15,15,15	0.66	0	21,21,21	0.88	1 (4%)
4	SO4	A	5	-	4,4,4	0.33	0	6,6,6	0.07	0
3	NDG	A	1158	-	15,15,15	0.71	0	21,21,21	1.38	4 (19%)
4	SO4	A	1	-	4,4,4	0.21	0	6,6,6	0.10	0
3	NDG	A	1438	-	15,15,15	0.79	1 (6%)	21,21,21	0.90	0
3	NDG	A	1399	-	15,15,15	0.71	0	21,21,21	1.38	3 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	A	1140	1	14,14,15	0.65	0	17,19,21	0.68	1 (5%)
4	SO4	A	4	-	4,4,4	0.29	0	6,6,6	0.14	0
4	SO4	A	3	-	4,4,4	0.22	0	6,6,6	0.11	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	NDG	A	1438	-	-	6/6/26/26	0/1/1/1
2	NAG	A	1140	1	-	3/6/23/26	0/1/1/1
3	NDG	A	1158	-	-	4/6/26/26	0/1/1/1
3	NDG	A	1439	-	-	4/6/26/26	0/1/1/1
3	NDG	A	1399	-	-	4/6/26/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1438	NDG	C8-C7	2.04	1.54	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1399	NDG	C4-C3-C2	3.86	116.00	110.34
3	A	1158	NDG	C4-C3-C2	3.14	114.94	110.34
3	A	1158	NDG	C1-C2-C3	3.04	114.69	110.54
3	A	1399	NDG	C3-C4-C5	2.92	115.44	110.24
3	A	1158	NDG	C1-C2-N2	-2.58	107.74	110.73
3	A	1399	NDG	C1-C2-N2	-2.23	108.14	110.73
3	A	1158	NDG	C3-C2-N2	-2.14	106.58	110.62
2	A	1140	NAG	C2-N2-C7	-2.07	119.95	122.90
3	A	1439	NDG	C4-C3-C2	2.05	113.34	110.34

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1439	NDG	C8-C7-N2-C2
3	A	1439	NDG	O7-C7-N2-C2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms
3	A	1158	NDG	C8-C7-N2-C2
3	A	1158	NDG	O7-C7-N2-C2
3	A	1438	NDG	C8-C7-N2-C2
3	A	1438	NDG	O7-C7-N2-C2
3	A	1399	NDG	C8-C7-N2-C2
3	A	1399	NDG	O7-C7-N2-C2
2	A	1140	NAG	C8-C7-N2-C2
2	A	1140	NAG	O7-C7-N2-C2
3	A	1438	NDG	C4-C5-C6-O6
3	A	1439	NDG	O5-C5-C6-O6
3	A	1158	NDG	O5-C5-C6-O6
3	A	1158	NDG	C4-C5-C6-O6
3	A	1439	NDG	C4-C5-C6-O6
3	A	1438	NDG	O5-C5-C6-O6
3	A	1438	NDG	C3-C2-N2-C7
3	A	1399	NDG	C4-C5-C6-O6
3	A	1438	NDG	C1-C2-N2-C7
3	A	1399	NDG	O5-C5-C6-O6
2	A	1140	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1439	NDG	2	0
3	A	1158	NDG	3	0
3	A	1438	NDG	7	0
3	A	1399	NDG	5	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	423/423 (100%)	0.29	25 (5%) 22   18	11, 31, 53, 71	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	90	ARG	5.3
1	A	93	ALA	5.0
1	A	91	GLU	4.5
1	A	375	TRP	4.3
1	A	199	PHE	4.2
1	A	353	VAL	3.7
1	A	403	HIS	3.6
1	A	168	HIS	3.3
1	A	37	ASP	3.3
1	A	65	MET	3.2
1	A	32	LEU	3.0
1	A	94	SER	2.9
1	A	406	VAL	2.8
1	A	68	HIS	2.5
1	A	95	LYS	2.4
1	A	221	ASN	2.4
1	A	354	ASP	2.4
1	A	160	SER	2.4
1	A	197	ASN	2.3
1	A	161	PHE	2.3
1	A	398	PHE	2.3
1	A	66	ASN	2.3
1	A	89	LYS	2.3
1	A	92	LYS	2.3
1	A	401	THR	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(Å <sup>2</sup> )	Q<0.9
4	SO4	A	5	5/5	0.63	0.83	94,95,95,95	0
3	NDG	A	1439	15/15	0.65	0.33	43,47,49,50	0
3	NDG	A	1399	15/15	0.67	0.56	39,44,50,50	0
3	NDG	A	1438	15/15	0.77	0.26	28,34,36,36	0
2	NAG	A	1140	14/15	0.79	0.29	47,52,54,55	0
3	NDG	A	1158	15/15	0.83	0.29	25,29,39,41	0
4	SO4	A	4	5/5	0.90	0.29	64,65,66,66	0
4	SO4	A	3	5/5	0.97	0.26	52,52,53,53	0
4	SO4	A	1	5/5	0.98	0.14	31,31,31,32	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.