



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 10:02 am GMT

PDB ID : 3NZS
Title : Structure-based Optimization of Pyrazolo -Pyrimidine and -Pyridine Inhibitors of PI3-Kinase
Authors : Murray, J.M.; Wiesmann, C.
Deposited on : 2010-07-16
Resolution : 2.75 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

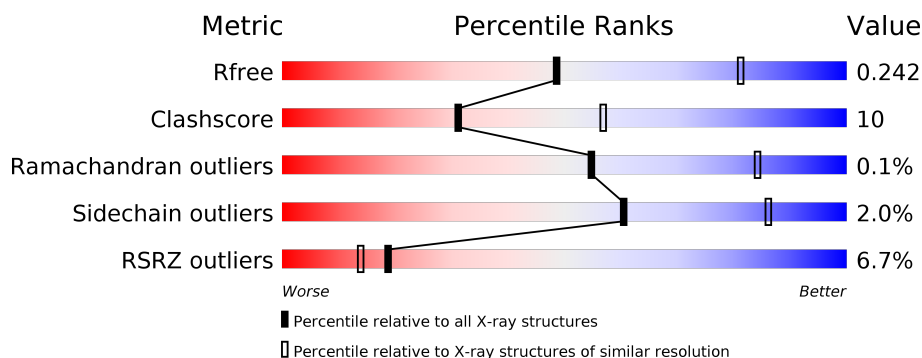
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.75 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	3666 (2.80-2.72)
Clashscore	112137	4174 (2.80-2.72)
Ramachandran outliers	110173	4103 (2.80-2.72)
Sidechain outliers	110143	4106 (2.80-2.72)
RSRZ outliers	101464	3697 (2.80-2.72)

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. 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	954	<div> <div>6%</div> <div>67%</div> <div>19%</div> <div>•</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6739 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.

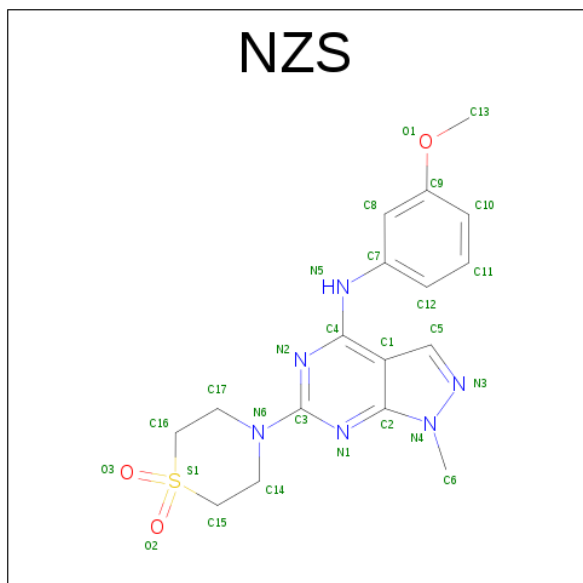
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	828	Total	C	N	O	S	29	0	0
			6712	4319	1144	1215	34			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1095	HIS	-	EXPRESSION TAG	UNP P48736
A	1096	HIS	-	EXPRESSION TAG	UNP P48736
A	1097	HIS	-	EXPRESSION TAG	UNP P48736
A	1098	HIS	-	EXPRESSION TAG	UNP P48736
A	1099	HIS	-	EXPRESSION TAG	UNP P48736
A	1100	HIS	-	EXPRESSION TAG	UNP P48736

- Molecule 2 is 6-(1,1-DIOXIDOTHIOMORPHOLIN-4-YL)-N-(3-METHOXYPHENYL)-1-METHYL-1H-PYRAZOLO[3,4-D]PYRIMIDIN-4-AMINE (three-letter code: NZS) (formula: C₁₇H₂₀N₆O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			27	17	6	3	1		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.97Å 67.97Å 106.99Å 90.00° 95.57° 90.00°	Depositor
Resolution (Å)	19.97 – 2.75 19.97 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.4 (19.97-2.75) 99.4 (19.97-2.75)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.75Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_392)	Depositor
R, R_{free}	0.210 , 0.243 0.213 , 0.242	Depositor DCC
R_{free} test set	1361 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	73.6	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 72.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6739	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NZS

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	0.27	0/6857	0.40	2/9281 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	915	SER	C-N-CD	-9.31	100.12	120.60
1	A	1092	LEU	CA-CB-CG	-5.23	103.28	115.30

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	6712	0	6758	136	0
2	A	27	0	20	5	0
All	All	6739	0	6778	138	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 10.

All (138) 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:968:ILE:C	1:A:968:ILE:HD12	1.56	1.23
1:A:917:THR:OG1	1:A:919:GLU:HG2	1.58	1.04
1:A:968:ILE:C	1:A:968:ILE:CD1	2.30	0.97
1:A:955:THR:HG22	1:A:957:THR:H	1.45	0.82
1:A:1087:PHE:O	1:A:1091:VAL:HB	1.80	0.81
1:A:890:LYS:HE2	2:A:1:NZS:H13A	1.71	0.72
2:A:1:NZS:N2	2:A:1:NZS:H8	2.04	0.72
1:A:693:HIS:CD2	1:A:789:PRO:HG3	2.26	0.70
1:A:917:THR:OG1	1:A:919:GLU:CG	2.37	0.70
1:A:1035:LEU:HD12	1:A:1048:ILE:HG12	1.74	0.68
1:A:1041:GLN:HG2	1:A:1042:LEU:HD13	1.74	0.67
1:A:779:LEU:HG	1:A:780:PRO:HD2	1.79	0.65
1:A:233:ILE:HD11	1:A:248:PHE:HD1	1.60	0.65
1:A:1091:VAL:O	1:A:1092:LEU:HD23	1.96	0.64
1:A:182:THR:HB	1:A:183:PRO:HD3	1.82	0.62
1:A:625:GLY:HA2	1:A:1026:LEU:HD23	1.82	0.61
1:A:734:GLN:O	1:A:738:VAL:HG12	2.00	0.61
1:A:579:ARG:HB2	1:A:610:LEU:HD11	1.82	0.61
1:A:529:LEU:HD12	1:A:530:PRO:HD2	1.84	0.60
1:A:739:ILE:HD13	1:A:872:THR:HG21	1.84	0.59
1:A:767:LEU:HD22	1:A:803:VAL:HG23	1.84	0.59
1:A:225:HIS:CD2	1:A:225:HIS:N	2.70	0.58
1:A:809:LYS:N	1:A:810:PRO:HD3	2.17	0.58
1:A:207:LEU:HD12	1:A:208:PRO:HD2	1.86	0.58
1:A:882:VAL:HG23	2:A:1:NZS:H6	1.85	0.58
1:A:625:GLY:O	1:A:629:GLN:HG3	2.04	0.57
1:A:218:ASN:O	1:A:237:PRO:HD3	2.05	0.56
1:A:280:TYR:HB3	1:A:282:VAL:HG23	1.87	0.55
1:A:593:PHE:CZ	1:A:611:LEU:HD21	2.42	0.55
1:A:702:GLU:O	1:A:706:SER:HB3	2.06	0.54
1:A:373:LEU:HB2	1:A:404:PHE:HE2	1.73	0.54
1:A:425:LYS:HD2	1:A:672:TYR:OH	2.08	0.54
1:A:887:THR:HG22	1:A:889:ALA:H	1.73	0.53
1:A:364:LYS:HE3	1:A:413:TRP:CE2	2.44	0.53
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.89	0.53
2:A:1:NZS:N2	2:A:1:NZS:C8	2.67	0.53
1:A:988:THR:HG21	1:A:1083:GLN:HG3	1.91	0.53
1:A:373:LEU:HB2	1:A:404:PHE:CE2	2.44	0.53
1:A:741:MET:HE1	1:A:780:PRO:HD2	1.89	0.53
1:A:640:VAL:O	1:A:643:ILE:HG12	2.09	0.52
1:A:887:THR:HG22	1:A:889:ALA:N	2.25	0.52
1:A:779:LEU:HD23	1:A:780:PRO:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:TRP:HA	1:A:421:LYS:HB2	1.91	0.52
1:A:589:TYR:CD2	1:A:593:PHE:HE1	2.27	0.52
1:A:768:LYS:O	1:A:772:GLU:HG3	2.09	0.52
1:A:148:GLN:O	1:A:152:ARG:HG3	2.10	0.52
1:A:589:TYR:HD2	1:A:593:PHE:HE1	1.59	0.51
1:A:912:LYS:HG3	1:A:921:PHE:CE1	2.45	0.51
1:A:738:VAL:HA	1:A:741:MET:HE2	1.92	0.51
1:A:917:THR:HG1	1:A:919:GLU:HG2	1.72	0.51
1:A:947:ARG:NH2	1:A:964:ASP:O	2.43	0.51
1:A:1070:ASP:O	1:A:1074:VAL:HG23	2.10	0.51
1:A:477:ARG:HG2	1:A:478:GLY:N	2.26	0.51
1:A:1041:GLN:HG2	1:A:1042:LEU:CD1	2.41	0.50
1:A:498:ASN:ND2	1:A:1040:PRO:HA	2.27	0.50
1:A:911:LEU:O	1:A:915:SER:OG	2.29	0.50
1:A:838:LEU:O	1:A:842:MET:HG3	2.12	0.50
1:A:402:LYS:HG3	1:A:403:PRO:HD2	1.94	0.49
1:A:776:ASN:O	1:A:777:SER:OG	2.25	0.49
1:A:463:TYR:CE1	1:A:501:LYS:HA	2.47	0.49
1:A:917:THR:HG1	1:A:919:GLU:CG	2.24	0.49
1:A:304:HIS:CG	1:A:823:LEU:HD21	2.48	0.48
1:A:963:ILE:HD12	2:A:1:NZS:N6	2.28	0.48
1:A:366:ARG:HB2	1:A:517:SER:HB2	1.96	0.48
1:A:554:GLN:O	1:A:558:ILE:HG13	2.13	0.48
1:A:224:ILE:C	1:A:225:HIS:HD2	2.18	0.47
1:A:625:GLY:CA	1:A:1026:LEU:HD23	2.43	0.47
1:A:1035:LEU:HB3	1:A:1042:LEU:O	2.15	0.47
1:A:149:ALA:HA	1:A:152:ARG:HD2	1.97	0.47
1:A:925:VAL:O	1:A:929:VAL:HG23	2.15	0.47
1:A:586:PRO:HA	1:A:589:TYR:CD1	2.50	0.46
1:A:233:ILE:HD11	1:A:248:PHE:CD1	2.45	0.46
1:A:697:TRP:CH2	1:A:739:ILE:HD12	2.51	0.46
1:A:245:LEU:O	1:A:249:PHE:HD1	1.99	0.46
1:A:898:ASN:O	1:A:1087:PHE:HZ	1.98	0.46
1:A:224:ILE:C	1:A:225:HIS:CD2	2.89	0.46
1:A:201:TRP:CE2	1:A:291:GLN:HG3	2.51	0.46
1:A:775:GLN:NE2	1:A:795:ALA:HB1	2.31	0.45
1:A:893:GLN:HA	1:A:897:GLY:HA2	1.99	0.45
1:A:731:ASP:O	1:A:735:GLN:HG3	2.16	0.45
1:A:470:ASP:HB3	1:A:476:ARG:HH21	1.81	0.45
1:A:806:SER:OG	1:A:807:LYS:N	2.50	0.45
1:A:509:ASP:OD2	1:A:512:ASN:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:944:ILE:HG22	1:A:968:ILE:HG13	2.00	0.44
1:A:996:GLY:O	1:A:1003:SER:HB2	2.18	0.44
1:A:500:ASP:HB3	1:A:708:HIS:CD2	2.52	0.44
1:A:800:LYS:HB2	1:A:814:GLU:HG3	2.00	0.43
1:A:1013:CYS:HB3	1:A:1068:PHE:CE2	2.52	0.43
1:A:905:GLU:HG2	1:A:993:PHE:CE1	2.53	0.43
1:A:887:THR:HB	1:A:890:LYS:HG3	2.01	0.43
1:A:775:GLN:HE21	1:A:795:ALA:HB1	1.84	0.43
1:A:831:ILE:HG13	1:A:881:ILE:HG12	2.01	0.43
1:A:733:THR:O	1:A:737:GLN:HG3	2.18	0.43
1:A:891:ILE:HG22	1:A:906:VAL:HG12	2.00	0.43
1:A:498:ASN:HD21	1:A:1040:PRO:HA	1.84	0.43
1:A:583:LEU:HD22	1:A:610:LEU:CD2	2.49	0.43
1:A:661:LEU:O	1:A:665:GLN:HG2	2.19	0.43
1:A:225:HIS:HD2	1:A:225:HIS:N	2.16	0.42
1:A:799:GLU:H	1:A:799:GLU:CD	2.23	0.42
1:A:889:ALA:O	1:A:893:GLN:HG3	2.19	0.42
1:A:271:VAL:CG2	1:A:282:VAL:HG22	2.50	0.42
1:A:864:LEU:C	1:A:866:PRO:HD3	2.40	0.42
1:A:364:LYS:HE3	1:A:413:TRP:NE1	2.34	0.42
1:A:865:LEU:HD12	1:A:865:LEU:HA	1.78	0.42
1:A:935:TYR:CE1	1:A:961:PHE:HA	2.55	0.42
1:A:887:THR:CG2	1:A:950:ASP:HA	2.50	0.42
1:A:180:LEU:C	1:A:183:PRO:HD2	2.40	0.42
1:A:232:THR:HG22	1:A:233:ILE:N	2.34	0.42
1:A:302:GLU:HG3	1:A:304:HIS:CD2	2.55	0.42
1:A:808:LYS:HD3	1:A:835:GLY:HA3	2.01	0.42
1:A:1092:LEU:HA	1:A:1092:LEU:HD23	1.69	0.42
1:A:198:MET:SD	1:A:282:VAL:HG21	2.60	0.42
1:A:221:PHE:CE1	1:A:234:LYS:HG2	2.55	0.42
1:A:948:HIS:HB2	1:A:1090:LEU:HD12	2.02	0.42
1:A:622:LEU:HD13	1:A:647:LYS:HB3	2.01	0.41
1:A:738:VAL:O	1:A:742:LEU:HG	2.19	0.41
1:A:953:MET:SD	1:A:963:ILE:HD13	2.60	0.41
1:A:507:ASN:HA	1:A:508:PRO:HD3	1.92	0.41
1:A:233:ILE:CD1	1:A:248:PHE:HD1	2.30	0.41
1:A:800:LYS:CB	1:A:814:GLU:HG3	2.50	0.41
1:A:852:GLU:HG3	1:A:864:LEU:HD12	2.02	0.41
1:A:917:THR:HG1	1:A:920:LYS:H	1.69	0.41
1:A:867:TYR:OH	1:A:963:ILE:HA	2.21	0.41
1:A:1026:LEU:HD22	1:A:1026:LEU:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:889:ALA:HB2	1:A:949:ASN:OD1	2.21	0.41
1:A:939:THR:OG1	1:A:945:GLY:HA2	2.21	0.41
1:A:802:LYS:HG3	1:A:812:TRP:HB3	2.03	0.40
1:A:905:GLU:HG2	1:A:993:PHE:CZ	2.56	0.40
1:A:635:PHE:O	1:A:641:ARG:HD2	2.22	0.40
1:A:181:VAL:O	1:A:185:MET:HG3	2.22	0.40
1:A:689:LYS:HG2	1:A:728:MET:SD	2.61	0.40
1:A:738:VAL:HA	1:A:741:MET:CE	2.50	0.40
1:A:767:LEU:HD22	1:A:803:VAL:CG2	2.49	0.40
1:A:840:GLN:O	1:A:844:ILE:HG12	2.20	0.40
1:A:904:ASP:O	1:A:990:ASP:HA	2.21	0.40
1:A:201:TRP:NE1	1:A:291:GLN:HG3	2.36	0.40
1:A:831:ILE:HB	1:A:879:ILE:HB	2.02	0.40
1:A:989:PRO:HA	1:A:992:LEU:HD12	2.04	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	810/954 (85%)	773 (95%)	36 (4%)	1 (0%)	55 84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	916	PRO

5.3.2 Protein sidechains [i](#)

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

resolution.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	744/854 (87%)	729 (98%)	15 (2%)	60 86

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	225	HIS
1	A	521	ASP
1	A	610	LEU
1	A	738	VAL
1	A	832	PHE
1	A	865	LEU
1	A	915	SER
1	A	917	THR
1	A	947	ARG
1	A	959	ASN
1	A	968	ILE
1	A	1026	LEU
1	A	1027	LEU
1	A	1039	MET
1	A	1089	HIS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	GLN
1	A	391	GLN
1	A	769	GLN
1	A	773	ASN
1	A	775	GLN
1	A	840	GLN
1	A	959	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](#)

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	NZS	A	1	-	28,30,30	3.98	6 (21%)	31,44,44	2.94	11 (35%)

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	NZS	A	1	-	-	0/10/22/22	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	NZS	C15-S1	-13.99	1.66	1.76
2	A	1	NZS	C16-S1	-13.93	1.66	1.76
2	A	1	NZS	C4-C1	-4.74	1.39	1.44
2	A	1	NZS	C7-N5	-2.08	1.36	1.40
2	A	1	NZS	C4-N2	2.02	1.35	1.33
2	A	1	NZS	C3-N6	3.21	1.41	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	NZS	O2-S1-O3	-8.12	109.86	117.83
2	A	1	NZS	C17-N6-C3	-6.38	111.72	121.76
2	A	1	NZS	C14-N6-C3	-5.89	112.50	121.76
2	A	1	NZS	C7-N5-C4	-3.16	121.58	128.53
2	A	1	NZS	C1-C5-N3	-2.99	104.45	110.70
2	A	1	NZS	N1-C3-N6	2.30	119.69	117.12
2	A	1	NZS	N2-C3-N6	2.71	120.12	117.11
2	A	1	NZS	C3-N2-C4	3.01	121.47	115.45
2	A	1	NZS	C6-N4-C2	3.79	132.47	124.48
2	A	1	NZS	C3-N1-C2	3.84	119.50	115.11
2	A	1	NZS	C5-C1-C2	6.85	111.53	105.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	NZS	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

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	825/954 (86%)	0.20	55 (6%) 19 14	34, 93, 159, 232	1 (0%)

All (55) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1042	LEU	16.2
1	A	1041	GLN	7.6
1	A	895	THR	7.3
1	A	823	LEU	6.3
1	A	378	ASP	6.3
1	A	778	GLN	6.2
1	A	898	ASN	5.5
1	A	379	LEU	5.1
1	A	1000	LYS	4.7
1	A	374	PRO	4.1
1	A	373	LEU	4.1
1	A	398	ARG	4.0
1	A	320	LYS	3.9
1	A	210	TYR	3.8
1	A	497	PHE	3.8
1	A	1092	LEU	3.7
1	A	777	SER	3.7
1	A	1089	HIS	3.6
1	A	231	GLN	3.5
1	A	217	ASN	3.3
1	A	148	GLN	3.3
1	A	894	SER	3.3
1	A	1012	ILE	3.1
1	A	226	ARG	3.1
1	A	1090	LEU	3.0
1	A	967	HIS	3.0
1	A	824	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	1091	VAL	2.9
1	A	758	ASP	2.9
1	A	1084	PHE	2.7
1	A	239	ASP	2.7
1	A	319	ARG	2.7
1	A	404	PHE	2.6
1	A	919	GLU	2.5
1	A	546	GLU	2.5
1	A	553	LYS	2.4
1	A	909	HIS	2.3
1	A	759	VAL	2.3
1	A	178	ARG	2.3
1	A	385	ALA	2.3
1	A	227	SER	2.2
1	A	519	LEU	2.2
1	A	270	PHE	2.2
1	A	152	ARG	2.2
1	A	269	ASP	2.1
1	A	295	HIS	2.1
1	A	359	ARG	2.1
1	A	968	ILE	2.1
1	A	820	PRO	2.1
1	A	993	PHE	2.1
1	A	530	PRO	2.1
1	A	1076	ARG	2.1
1	A	811	LEU	2.0
1	A	825	ASN	2.0
1	A	619	GLN	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, 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	LLDF	B-factors(\AA^2)	Q<0.9
2	NZS	A	1	27/27	0.94	0.17	0.17	69,95,109,112	0

6.5 Other polymers [i](#)

There are no such residues in this entry.