



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 03:05 PM UTC

PDB ID : 4O88 / pdb_00004o88
Title : Crystal structure of a C-tagged Nuclease
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Deposited on : 2013-12-26
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

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

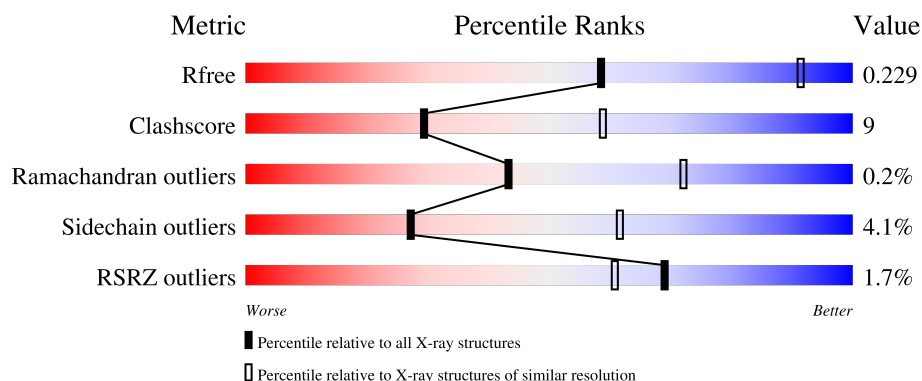
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (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 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	325	
1	B	325	

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	SO4	A	402	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5252 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 N-tagged Nuclease.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	S	0	2	0
			2506	1569	435	498	4			
1	B	314	Total	C	N	O	S	0	1	0
			2485	1555	430	496	4			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	320	LEU	-	expression tag	UNP Q707V3
A	321	GLU	-	expression tag	UNP Q707V3
A	322	HIS	-	expression tag	UNP Q707V3
A	323	HIS	-	expression tag	UNP Q707V3
A	324	HIS	-	expression tag	UNP Q707V3
A	325	HIS	-	expression tag	UNP Q707V3
A	326	HIS	-	expression tag	UNP Q707V3
A	327	HIS	-	expression tag	UNP Q707V3
B	320	LEU	-	expression tag	UNP Q707V3
B	321	GLU	-	expression tag	UNP Q707V3
B	322	HIS	-	expression tag	UNP Q707V3
B	323	HIS	-	expression tag	UNP Q707V3
B	324	HIS	-	expression tag	UNP Q707V3
B	325	HIS	-	expression tag	UNP Q707V3
B	326	HIS	-	expression tag	UNP Q707V3
B	327	HIS	-	expression tag	UNP Q707V3

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Cl	0	0
			1	1		
2	B	1	Total	Cl	0	0
			1	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

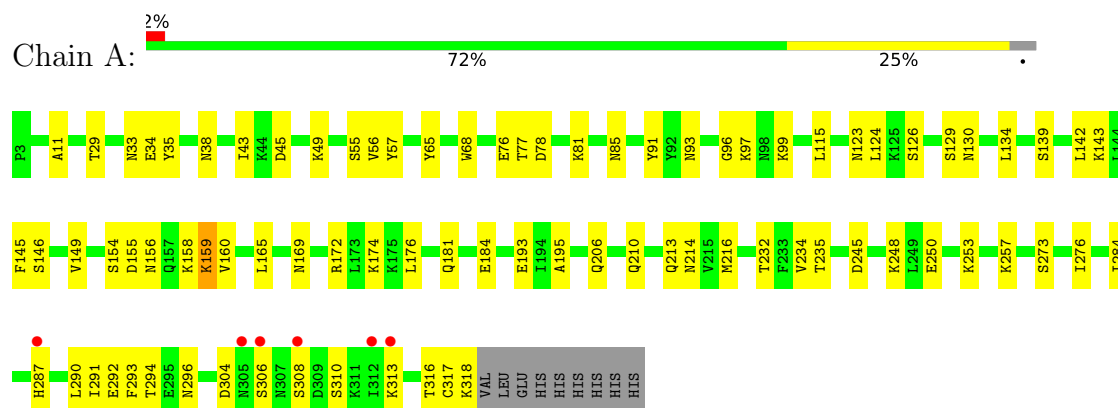
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	103	Total	O	0	0
			103	103		
4	B	61	Total	O	0	0
			61	61		

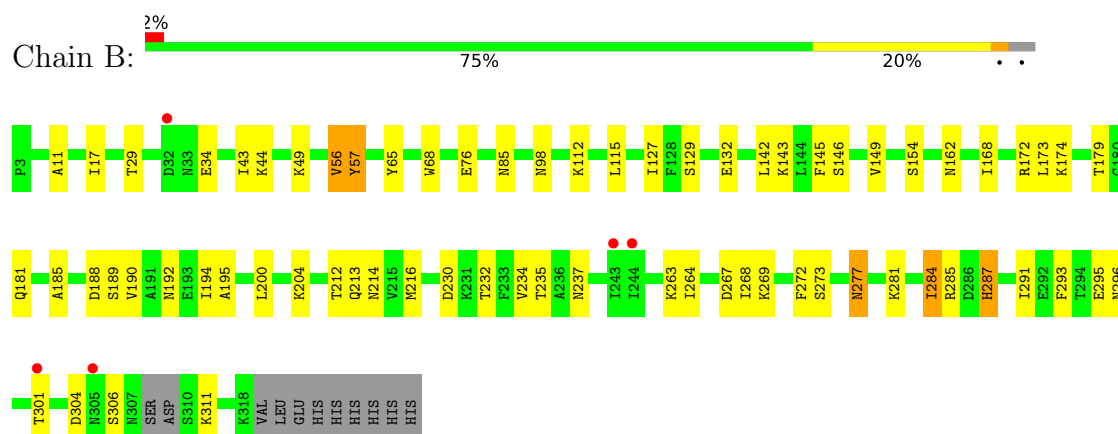
3 Residue-property plots

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: N-tagged Nuclease



• Molecule 1: N-tagged Nuclease



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	61.88Å 77.45Å 147.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.95 – 2.90 45.95 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (45.95-2.90) 98.6 (45.95-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.188 , 0.247 (Not available) , 0.229	Depositor DCC
R_{free} test set	611 reflections (0.28%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.637	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5252	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.27 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.0154e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: CL, 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	0.42	0/2545	0.85	3/3431 (0.1%)
1	B	0.40	0/2520	0.86	6/3398 (0.2%)
All	All	0.41	0/5065	0.86	9/6829 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	311	LYS	N-CA-C	6.92	120.25	110.50
1	B	57	TYR	N-CA-C	6.23	119.00	111.40
1	B	232	THR	N-CA-C	6.10	118.01	111.36
1	B	56	VAL	N-CA-C	5.72	115.91	110.53
1	A	93	ASN	CA-C-N	5.26	126.42	119.84
1	A	93	ASN	C-N-CA	5.26	126.42	119.84
1	B	98	ASN	N-CA-C	5.17	118.44	110.42
1	B	306	SER	N-CA-C	5.16	117.34	107.75
1	A	232	THR	N-CA-C	5.12	116.94	111.36

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	2506	0	2493	48	0
1	B	2485	0	2459	38	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	60	0	0	4	0
3	B	35	0	0	1	0
4	A	103	0	0	2	0
4	B	61	0	0	2	0
All	All	5252	0	4952	86	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 9.

All (86) 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:B:188:ASP:O	1:B:192:ASN:ND2	2.17	0.77
1:A:213:GLN:NE2	4:A:562:HOH:O	2.17	0.71
1:B:273:SER:HB2	1:B:295:GLU:HG2	1.73	0.71
1:B:29:THR:OG1	1:B:34:GLU:OE2	2.08	0.70
1:B:132:GLU:N	1:B:132:GLU:OE1	2.25	0.69
1:A:43:ILE:HD13	1:A:68:TRP:HZ2	1.58	0.68
1:A:181:GLN:NE2	1:A:210:GLN:HE22	1.90	0.67
1:B:172:ARG:HE	1:B:287:HIS:CD2	2.12	0.67
1:B:43:ILE:HD13	1:B:68:TRP:HZ2	1.63	0.64
1:A:172:ARG:HD3	1:A:287:HIS:CE1	2.31	0.64
1:A:29:THR:OG1	1:A:34:GLU:OE2	2.19	0.59
1:A:81:LYS:O	1:A:85:ASN:ND2	2.31	0.59
1:A:145:PHE:O	1:A:149:VAL:HG23	2.02	0.58
1:A:29:THR:HB	1:A:316:THR:HA	1.87	0.56
1:B:179:THR:HG23	1:B:181:GLN:HB2	1.87	0.56
1:B:11:ALA:HB1	1:B:65:TYR:HB3	1.87	0.56
1:B:281:LYS:HA	1:B:285:ARG:HD3	1.88	0.55
1:A:45:ASP:O	1:A:49[A]:LYS:HG2	2.08	0.53
1:A:11:ALA:HB1	1:A:65:TYR:HB3	1.91	0.53
1:B:168:ILE:O	1:B:172:ARG:HB2	2.09	0.52
1:A:35:TYR:CZ	1:A:134:LEU:HD13	2.45	0.52
1:B:185:ALA:HB2	1:B:284:ILE:HD11	1.92	0.51
1:B:237:ASN:ND2	4:B:537:HOH:O	2.34	0.51
1:A:154:SER:OG	3:A:403:SO4:O4	2.24	0.50
1:A:176:LEU:HD13	1:A:287:HIS:HD2	1.75	0.50
1:A:91:TYR:HB3	1:A:99:LYS:HG2	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LEU:HD22	1:A:290:LEU:HD11	1.93	0.49
1:B:154:SER:OG	3:B:407:SO4:O1	2.29	0.49
1:B:173:LEU:HD22	1:B:269:LYS:HG3	1.95	0.49
1:B:85:ASN:OD1	1:B:174:LYS:NZ	2.37	0.49
1:B:195:ALA:HB2	1:B:216:MET:SD	2.52	0.49
1:A:143:LYS:HG3	1:A:293:PHE:CE1	2.47	0.48
1:A:124:LEU:N	3:A:402:SO4:O1	2.39	0.48
1:A:181:GLN:HE21	1:A:210:GLN:HE22	1.59	0.48
1:B:57:TYR:OH	1:B:76:GLU:OE2	2.22	0.48
1:A:142:LEU:O	1:A:146:SER:OG	2.23	0.48
1:A:35:TYR:HA	1:A:130:ASN:HD21	1.79	0.48
1:A:165:LEU:HD22	1:A:294:THR:HG22	1.95	0.48
1:A:29:THR:HA	1:A:33:ASN:O	2.14	0.47
1:A:57:TYR:OH	1:A:76:GLU:OE2	2.22	0.47
1:A:276:ILE:HD11	1:A:292:GLU:HB2	1.97	0.47
1:A:97:LYS:N	3:A:410:SO4:O1	2.48	0.47
1:A:306:SER:HB3	1:A:310:SER:OG	2.15	0.47
1:B:263:LYS:O	1:B:267:ASP:HB2	2.15	0.47
1:B:287:HIS:O	1:B:291:ILE:HG13	2.14	0.47
1:B:268:ILE:O	1:B:272:PHE:N	2.45	0.47
1:B:145:PHE:O	1:B:149:VAL:HG23	2.14	0.46
1:B:143:LYS:HG3	1:B:293:PHE:CE1	2.51	0.46
1:A:154:SER:O	1:A:158:LYS:HG3	2.16	0.46
1:A:234:VAL:HG12	1:A:235:THR:N	2.31	0.46
1:B:17:ILE:HD11	1:B:127:ILE:HG23	1.96	0.46
1:B:142:LEU:O	1:B:146:SER:OG	2.20	0.45
1:B:264:ILE:O	1:B:268:ILE:HG13	2.16	0.45
1:A:43:ILE:HD13	1:A:68:TRP:CZ2	2.44	0.45
1:A:77:THR:OG1	1:A:78:ASP:N	2.46	0.45
1:B:277:ASN:HD22	1:B:277:ASN:HA	1.58	0.45
1:A:287:HIS:O	1:A:291:ILE:HG13	2.17	0.45
1:A:38:ASN:OD1	1:A:129:SER:OG	2.33	0.45
1:B:234:VAL:HG12	1:B:235:THR:N	2.31	0.45
1:B:56:VAL:HG21	1:B:115:LEU:HD21	1.99	0.45
1:B:234:VAL:HG12	1:B:235:THR:H	1.82	0.45
1:A:123[A]:ASN:OD1	1:A:126:SER:OG	2.29	0.45
1:A:245:ASP:HB3	1:A:248:LYS:HB2	1.98	0.44
1:A:273:SER:OG	1:A:296:ASN:ND2	2.50	0.44
1:A:169:ASN:ND2	1:A:294:THR:OG1	2.24	0.44
1:B:213:GLN:NE2	4:B:545:HOH:O	2.40	0.44
1:B:44:LYS:HB2	1:B:44:LYS:HE3	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:VAL:HG21	1:A:115:LEU:HD11	1.99	0.44
1:A:234:VAL:HG12	1:A:235:THR:H	1.82	0.43
1:A:290:LEU:HD12	1:A:290:LEU:HA	1.87	0.43
1:B:200:LEU:HD11	1:B:264:ILE:HD12	2.01	0.43
1:A:317:CYS:SG	1:A:318:LYS:N	2.90	0.43
1:A:195:ALA:HB2	1:A:216:MET:SD	2.59	0.43
1:B:204:LYS:HG2	1:B:212:THR:CG2	2.49	0.43
1:B:194:ILE:HD13	1:B:268:ILE:HG12	2.01	0.42
1:A:155:ASP:O	1:A:159:LYS:HG2	2.19	0.42
1:B:56:VAL:HG12	1:B:112:LYS:HG2	2.00	0.42
1:A:123[A]:ASN:ND2	3:A:402:SO4:O3	2.53	0.42
1:A:296:ASN:OD1	4:A:550:HOH:O	2.21	0.42
1:B:179:THR:HG23	1:B:181:GLN:H	1.85	0.41
1:A:156:ASN:O	1:A:160:VAL:HG23	2.19	0.41
1:B:273:SER:OG	1:B:296:ASN:OD1	2.37	0.41
1:A:65:TYR:HA	1:A:68:TRP:CD1	2.55	0.41
1:A:206:GLN:HG3	1:A:210:GLN:O	2.21	0.41
1:B:190:VAL:O	1:B:194:ILE:HG13	2.21	0.40
1:A:250:GLU:O	1:A:253:LYS:HB2	2.21	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	316/325 (97%)	311 (98%)	4 (1%)	1 (0%)	36	65
1	B	311/325 (96%)	304 (98%)	7 (2%)	0	100	100
All	All	627/650 (96%)	615 (98%)	11 (2%)	1 (0%)	43	72

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	96	GLY

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	282/297 (95%)	270 (96%)	12 (4%)	26	60
1	B	279/297 (94%)	268 (96%)	11 (4%)	28	63
All	All	561/594 (94%)	538 (96%)	23 (4%)	27	61

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	55	SER
1	A	139	SER
1	A	159	LYS
1	A	174	LYS
1	A	184	GLU
1	A	193	GLU
1	A	214	ASN
1	A	257	LYS
1	A	284	ILE
1	A	304	ASP
1	A	308	SER
1	A	313	LYS
1	B	49	LYS
1	B	129	SER
1	B	162	ASN
1	B	189	SER
1	B	214	ASN
1	B	230	ASP
1	B	277	ASN
1	B	284	ILE
1	B	287	HIS
1	B	301	THR
1	B	304	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	63	ASN
1	A	118	ASN
1	A	210	GLN
1	A	296	ASN
1	B	63	ASN
1	B	93	ASN
1	B	162	ASN
1	B	220	ASN
1	B	277	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 21 ligands modelled in this entry, 2 are monoatomic - leaving 19 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	$\# Z > 2$
3	SO4	A	411	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	A	412	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	A	404	-	4,4,4	0.23	0	6,6,6	0.10	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	A	402	-	4,4,4	0.22	0	6,6,6	0.15	0
3	SO4	A	408	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	B	402	-	4,4,4	0.23	0	6,6,6	0.11	0
3	SO4	A	405	-	4,4,4	0.24	0	6,6,6	0.04	0
3	SO4	B	405	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	A	409	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	B	406	-	4,4,4	0.25	0	6,6,6	0.07	0
3	SO4	A	413	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	408	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	A	406	-	4,4,4	0.23	0	6,6,6	0.12	0
3	SO4	A	403	-	4,4,4	0.24	0	6,6,6	0.08	0
3	SO4	B	403	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	A	407	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	B	407	-	4,4,4	0.23	0	6,6,6	0.10	0
3	SO4	B	404	-	4,4,4	0.24	0	6,6,6	0.06	0
3	SO4	A	410	-	4,4,4	0.23	0	6,6,6	0.06	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	SO4	2	0
3	A	403	SO4	1	0
3	B	407	SO4	1	0
3	A	410	SO4	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, 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	316/325 (97%)	-0.23	6 (1%) 66 58	17, 36, 73, 115	2 (0%)
1	B	314/325 (96%)	0.00	5 (1%) 70 62	24, 45, 81, 105	1 (0%)
All	All	630/650 (96%)	-0.11	11 (1%) 69 61	17, 40, 79, 115	3 (0%)

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	308	SER	3.3
1	A	306	SER	3.1
1	B	243	ILE	3.0
1	B	305	ASN	2.8
1	A	305	ASN	2.7
1	A	312	ILE	2.6
1	A	287	HIS	2.4
1	B	32	ASP	2.4
1	A	313	LYS	2.2
1	B	244	ILE	2.1
1	B	301	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 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	SO4	B	406	5/5	0.73	0.21	81,86,93,93	0
3	SO4	A	413	5/5	0.74	0.11	124,124,126,128	0
3	SO4	B	407	5/5	0.74	0.16	97,102,107,108	0
3	SO4	B	403	5/5	0.77	0.26	106,107,109,109	0
3	SO4	B	405	5/5	0.78	0.10	127,128,130,133	0
3	SO4	A	411	5/5	0.78	0.16	101,101,105,107	0
3	SO4	A	412	5/5	0.78	0.14	110,113,113,116	0
3	SO4	A	410	5/5	0.79	0.17	95,98,99,103	0
3	SO4	A	407	5/5	0.79	0.29	90,93,95,95	0
3	SO4	A	408	5/5	0.82	0.13	104,106,107,108	0
3	SO4	A	406	5/5	0.86	0.14	87,87,90,91	0
3	SO4	A	405	5/5	0.87	0.18	87,88,92,93	0
3	SO4	A	404	5/5	0.87	0.12	93,94,96,97	0
3	SO4	B	404	5/5	0.88	0.20	81,82,85,86	0
3	SO4	B	408	5/5	0.88	0.09	109,110,115,116	0
3	SO4	A	403	5/5	0.91	0.11	87,89,90,93	0
3	SO4	A	409	5/5	0.91	0.24	104,105,107,108	0
3	SO4	B	402	5/5	0.94	0.08	42,50,59,64	0
2	CL	A	401	1/1	0.96	0.05	55,55,55,55	0
2	CL	B	401	1/1	0.96	0.07	57,57,57,57	0
3	SO4	A	402	5/5	0.97	0.07	48,51,52,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.