



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:34 AM UTC

PDB ID : 5QJ9 / pdb_00005qj9
Title : PanDDA analysis group deposition of models with modelled events (e.g. bound ligands) – Crystal Structure of NUDT5 in complex with Z768399682
Authors : Dubianok, Y.; Collins, P.; Krojer, T.; Wright, N.; Strain-Damerell, C.; Burgess-Brown, N.; Bountra, C.; Arrowsmith, C.H.; Edwards, A.; Huber, K.; von Delft, F.
Deposited on : 2018-11-12
Resolution : 1.85 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:

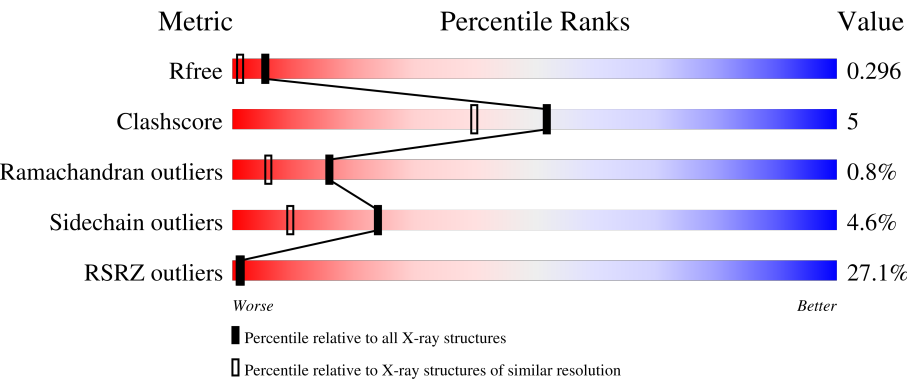
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry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

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.85 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	3428 (1.86-1.86)
Clashscore	190562	3579 (1.86-1.86)
Ramachandran outliers	187476	3553 (1.86-1.86)
Sidechain outliers	187428	3553 (1.86-1.86)
RSRZ outliers	180081	3429 (1.86-1.86)

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	209	12% 79%12%7%
1	B	209	15% 81%11%7%
1	C	209	23% 77%14%8%
1	D	209	50% 67%23%9%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6060 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 ADP-sugar pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1450	917	242	283	8			
1	B	194	Total	C	N	O	S	0	0	0
			1464	924	244	288	8			
1	C	192	Total	C	N	O	S	0	0	0
			1412	890	238	277	7			
1	D	190	Total	C	N	O	S	0	1	0
			1406	888	238	272	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	expression tag	UNP Q9UKK9
B	0	SER	-	expression tag	UNP Q9UKK9
C	0	SER	-	expression tag	UNP Q9UKK9
D	0	SER	-	expression tag	UNP Q9UKK9

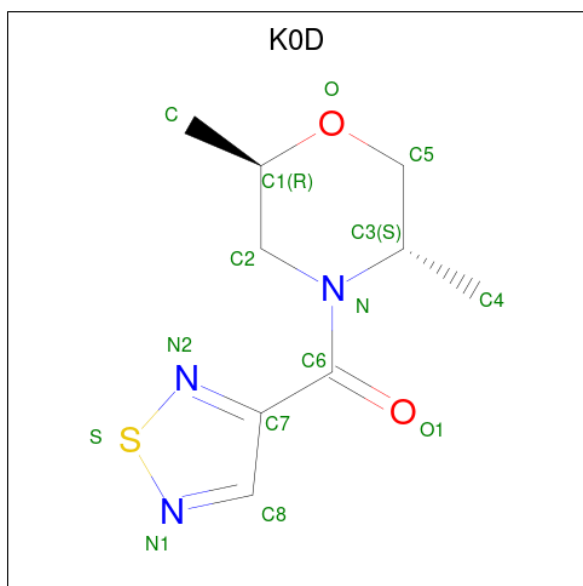
- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		
2	B	2	Total	Mg	0	0
			2	2		
2	C	2	Total	Mg	0	0
			2	2		
2	D	2	Total	Mg	0	0
			2	2		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is [(2R,5S)-2,5-dimethylmorpholin-4-yl](1,2,5-thiadiazol-3-yl)methanone (CCD ID: K0D) (formula: C₉H₁₃N₃O₂S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
4	B	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
4	C	1	Total	C	N	O	S	0	0
			15	9	3	2	1		
4	C	1	Total	C	N	O	S	0	0
			15	9	3	2	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		

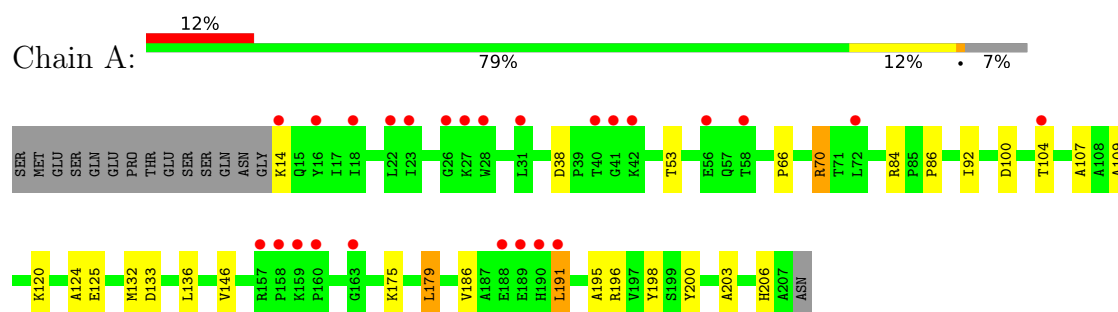
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	74	Total	O	0	0
			74	74		
6	B	73	Total	O	0	0
			73	73		
6	C	70	Total	O	0	0
			70	70		
6	D	30	Total	O	0	0
			30	30		

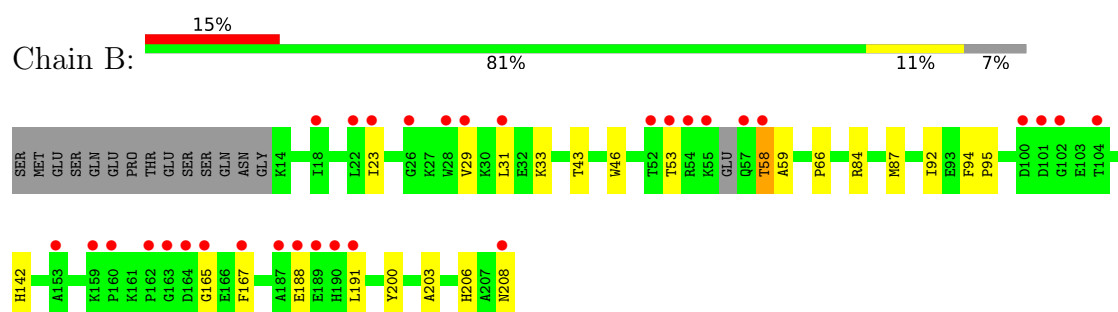
3 Residue-property plots [i](#)

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.

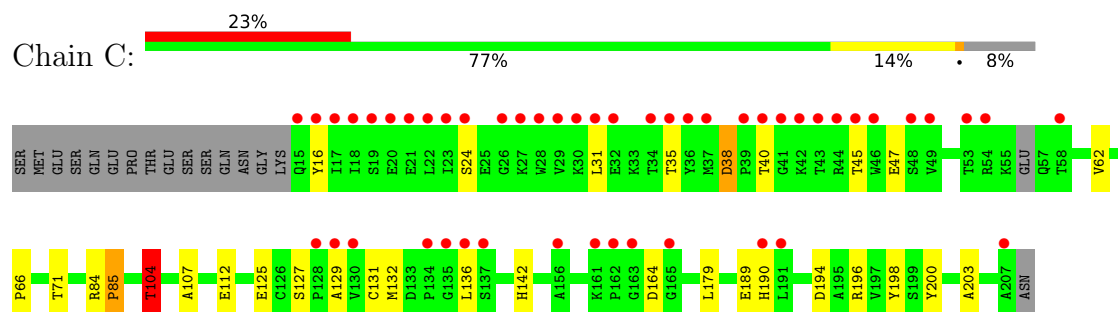
- Molecule 1: ADP-sugar pyrophosphatase



- Molecule 1: ADP-sugar pyrophosphatase

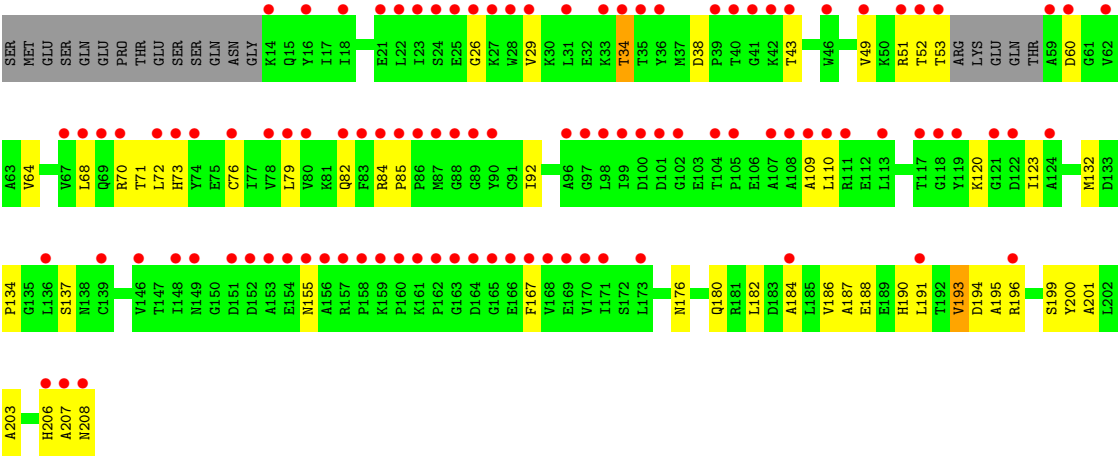


- Molecule 1: ADP-sugar pyrophosphatase



- Molecule 1: ADP-sugar pyrophosphatase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	49.59Å 59.88Å 79.67Å 79.45° 81.18° 75.37°	Depositor
Resolution (Å)	77.83 – 1.85 77.83 – 1.85	Depositor EDS
% Data completeness (in resolution range)	96.3 (77.83-1.85) 96.3 (77.83-1.85)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.43 (at 1.84Å)	Xtriage
Refinement program	REFMAC 5.8.0189	Depositor
R, R_{free}	0.242 , 0.288 0.256 , 0.296	Depositor DCC
R_{free} test set	3702 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.160	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6060	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.74% 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: EDO, K0D, MG, CL

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	1.20	5/1478 (0.3%)	1.11	5/2019 (0.2%)
1	B	1.08	0/1492	1.08	2/2035 (0.1%)
1	C	1.16	2/1439 (0.1%)	1.19	8/1969 (0.4%)
1	D	1.12	2/1432 (0.1%)	1.16	6/1956 (0.3%)
All	All	1.14	9/5841 (0.2%)	1.13	21/7979 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	84	ARG	C-O	-6.83	1.19	1.25
1	C	104	THR	CA-C	6.19	1.60	1.53
1	A	109	ALA	N-CA	5.96	1.53	1.46
1	A	124	ALA	CA-C	-5.30	1.47	1.52
1	D	201	ALA	CA-C	5.22	1.59	1.52
1	C	129	ALA	N-CA	5.21	1.52	1.46
1	A	179	LEU	N-CA	-5.21	1.40	1.46
1	A	146	VAL	N-CA	-5.19	1.40	1.46
1	A	100	ASP	N-CA	5.04	1.52	1.45

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	85	PRO	N-CA-C	9.96	122.85	110.70
1	C	38	ASP	CA-C-N	8.26	130.16	119.84
1	C	38	ASP	C-N-CA	8.26	130.16	119.84
1	D	60	ASP	N-CA-C	6.84	118.39	111.07
1	D	193	VAL	N-CA-C	-6.34	99.14	108.97
1	C	104	THR	CB-CA-C	6.09	118.21	109.26
1	B	84	ARG	CA-C-N	-5.88	114.32	120.38
1	B	84	ARG	C-N-CA	-5.88	114.32	120.38
1	C	45	THR	N-CA-C	5.82	117.63	108.96
1	D	176	ASN	N-CA-C	5.66	119.29	112.38
1	A	84	ARG	CA-C-N	-5.63	114.58	120.38
1	A	84	ARG	C-N-CA	-5.63	114.58	120.38
1	D	199	SER	N-CA-C	-5.48	105.39	111.36
1	C	190	HIS	N-CA-CB	5.41	118.60	109.94
1	A	195	ALA	N-CA-C	5.29	117.04	111.28
1	C	85	PRO	N-CA-C	5.27	117.13	110.70
1	A	133	ASP	CA-C-N	5.20	124.81	119.56
1	A	133	ASP	C-N-CA	5.20	124.81	119.56
1	C	127	SER	CA-C-N	-5.16	115.26	120.21
1	C	127	SER	C-N-CA	-5.16	115.26	120.21
1	D	26	GLY	N-CA-C	5.13	117.76	110.74

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	58	THR	Peptide

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	1450	0	1405	17	0
1	B	1464	0	1414	16	0
1	C	1412	0	1320	15	0
1	D	1406	0	1345	25	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
4	A	15	0	0	0	0
4	B	15	0	0	0	0
4	C	30	0	0	1	0
5	A	4	0	6	0	0
5	B	4	0	6	0	0
5	C	4	0	6	0	0
6	A	74	0	0	2	0
6	B	73	0	0	0	0
6	C	70	0	0	2	0
6	D	30	0	0	1	0
All	All	6060	0	5502	58	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 5.

All (58) 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:C:125:GLU:OE1	6:C:401:HOH:O	2.01	0.78
1:D:120:LYS:H	1:D:155:ASN:HD21	1.35	0.73
1:A:206:HIS:HD2	1:B:200:TYR:OH	1.78	0.67
1:A:104:THR:HG23	1:A:107:ALA:H	1.59	0.66
1:C:203:ALA:HB3	1:D:203:ALA:HB3	1.82	0.60
1:A:203:ALA:HB3	1:B:203:ALA:HB3	1.84	0.59
1:C:104:THR:HG22	1:C:107:ALA:H	1.68	0.58
1:D:190:HIS:O	1:D:191:LEU:HB3	2.04	0.58
1:A:132:MET:HE1	1:A:196:ARG:CZ	2.34	0.58
1:D:191:LEU:C	1:D:191:LEU:HD12	2.29	0.57
1:C:179:LEU:HD11	1:C:198:TYR:CZ	2.40	0.56
1:C:194:ASP:OD2	1:C:196:ARG:NH2	2.38	0.56
1:D:71:THR:O	1:D:73:HIS:ND1	2.38	0.55
1:A:70:ARG:NH1	6:A:402:HOH:O	2.39	0.55
1:C:200:TYR:CD1	1:D:203:ALA:HB2	2.41	0.55
1:C:203:ALA:HB2	1:D:200:TYR:CD1	2.41	0.55
1:C:112:GLU:OE2	6:C:402:HOH:O	2.18	0.54
1:D:182:LEU:O	1:D:186:VAL:HG23	2.10	0.52
1:B:58:THR:CB	1:B:142:HIS:NE2	2.74	0.51
1:D:180:GLN:CB	6:D:418:HOH:O	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:38:ASP:HB2	1:D:167:PHE:CE2	2.47	0.50
1:C:132:MET:HE1	1:C:196:ARG:CZ	2.41	0.50
1:A:136:LEU:CD1	1:B:29:VAL:HG21	2.42	0.49
1:D:49:VAL:O	1:D:137:SER:HA	2.12	0.49
1:A:200:TYR:CD1	1:B:203:ALA:HB2	2.49	0.48
1:D:64:VAL:HG22	1:D:109:ALA:HB1	1.96	0.47
1:C:62:VAL:HG12	1:C:142:HIS:HB2	1.97	0.47
1:A:125:GLU:OE1	1:B:206:HIS:HE1	1.97	0.47
1:B:165:GLY:O	1:B:167:PHE:CD1	2.68	0.47
1:B:23:ILE:HD12	1:B:31:LEU:CD2	2.46	0.46
1:D:110:LEU:HG	1:D:123:ILE:HD11	1.99	0.46
1:A:104:THR:CG2	1:A:107:ALA:H	2.27	0.45
1:C:131:CYS:SG	1:D:194:ASP:HA	2.56	0.45
1:D:52:THR:O	1:D:53:THR:CB	2.64	0.45
1:D:195:ALA:HB3	1:D:196[B]:ARG:NH1	2.31	0.45
1:A:175:LYS:NZ	1:B:206:HIS:O	2.46	0.45
1:B:23:ILE:HD12	1:B:31:LEU:HD22	1.97	0.45
1:A:86:PRO:HD3	1:B:46:TRP:CD1	2.52	0.45
1:D:120:LYS:N	1:D:155:ASN:HD21	2.10	0.45
1:A:179:LEU:HD11	1:A:198:TYR:CZ	2.53	0.44
1:A:120:LYS:NZ	6:A:408:HOH:O	2.51	0.43
1:A:206:HIS:CD2	1:B:200:TYR:OH	2.66	0.43
1:D:132:MET:HE1	1:D:196[A]:ARG:HD2	2.00	0.43
1:D:29:VAL:HA	1:D:51:ARG:HA	2.01	0.43
1:A:186:VAL:HG22	1:A:191:LEU:HD21	2.01	0.42
1:D:79:LEU:HD13	1:D:92:ILE:HG22	2.01	0.42
1:A:38:ASP:C	1:A:38:ASP:OD1	2.62	0.42
1:D:182:LEU:HD22	1:D:193:VAL:CG1	2.50	0.42
1:D:203:ALA:O	1:D:206:HIS:O	2.38	0.41
1:A:92:ILE:HD11	1:A:191:LEU:HD11	2.03	0.41
1:B:87:MET:HE3	1:B:87:MET:HB3	1.98	0.41
1:C:47:GLU:N	4:C:305:K0D:N1	2.58	0.41
1:B:94:PHE:O	1:B:95:PRO:C	2.62	0.41
1:C:85:PRO:HB3	1:D:34:THR:HG21	2.01	0.40
1:D:184:ALA:O	1:D:187:ALA:N	2.54	0.40
1:B:92:ILE:HD11	1:B:191:LEU:HD13	2.04	0.40
1:C:84:ARG:HG3	1:D:134:PRO:HB2	2.04	0.40
1:B:23:ILE:HD11	1:B:33:LYS:HB2	2.02	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	192/209 (92%)	188 (98%)	3 (2%)	1 (0%)	24	13
1	B	190/209 (91%)	184 (97%)	4 (2%)	2 (1%)	11	3
1	C	188/209 (90%)	181 (96%)	5 (3%)	2 (1%)	11	3
1	D	187/209 (90%)	169 (90%)	17 (9%)	1 (0%)	24	13
All	All	757/836 (91%)	722 (95%)	29 (4%)	6 (1%)	16	6

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	207	ALA
1	B	59	ALA
1	C	24	SER
1	B	66	PRO
1	C	66	PRO
1	A	66	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	151/179 (84%)	147 (97%)	4 (3%)	40	25
1	B	154/179 (86%)	150 (97%)	4 (3%)	40	25
1	C	141/179 (79%)	132 (94%)	9 (6%)	16	4
1	D	143/179 (80%)	133 (93%)	10 (7%)	14	3

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	589/716 (82%)	562 (95%)	27 (5%)	24 9

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	LYS
1	A	53	THR
1	A	70	ARG
1	A	191	LEU
1	B	43	THR
1	B	53	THR
1	B	188	GLU
1	B	208	ASN
1	C	16	TYR
1	C	31	LEU
1	C	35	THR
1	C	40	THR
1	C	71	THR
1	C	104	THR
1	C	136	LEU
1	C	164	ASP
1	C	189	GLU
1	D	34	THR
1	D	38	ASP
1	D	43	THR
1	D	68	LEU
1	D	70	ARG
1	D	72	LEU
1	D	76	CYS
1	D	82	GLN
1	D	188	GLU
1	D	208	ASN

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

Mol	Chain	Res	Type
1	A	73	HIS
1	A	82	GLN
1	A	206	HIS
1	B	190	HIS
1	B	206	HIS

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Mol	Chain	Res	Type
1	B	208	ASN
1	C	206	HIS
1	D	82	GLN
1	D	149	ASN
1	D	155	ASN
1	D	208	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 16 ligands modelled in this entry, 9 are monoatomic - leaving 7 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$
4	K0D	C	304	-	15,16,16	2.67	7 (46%)	20,22,22	3.29	11 (55%)
5	EDO	B	301	-	3,3,3	0.57	0	2,2,2	0.38	0
5	EDO	A	305	-	3,3,3	0.38	0	2,2,2	0.26	0
4	K0D	B	304	-	15,16,16	2.41	7 (46%)	20,22,22	2.38	3 (15%)
5	EDO	C	301	-	3,3,3	0.54	0	2,2,2	0.08	0
4	K0D	A	304	-	15,16,16	2.65	7 (46%)	20,22,22	2.25	4 (20%)
4	K0D	C	305	-	15,16,16	3.21	6 (40%)	20,22,22	2.56	6 (30%)

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
4	K0D	C	304	-	-	3/8/21/21	0/2/2/2
5	EDO	B	301	-	-	0/1/1/1	-
5	EDO	A	305	-	-	0/1/1/1	-
4	K0D	B	304	-	-	2/8/21/21	0/2/2/2
5	EDO	C	301	-	-	0/1/1/1	-
4	K0D	A	304	-	-	3/8/21/21	0/2/2/2
4	K0D	C	305	-	-	2/8/21/21	0/2/2/2

All (27) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	305	K0D	S-N2	5.85	1.71	1.62
4	C	305	K0D	C3-N	5.67	1.54	1.47
4	C	305	K0D	C6-N	5.36	1.42	1.34
4	A	304	K0D	C6-N	5.14	1.42	1.34
4	C	304	K0D	C3-N	5.13	1.53	1.47
4	C	305	K0D	S-N1	4.66	1.69	1.62
4	C	305	K0D	C2-N	4.42	1.52	1.46
4	C	304	K0D	C8-C7	4.36	1.49	1.40
4	B	304	K0D	C7-N2	-4.21	1.29	1.35
4	A	304	K0D	C3-N	4.14	1.52	1.47
4	B	304	K0D	C8-C7	4.13	1.49	1.40
4	C	304	K0D	C6-N	4.08	1.40	1.34
4	A	304	K0D	S-N1	3.80	1.68	1.62
4	A	304	K0D	C8-C7	3.68	1.48	1.40
4	B	304	K0D	C6-N	3.61	1.40	1.34
4	C	304	K0D	S-N2	3.52	1.68	1.62
4	A	304	K0D	S-N2	3.45	1.68	1.62
4	B	304	K0D	C2-N	3.41	1.50	1.46
4	C	304	K0D	C5-C3	2.98	1.60	1.51
4	B	304	K0D	C3-N	2.97	1.51	1.47
4	C	304	K0D	C7-N2	-2.87	1.31	1.35
4	A	304	K0D	C7-N2	-2.63	1.31	1.35
4	A	304	K0D	C2-N	2.62	1.49	1.46
4	C	305	K0D	C8-C7	2.60	1.45	1.40
4	B	304	K0D	S-N1	2.49	1.66	1.62
4	C	304	K0D	S-N1	2.31	1.66	1.62
4	B	304	K0D	S-N2	2.26	1.66	1.62

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	304	K0D	C2-N-C3	-8.63	107.56	115.72
4	B	304	K0D	C8-C7-N2	7.75	114.33	107.88
4	A	304	K0D	C8-C7-N2	7.22	113.89	107.88
4	C	305	K0D	C8-C7-N2	6.34	113.16	107.88
4	C	305	K0D	C7-C8-N1	5.30	114.18	109.77
4	C	304	K0D	C7-C8-N1	5.13	114.03	109.77
4	C	305	K0D	N2-S-N1	-4.97	95.03	100.70
4	B	304	K0D	C7-C8-N1	4.96	113.89	109.77
4	A	304	K0D	C7-C8-N1	4.79	113.76	109.77
4	C	304	K0D	C8-C7-N2	4.69	111.78	107.88
4	C	304	K0D	C4-C3-N	4.63	118.94	111.55
4	C	304	K0D	C7-C6-N	3.97	124.97	120.45
4	C	305	K0D	C7-N2-S	3.75	108.75	106.23
4	B	304	K0D	C5-O-C1	3.60	117.09	111.80
4	C	304	K0D	C7-N2-S	3.16	108.36	106.23
4	C	304	K0D	O-C5-C3	2.94	115.80	111.21
4	C	304	K0D	N2-S-N1	-2.92	97.38	100.70
4	C	304	K0D	O1-C6-C7	-2.44	114.86	118.65
4	A	304	K0D	N2-S-N1	-2.39	97.98	100.70
4	C	305	K0D	C7-C6-N	2.30	123.07	120.45
4	A	304	K0D	C7-C6-N	2.20	122.96	120.45
4	C	304	K0D	C3-N-C6	2.15	125.67	120.32
4	C	305	K0D	C8-N1-S	2.13	108.88	106.74
4	C	304	K0D	C1-C2-N	-2.07	104.78	111.31

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	304	K0D	N-C6-C7-C8
4	A	304	K0D	O1-C6-C7-C8
4	A	304	K0D	O1-C6-C7-N2
4	C	304	K0D	O1-C6-N-C3
4	C	305	K0D	O1-C6-C7-N2
4	B	304	K0D	O1-C6-C7-N2
4	B	304	K0D	O1-C6-C7-C8
4	C	305	K0D	O1-C6-C7-C8
4	C	304	K0D	O1-C6-C7-N2
4	C	304	K0D	O1-C6-C7-C8

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	305	K0D	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

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	194/209 (92%)	0.79	25 (12%) 7 7	16, 28, 50, 62	6 (3%)
1	B	194/209 (92%)	1.01	31 (15%) 5 4	19, 32, 55, 74	6 (3%)
1	C	192/209 (91%)	1.36	49 (25%) 1 1	19, 35, 64, 78	10 (5%)
1	D	190/209 (90%)	2.35	104 (54%) 0 0	14, 44, 68, 91	19 (10%)
All	All	770/836 (92%)	1.37	209 (27%) 1 1	14, 35, 62, 91	41 (5%)

All (209) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	207	ALA	14.3
1	B	191	LEU	11.0
1	A	191	LEU	10.2
1	B	57	GLN	9.7
1	A	190	HIS	9.5
1	D	206	HIS	9.2
1	B	54	ARG	9.1
1	B	190	HIS	8.5
1	A	189	GLU	8.3
1	D	208	ASN	8.1
1	B	188	GLU	7.5
1	B	189	GLU	7.0
1	A	188	GLU	6.7
1	C	54	ARG	6.5
1	D	29	VAL	6.2
1	C	18	ILE	6.1
1	A	28	TRP	6.1
1	D	167	PHE	6.0
1	C	23	ILE	6.0
1	D	168	VAL	6.0
1	D	28	TRP	5.8

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Mol	Chain	Res	Type	RSRZ
1	D	160	PRO	5.7
1	C	22	LEU	5.4
1	D	119	TYR	5.3
1	C	39	PRO	5.1
1	D	31	LEU	5.1
1	C	43	THR	5.0
1	D	74	TYR	5.0
1	D	99	ILE	5.0
1	C	17	ILE	4.9
1	C	29	VAL	4.8
1	D	23	ILE	4.7
1	C	28	TRP	4.7
1	D	26	GLY	4.7
1	C	26	GLY	4.6
1	C	31	LEU	4.6
1	B	28	TRP	4.6
1	C	46	TRP	4.6
1	D	90	TYR	4.6
1	D	88	GLY	4.5
1	C	16	TYR	4.5
1	D	161	LYS	4.4
1	A	41	GLY	4.4
1	C	37	MET	4.3
1	B	165	GLY	4.2
1	D	156	ALA	4.1
1	B	101	ASP	4.1
1	D	191	LEU	4.0
1	D	27	LYS	4.0
1	D	158	PRO	4.0
1	D	59	ALA	3.9
1	D	153	ALA	3.9
1	C	15	GLN	3.9
1	D	152	ASP	3.9
1	C	53	THR	3.9
1	D	155	ASN	3.8
1	C	24	SER	3.8
1	D	40	THR	3.8
1	C	49	VAL	3.8
1	C	58	THR	3.7
1	D	22	LEU	3.7
1	D	78	VAL	3.7
1	D	89	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	40	THR	3.7
1	D	87	MET	3.6
1	D	53	THR	3.6
1	C	32	GLU	3.6
1	D	164	ASP	3.6
1	A	27	LYS	3.6
1	C	35	THR	3.6
1	C	136	LEU	3.6
1	D	171	ILE	3.6
1	B	58	THR	3.6
1	D	97	GLY	3.5
1	C	207	ALA	3.5
1	D	16	TYR	3.4
1	D	49	VAL	3.4
1	D	96	ALA	3.4
1	D	162	PRO	3.4
1	D	151	ASP	3.3
1	B	55	LYS	3.3
1	B	163	GLY	3.3
1	D	148	ILE	3.3
1	D	100	ASP	3.2
1	C	34	THR	3.2
1	D	110	LEU	3.2
1	C	135	GLY	3.2
1	A	157	ARG	3.2
1	D	70	ARG	3.2
1	C	137	SER	3.2
1	C	129	ALA	3.1
1	D	146	VAL	3.1
1	C	36	TYR	3.1
1	D	68	LEU	3.1
1	B	208	ASN	3.1
1	D	85	PRO	3.1
1	A	31	LEU	3.1
1	A	72	LEU	3.1
1	C	19	SER	3.1
1	D	24	SER	3.1
1	A	163	GLY	3.1
1	D	98	LEU	3.0
1	D	108	ALA	3.0
1	D	122	ASP	3.0
1	D	184	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	165	GLY	3.0
1	D	149	ASN	3.0
1	B	162	PRO	2.9
1	D	121	GLY	2.9
1	D	107	ALA	2.9
1	D	196[A]	ARG	2.9
1	C	48	SER	2.9
1	C	45	THR	2.9
1	D	43	THR	2.9
1	D	86	PRO	2.9
1	B	167	PHE	2.9
1	A	14	LYS	2.9
1	C	163	GLY	2.9
1	D	163	GLY	2.9
1	C	162	PRO	2.8
1	D	51	ARG	2.8
1	D	136	LEU	2.8
1	A	58	THR	2.8
1	A	56	GLU	2.8
1	B	159	LYS	2.8
1	D	154	GLU	2.8
1	D	159	LYS	2.7
1	D	102	GLY	2.7
1	B	164	ASP	2.7
1	D	62	VAL	2.7
1	A	16	TYR	2.7
1	C	20	GLU	2.7
1	C	42	LYS	2.7
1	A	40	THR	2.7
1	C	27	LYS	2.7
1	D	169	GLU	2.6
1	A	18	ILE	2.6
1	D	109	ALA	2.6
1	D	117	THR	2.6
1	D	34	THR	2.6
1	B	22	LEU	2.5
1	D	46	TRP	2.5
1	A	23	ILE	2.5
1	C	161	LYS	2.5
1	D	14	LYS	2.5
1	D	82	GLN	2.5
1	C	21	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	30	LYS	2.5
1	D	173	LEU	2.5
1	C	190	HIS	2.5
1	A	104	THR	2.5
1	B	104	THR	2.5
1	D	33	LYS	2.5
1	D	35	THR	2.5
1	D	104	THR	2.5
1	D	60	ASP	2.5
1	B	160	PRO	2.5
1	A	159	LYS	2.4
1	D	118	GLY	2.4
1	D	139	CYS	2.4
1	B	102	GLY	2.4
1	D	80	VAL	2.4
1	B	53	THR	2.3
1	C	134	PRO	2.3
1	D	157	ARG	2.3
1	B	31	LEU	2.3
1	B	153	ALA	2.3
1	B	23	ILE	2.3
1	D	25	GLU	2.3
1	D	69	GLN	2.3
1	D	113	LEU	2.3
1	D	105	PRO	2.3
1	D	41	GLY	2.3
1	B	26	GLY	2.2
1	D	36	TYR	2.2
1	B	29	VAL	2.2
1	D	84	ARG	2.2
1	A	22	LEU	2.2
1	D	79	LEU	2.2
1	D	166	GLU	2.2
1	D	76	CYS	2.2
1	C	156	ALA	2.2
1	D	83	PHE	2.2
1	D	18	ILE	2.2
1	A	42	LYS	2.2
1	A	158	PRO	2.2
1	C	44	ARG	2.2
1	A	26	GLY	2.1
1	D	165	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	111	ARG	2.1
1	B	100	ASP	2.1
1	D	52	THR	2.1
1	C	130	VAL	2.1
1	C	128	PRO	2.1
1	D	39	PRO	2.1
1	D	72	LEU	2.1
1	B	187	ALA	2.1
1	D	124	ALA	2.1
1	B	18	ILE	2.1
1	D	101	ASP	2.1
1	D	73	HIS	2.1
1	D	21	GLU	2.0
1	D	42	LYS	2.0
1	B	52	THR	2.0
1	A	160	PRO	2.0
1	D	67	VAL	2.0
1	C	191	LEU	2.0
1	C	41	GLY	2.0
1	D	170	VAL	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
4	K0D	C	305	15/15	0.79	0.22	45,52,61,63	15
3	CL	A	303	1/1	0.82	0.17	66,66,66,66	0
4	K0D	B	304	15/15	0.85	0.20	31,39,43,45	15

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	K0D	A	304	15/15	0.87	0.16	54,58,64,64	0
5	EDO	B	301	4/4	0.88	0.11	36,36,38,39	0
5	EDO	C	301	4/4	0.89	0.11	33,42,44,48	0
4	K0D	C	304	15/15	0.90	0.18	45,53,62,64	15
2	MG	A	302	1/1	0.91	0.08	52,52,52,52	0
2	MG	D	301	1/1	0.92	0.06	37,37,37,37	0
5	EDO	A	305	4/4	0.92	0.13	37,38,39,41	0
2	MG	B	303	1/1	0.93	0.07	61,61,61,61	0
2	MG	D	302	1/1	0.93	0.10	50,50,50,50	0
2	MG	C	302	1/1	0.94	0.07	50,50,50,50	0
2	MG	B	302	1/1	0.98	0.03	30,30,30,30	0
2	MG	A	301	1/1	0.99	0.04	29,29,29,29	0
2	MG	C	303	1/1	0.99	0.03	27,27,27,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.