



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:15 PM UTC

PDB ID : 2ISN / pdb_00002isn
Title : Crystal structure of a phosphatase from a pathogenic strain *Toxoplasma gondii*
Authors : Agarwal, R.; Burley, S.K.; Swaminathan, S.; New York SGX Research Center
for Structural Genomics (NYSGXRC)
Deposited on : 2006-10-18
Resolution : 1.90 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

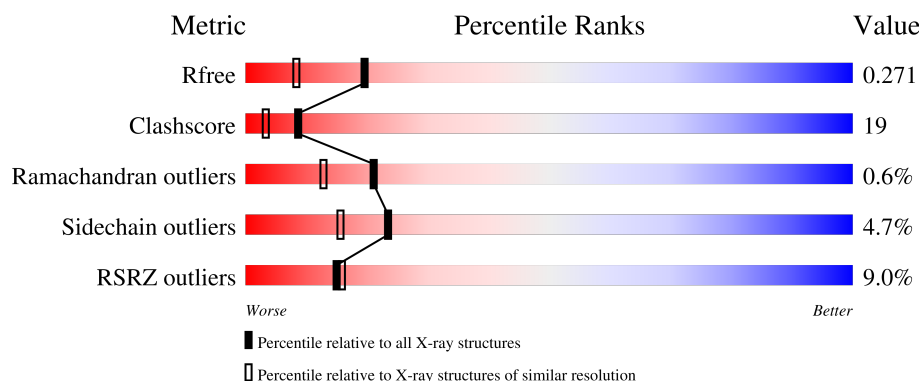
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 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	7789 (1.90-1.90)
Clashscore	190562	8410 (1.90-1.90)
Ramachandran outliers	187476	8333 (1.90-1.90)
Sidechain outliers	187428	8333 (1.90-1.90)
RSRZ outliers	180081	7790 (1.90-1.90)

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	364	8% 57% 31% 9%
1	B	364	8% 62% 25% 10%

2 Entry composition [i](#)

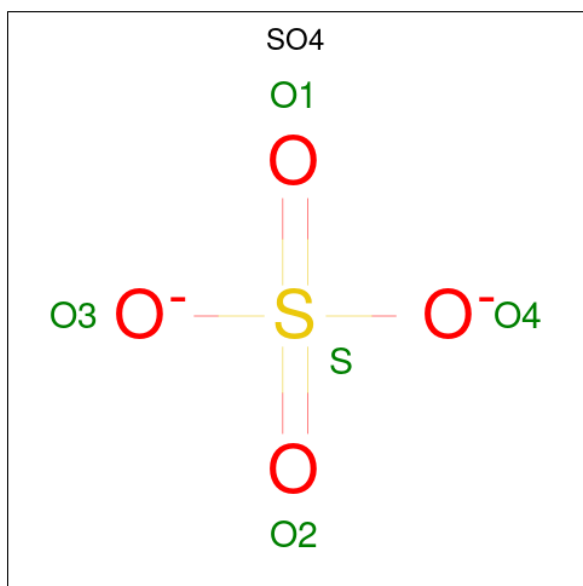
There are 4 unique types of molecules in this entry. The entry contains 5353 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 NYSGXRC-8828z, phosphatase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	Se	0	0	0
			2550	1609	443	488	3	7			
1	B	329	Total	C	N	O	S	Se	0	0	0
			2534	1599	440	485	3	7			

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 3 is PRASEODYMIUM ION (CCD ID: PR) (formula: Pr).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Pr 1	0	0
3	B	1	Total 1	Pr 1	0	0

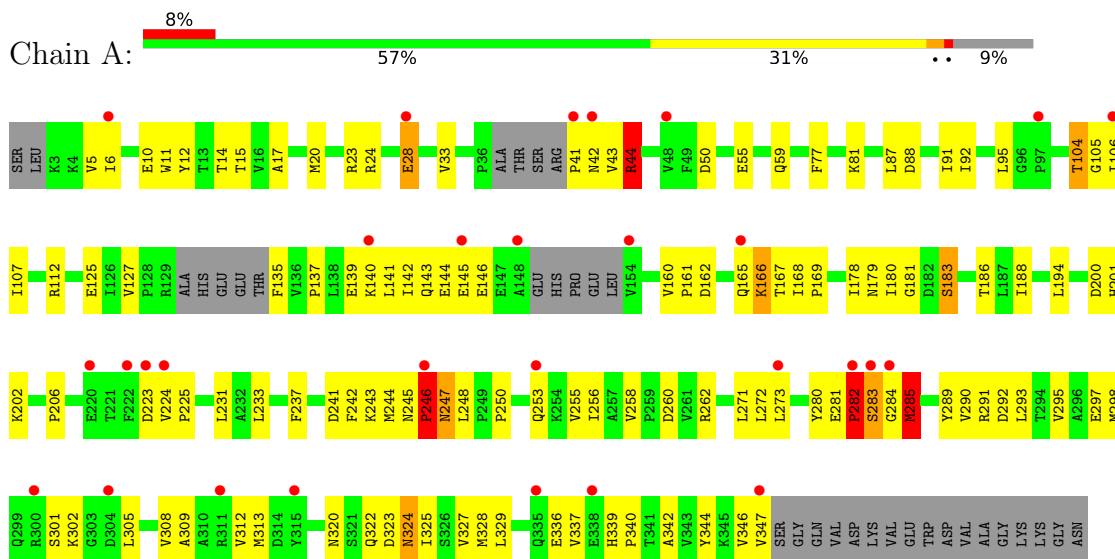
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	115	Total 115	O 115	0	0
4	B	137	Total 137	O 137	0	0

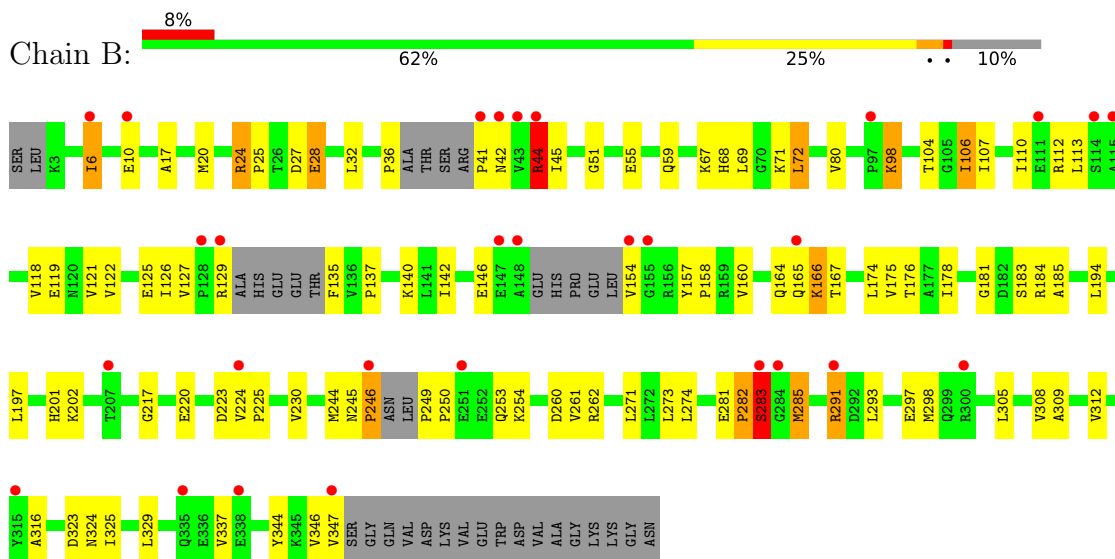
3 Residue-property plots

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: NYSGXRC-8828z, phosphatase



• Molecule 1: NYSGXRC-8828z, phosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	52.99Å 62.45Å 63.74Å 65.53° 70.21° 77.64°	Depositor
Resolution (Å)	43.06 – 1.90 43.06 – 1.90	Depositor EDS
% Data completeness (in resolution range)	96.6 (43.06-1.90) 96.7 (43.06-1.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.95 (at 1.89Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.241 , 0.279 0.236 , 0.271	Depositor DCC
R_{free} test set	1604 reflections (2.93%)	wwPDB-VP
Wilson B-factor (Å ²)	13.1	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 35.8	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	0.90	EDS
Total number of atoms	5353	wwPDB-VP
Average B, all atoms (Å ²)	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.05% 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: SO4, PR

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	0.47	3/2590 (0.1%)	1.07	19/3501 (0.5%)
1	B	0.52	2/2573 (0.1%)	1.06	20/3475 (0.6%)
All	All	0.50	5/5163 (0.1%)	1.06	39/6976 (0.6%)

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 (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	44	ARG	C-N	-15.06	1.15	1.33
1	A	44	ARG	C-N	-9.79	1.20	1.33
1	A	283	SER	CA-C	-7.39	1.43	1.53
1	B	285	MSE	CA-C	7.13	1.61	1.53
1	A	285	MSE	N-CA	6.21	1.54	1.46

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	ASN	N-CA-C	-13.39	94.34	114.16
1	B	44	ARG	O-C-N	-12.53	104.72	122.76
1	A	282	PRO	CA-C-N	-8.94	110.86	123.20
1	A	282	PRO	C-N-CA	-8.94	110.86	123.20
1	A	283	SER	O-C-N	8.03	133.66	122.83
1	A	223	ASP	N-CA-C	-7.75	102.16	111.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	183	SER	N-CA-C	-7.72	100.57	110.53
1	A	260	ASP	N-CA-C	-7.28	97.83	109.76
1	B	230	VAL	N-CA-C	7.02	118.08	111.48
1	B	183	SER	N-CA-C	-6.95	101.17	110.55
1	B	260	ASP	N-CA-C	-6.93	97.94	109.24
1	B	104	THR	N-CA-C	-6.78	101.79	110.53
1	A	283	SER	N-CA-C	6.44	117.63	108.54
1	B	285	MSE	N-CA-C	-6.35	96.75	108.24
1	B	230	VAL	CB-CA-C	-6.25	106.40	111.71
1	B	223	ASP	N-CA-C	-5.88	104.82	112.23
1	B	283	SER	CA-C-N	-5.88	113.88	122.46
1	B	283	SER	C-N-CA	-5.88	113.88	122.46
1	B	72	LEU	N-CA-C	5.84	118.80	110.10
1	A	104	THR	N-CA-C	-5.82	103.03	110.53
1	A	283	SER	CA-C-N	5.81	132.79	121.41
1	A	283	SER	C-N-CA	5.81	132.79	121.41
1	B	285	MSE	CB-CA-C	-5.76	103.30	112.05
1	A	324	ASN	N-CA-C	-5.74	102.41	110.50
1	A	282	PRO	CB-CA-C	5.73	118.73	111.39
1	B	44	ARG	CA-C-N	5.65	131.37	122.33
1	B	44	ARG	C-N-CA	5.65	131.37	122.33
1	A	5	VAL	N-CA-C	5.53	116.45	108.48
1	B	122	VAL	N-CA-C	-5.51	98.76	106.53
1	B	202	LYS	CA-C-N	5.46	125.55	119.32
1	B	202	LYS	C-N-CA	5.46	125.55	119.32
1	B	184	ARG	N-CA-C	5.45	117.47	109.24
1	A	320	ASN	N-CA-C	5.42	119.19	112.58
1	B	285	MSE	N-CA-CB	5.33	118.32	110.49
1	A	179	ASN	N-CA-C	5.32	118.15	109.59
1	B	98	LYS	N-CA-C	5.31	118.76	110.32
1	A	285	MSE	N-CA-C	5.25	121.98	110.80
1	A	342	ALA	N-CA-C	-5.02	100.11	108.34
1	A	14	THR	N-CA-C	-5.01	100.12	108.34

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	44	ARG	Mainchain

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	2550	0	2553	104	0
1	B	2534	0	2535	99	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	115	0	0	3	0
4	B	137	0	0	4	0
All	All	5353	0	5088	192	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 19.

All (192) 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:106:ILE:HD13	1:A:183:SER:HB2	1.30	1.11
1:A:33:VAL:HA	1:A:328:MSE:HE1	1.40	1.04
1:A:245:ASN:N	1:A:246:PRO:HD2	1.82	0.94
1:A:285:MSE:HE3	1:A:289:TYR:HD1	1.32	0.94
1:A:43:VAL:O	1:A:44:ARG:NH1	2.01	0.92
1:B:245:ASN:N	1:B:246:PRO:HD2	1.88	0.88
1:A:106:ILE:CD1	1:A:183:SER:HB2	2.03	0.87
1:B:246:PRO:HD3	1:B:253:GLN:NE2	1.93	0.82
1:B:118:VAL:HG22	1:B:167:THR:HG22	1.62	0.82
1:A:42:ASN:HD21	1:A:112:ARG:H	1.26	0.82
1:A:181:GLY:H	1:A:201:HIS:HD2	1.28	0.81
1:A:17:ALA:HB2	1:A:328:MSE:HE3	1.60	0.81
1:B:181:GLY:H	1:B:201:HIS:HD2	1.24	0.80
1:B:246:PRO:HD3	1:B:253:GLN:HE22	1.44	0.80
1:B:68:HIS:HA	1:B:71:LYS:HZ2	1.47	0.79
1:A:6:ILE:HD11	1:B:344:TYR:CD1	2.18	0.78
1:A:346:VAL:HG12	1:A:347:VAL:HG23	1.64	0.78
1:B:166:LYS:HA	1:B:166:LYS:HE3	1.65	0.78
1:A:28:GLU:HG2	4:A:532:HOH:O	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:ARG:HD2	1:A:323:ASP:HA	1.67	0.77
1:A:244:MSE:C	1:A:246:PRO:HD2	2.12	0.75
1:B:41:PRO:O	1:B:42:ASN:HB3	1.88	0.74
1:A:137:PRO:HG2	1:A:140:LYS:HG3	1.73	0.71
1:A:6:ILE:HD13	1:B:6:ILE:HG23	1.72	0.71
1:B:244:MSE:C	1:B:246:PRO:HD2	2.16	0.70
1:B:137:PRO:HG2	1:B:140:LYS:HG3	1.72	0.69
1:B:106:ILE:HD11	1:B:185:ALA:HB2	1.73	0.69
1:B:44:ARG:O	1:B:45:ILE:HD13	1.92	0.68
1:B:20:MSE:HG2	1:B:325:ILE:HB	1.75	0.68
1:A:250:PRO:HA	1:A:253:GLN:CD	2.19	0.68
1:A:339:HIS:CD2	1:B:67:LYS:HD3	2.28	0.67
1:A:250:PRO:HG2	4:A:613:HOH:O	1.93	0.67
1:A:166:LYS:HZ1	1:A:167:THR:H	1.44	0.66
1:A:33:VAL:CA	1:A:328:MSE:HE1	2.23	0.66
1:B:68:HIS:HA	1:B:71:LYS:NZ	2.10	0.65
1:B:121:VAL:HG12	1:B:126:ILE:HD13	1.79	0.64
1:A:23:ARG:HG2	1:A:23:ARG:HH11	1.62	0.64
1:A:42:ASN:ND2	1:A:112:ARG:H	1.97	0.63
1:B:166:LYS:CE	1:B:167:THR:H	2.11	0.63
1:A:105:GLY:C	1:A:106:ILE:HD12	2.23	0.62
1:A:166:LYS:NZ	1:A:167:THR:H	1.96	0.62
1:B:42:ASN:ND2	1:B:112:ARG:HB3	2.15	0.61
1:B:281:GLU:HB3	1:B:282:PRO:CD	2.30	0.61
1:B:137:PRO:HG2	1:B:140:LYS:CG	2.30	0.61
1:B:10:GLU:HA	1:B:337:VAL:HG21	1.83	0.60
1:A:241:ASP:O	1:A:244:MSE:HE2	2.01	0.59
1:B:166:LYS:HE3	1:B:167:THR:H	1.65	0.59
1:B:24:ARG:HG3	1:B:25:PRO:HD2	1.82	0.59
1:B:6:ILE:HD12	1:B:17:ALA:O	2.03	0.59
1:B:281:GLU:HB3	1:B:282:PRO:HD3	1.84	0.58
1:A:280:TYR:CE2	1:A:290:VAL:HG21	2.39	0.58
1:B:28:GLU:HG3	1:B:51:GLY:O	2.03	0.58
1:A:140:LYS:HG2	1:A:160:VAL:HG21	1.84	0.57
1:B:271:LEU:HD11	1:B:298:MSE:HE2	1.85	0.57
1:A:125:GLU:OE2	1:A:262:ARG:HD2	2.04	0.57
1:A:245:ASN:N	1:A:246:PRO:CD	2.64	0.57
1:A:181:GLY:H	1:A:201:HIS:CD2	2.18	0.57
1:B:135:PHE:N	4:B:628:HOH:O	2.37	0.57
1:A:105:GLY:O	1:A:106:ILE:HD12	2.04	0.56
1:B:6:ILE:HD12	1:B:6:ILE:H	1.71	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:PRO:HG2	1:B:36:PRO:HG3	1.87	0.56
1:A:6:ILE:HD13	1:B:6:ILE:CG2	2.35	0.55
1:B:140:LYS:HE3	1:B:160:VAL:HB	1.88	0.55
1:B:42:ASN:HD21	1:B:112:ARG:HB3	1.71	0.55
1:A:271:LEU:HD11	1:A:298:MSE:HE2	1.89	0.55
1:A:285:MSE:HE3	1:A:289:TYR:CD1	2.25	0.55
1:B:119:GLU:HA	1:B:129:ARG:HH21	1.72	0.55
1:A:17:ALA:CB	1:A:328:MSE:HE3	2.35	0.54
1:B:106:ILE:C	1:B:106:ILE:HD13	2.32	0.54
1:B:246:PRO:C	4:B:687:HOH:O	2.51	0.54
1:A:200:ASP:HB3	1:A:202:LYS:HZ2	1.72	0.54
1:A:106:ILE:HG12	1:A:183:SER:C	2.31	0.54
1:B:127:VAL:HG22	1:B:135:PHE:CE2	2.43	0.54
1:B:245:ASN:N	1:B:246:PRO:CD	2.67	0.54
1:B:55:GLU:O	1:B:59:GLN:HG3	2.08	0.53
1:B:69:LEU:HA	1:B:72:LEU:HD13	1.90	0.53
1:B:178:ILE:HD12	1:B:261:VAL:HG22	1.90	0.53
1:B:106:ILE:O	1:B:106:ILE:HG23	2.09	0.53
1:B:194:LEU:C	1:B:194:LEU:HD12	2.34	0.53
1:B:291:ARG:NH2	4:B:713:HOH:O	2.42	0.52
1:A:41:PRO:O	1:A:42:ASN:HB3	2.10	0.52
1:A:6:ILE:HG12	1:B:6:ILE:HG12	1.91	0.52
1:B:98:LYS:HG2	1:B:244:MSE:HE1	1.90	0.52
1:A:243:LYS:HB3	1:A:253:GLN:CD	2.35	0.52
1:A:42:ASN:HD21	1:A:112:ARG:N	2.04	0.51
1:A:42:ASN:ND2	1:A:42:ASN:O	2.43	0.51
1:A:305:LEU:O	1:A:308:VAL:HG12	2.11	0.51
1:A:309:ALA:O	1:A:312:VAL:HG12	2.10	0.51
1:A:301:SER:O	1:A:302:LYS:HB2	2.09	0.51
1:B:224:VAL:HG13	1:B:225:PRO:HD2	1.91	0.51
1:B:166:LYS:HE3	1:B:166:LYS:CA	2.37	0.51
1:B:176:THR:HG22	1:B:178:ILE:HD11	1.92	0.51
1:B:305:LEU:O	1:B:308:VAL:HG12	2.11	0.51
1:A:50:ASP:HB3	1:A:104:THR:OG1	2.11	0.50
1:A:166:LYS:HE3	1:A:167:THR:O	2.11	0.50
1:A:194:LEU:HD12	1:A:194:LEU:C	2.36	0.50
1:A:10:GLU:HA	1:A:337:VAL:HG21	1.93	0.50
1:A:17:ALA:HB2	1:A:328:MSE:CE	2.35	0.50
1:A:291:ARG:HD2	1:A:292:ASP:OD1	2.12	0.50
1:A:344:TYR:CD2	1:B:6:ILE:HD11	2.47	0.49
1:B:140:LYS:HG2	1:B:160:VAL:HG11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:LEU:O	1:A:91:ILE:HG13	2.12	0.49
1:A:44:ARG:HD3	1:A:44:ARG:HA	1.52	0.48
1:B:293:LEU:O	1:B:297:GLU:HG2	2.14	0.48
1:B:346:VAL:O	1:B:347:VAL:HB	2.13	0.48
1:B:309:ALA:O	1:B:312:VAL:HG12	2.14	0.48
1:A:77:PHE:CZ	1:A:81:LYS:HD3	2.49	0.47
1:A:243:LYS:HB3	1:A:253:GLN:OE1	2.15	0.47
1:A:104:THR:HG22	1:A:233:LEU:CD2	2.45	0.47
1:A:291:ARG:O	1:A:295:VAL:HG23	2.15	0.47
1:B:80:VAL:HG11	1:B:178:ILE:HD12	1.95	0.47
1:A:15:THR:HG22	1:A:328:MSE:HE2	1.95	0.47
1:B:69:LEU:O	1:B:72:LEU:HD13	2.15	0.47
1:B:323:ASP:OD1	1:B:324:ASN:N	2.43	0.47
1:B:164:GLN:HG2	1:B:165:GLN:N	2.29	0.47
1:A:20:MSE:HG2	1:A:325:ILE:HB	1.97	0.47
1:B:6:ILE:HD12	1:B:6:ILE:N	2.30	0.47
1:A:142:ILE:O	1:A:146:GLU:HG3	2.15	0.46
1:B:110:ILE:HD12	1:B:175:VAL:HG22	1.97	0.46
1:A:137:PRO:HG2	1:A:140:LYS:CG	2.43	0.46
1:A:43:VAL:O	1:A:44:ARG:HD3	2.15	0.46
1:A:243:LYS:HE3	1:A:255:VAL:HG23	1.97	0.46
1:A:23:ARG:HG2	1:A:23:ARG:NH1	2.28	0.46
1:A:247:ASN:O	1:A:248:LEU:HD12	2.16	0.46
1:A:344:TYR:CE2	1:B:6:ILE:HD11	2.50	0.46
1:A:242:PHE:HB3	1:A:255:VAL:HG22	1.98	0.46
1:A:188:ILE:HG13	1:A:273:LEU:HD21	1.99	0.45
1:A:231:LEU:HD12	1:A:255:VAL:HG11	1.98	0.45
1:B:308:VAL:HG13	1:B:329:LEU:CD1	2.47	0.45
1:A:127:VAL:HG22	1:A:135:PHE:CE2	2.52	0.45
1:B:106:ILE:CD1	1:B:185:ALA:HB2	2.44	0.45
1:A:340:PRO:HG2	1:B:36:PRO:CG	2.47	0.45
1:B:142:ILE:O	1:B:146:GLU:HG3	2.17	0.45
1:A:55:GLU:H	1:A:55:GLU:CD	2.25	0.45
1:A:346:VAL:HG21	1:B:27:ASP:HB3	1.99	0.45
1:B:346:VAL:HG12	1:B:347:VAL:HG23	1.99	0.45
1:A:28:GLU:CD	1:A:324:ASN:HD21	2.25	0.44
1:B:72:LEU:HD12	1:B:72:LEU:N	2.31	0.44
1:A:88:ASP:O	1:A:92:ILE:HG13	2.18	0.44
1:B:42:ASN:O	1:B:42:ASN:CG	2.60	0.44
1:B:245:ASN:O	1:B:246:PRO:C	2.61	0.44
1:A:140:LYS:O	1:A:144:GLU:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:PRO:CD	1:B:253:GLN:HE22	2.23	0.44
1:B:283:SER:C	1:B:285:MSE:H	2.25	0.44
1:B:106:ILE:HD12	1:B:274:LEU:HG	1.99	0.44
1:A:137:PRO:HD2	1:A:140:LYS:HD2	1.99	0.44
1:B:125:GLU:OE2	1:B:262:ARG:HD2	2.18	0.44
1:A:337:VAL:O	1:A:337:VAL:HG23	2.18	0.43
1:B:281:GLU:CB	1:B:282:PRO:CD	2.95	0.43
1:B:137:PRO:CG	1:B:140:LYS:HG3	2.44	0.43
1:A:186:THR:O	1:A:273:LEU:HD23	2.17	0.43
1:A:256:ILE:HD12	1:A:258:VAL:HB	1.99	0.43
1:B:36:PRO:HA	1:B:44:ARG:HH11	1.83	0.43
1:A:281:GLU:O	1:A:282:PRO:C	2.60	0.43
1:B:346:VAL:O	1:B:347:VAL:CB	2.65	0.43
1:A:166:LYS:CE	1:A:167:THR:H	2.32	0.43
1:B:224:VAL:HG12	1:B:225:PRO:N	2.34	0.43
1:A:242:PHE:CB	1:A:255:VAL:HG22	2.48	0.43
1:A:20:MSE:CG	1:A:325:ILE:HB	2.49	0.42
1:B:178:ILE:CD1	1:B:261:VAL:HG13	2.49	0.42
1:B:217:GLY:CA	1:B:254:LYS:HE2	2.49	0.42
1:A:224:VAL:CG1	1:A:225:PRO:HD2	2.49	0.42
1:A:55:GLU:O	1:A:59:GLN:HG3	2.20	0.42
1:B:67:LYS:O	1:B:71:LYS:HG3	2.19	0.42
1:B:140:LYS:HG2	1:B:160:VAL:HG21	2.01	0.42
1:B:224:VAL:HG12	4:B:638:HOH:O	2.19	0.42
1:B:273:LEU:C	1:B:273:LEU:HD23	2.45	0.42
1:B:285:MSE:HE2	1:B:316:ALA:HB2	2.02	0.41
1:A:42:ASN:O	1:A:42:ASN:CG	2.64	0.41
1:A:344:TYR:CG	1:B:6:ILE:HD11	2.55	0.41
1:B:166:LYS:HE3	1:B:167:THR:N	2.34	0.41
1:A:11:TRP:CG	1:A:12:TYR:H	2.37	0.41
1:A:139:GLU:O	1:A:143:GLN:HG3	2.21	0.41
1:B:185:ALA:HB1	1:B:197:LEU:HD12	2.02	0.41
1:A:313:MSE:SE	1:A:327:VAL:HG22	2.70	0.41
1:B:224:VAL:CG1	1:B:225:PRO:HD2	2.49	0.41
1:A:160:VAL:HA	1:A:161:PRO:HD3	1.90	0.41
1:A:293:LEU:O	1:A:297:GLU:HG2	2.21	0.41
1:A:91:ILE:O	1:A:95:LEU:HD13	2.20	0.41
1:A:140:LYS:HG3	1:A:160:VAL:HG11	2.02	0.41
1:A:180:ILE:HD12	1:A:237:PHE:CE2	2.56	0.41
1:B:157:TYR:HA	1:B:158:PRO:HD3	1.84	0.41
1:B:249:PRO:HA	1:B:250:PRO:HD3	2.00	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:ILE:HB	1:A:178:ILE:HB	2.04	0.40
1:B:107:ILE:HB	1:B:178:ILE:HB	2.03	0.40
1:A:322:GLN:NE2	4:A:611:HOH:O	2.54	0.40
1:B:106:ILE:C	1:B:106:ILE:CD1	2.94	0.40
1:B:282:PRO:HB2	1:B:285:MSE:CG	2.51	0.40
1:A:95:LEU:N	1:A:95:LEU:HD12	2.37	0.40
1:A:308:VAL:HG13	1:A:329:LEU:CD1	2.51	0.40
1:A:168:ILE:HA	1:A:169:PRO:HD2	1.96	0.40
1:B:113:LEU:HD21	1:B:174:LEU:HG	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	323/364 (89%)	306 (95%)	13 (4%)	4 (1%)	10	4
1	B	319/364 (88%)	310 (97%)	9 (3%)	0	100	100
All	All	642/728 (88%)	616 (96%)	22 (3%)	4 (1%)	21	13

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	246	PRO
1	A	285	MSE
1	A	284	GLY
1	A	206	PRO

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	277/297 (93%)	264 (95%)	13 (5%)	23	15
1	B	275/297 (93%)	262 (95%)	13 (5%)	23	15
All	All	552/594 (93%)	526 (95%)	26 (5%)	23	15

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

Mol	Chain	Res	Type
1	A	28	GLU
1	A	44	ARG
1	A	141	LEU
1	A	145	GLU
1	A	162	ASP
1	A	165	GLN
1	A	166	LYS
1	A	246	PRO
1	A	272	LEU
1	A	282	PRO
1	A	283	SER
1	A	285	MSE
1	A	336	GLU
1	B	6	ILE
1	B	24	ARG
1	B	28	GLU
1	B	32	LEU
1	B	44	ARG
1	B	106	ILE
1	B	154	VAL
1	B	166	LYS
1	B	220	GLU
1	B	246	PRO
1	B	282	PRO
1	B	283	SER
1	B	291	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	ASN
1	A	64	HIS
1	A	68	HIS
1	A	143	GLN
1	A	165	GLN
1	A	201	HIS
1	A	253	GLN
1	A	322	GLN
1	A	324	ASN
1	A	334	ASN
1	A	339	HIS
1	B	42	ASN
1	B	99	HIS
1	B	143	GLN
1	B	201	HIS
1	B	263	GLN
1	B	324	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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	$\# Z > 2$
2	SO4	B	600	-	4,4,4	0.38	0	6,6,6	0.11	0
2	SO4	A	400	-	4,4,4	0.34	0	6,6,6	0.17	0
2	SO4	B	500	-	4,4,4	0.38	0	6,6,6	0.09	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.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	B	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	44:ARG	C	45:ILE	N	1.15

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	324/364 (89%)	0.70	29 (8%) 15 16	8, 13, 18, 21	0
1	B	322/364 (88%)	0.70	29 (9%) 15 16	8, 12, 18, 21	0
All	All	646/728 (88%)	0.70	58 (8%) 15 16	8, 13, 18, 21	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	154	VAL	7.1
1	B	246	PRO	6.9
1	B	284	GLY	6.7
1	A	283	SER	6.6
1	A	246	PRO	6.3
1	B	347	VAL	6.2
1	A	347	VAL	5.0
1	A	154	VAL	4.8
1	A	284	GLY	4.7
1	B	315	TYR	4.3
1	B	42	ASN	4.0
1	A	253	GLN	3.9
1	B	41	PRO	3.7
1	B	129	ARG	3.6
1	B	165	GLN	3.4
1	A	224	VAL	3.4
1	A	41	PRO	3.3
1	B	115	ALA	3.2
1	B	335	GLN	3.1
1	A	165	GLN	3.0
1	A	106	ILE	3.0
1	B	43	VAL	2.9
1	A	300	ARG	2.9
1	A	273	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	148	ALA	2.9
1	A	282	PRO	2.9
1	B	283	SER	2.9
1	B	6	ILE	2.8
1	B	155	GLY	2.8
1	B	207	THR	2.6
1	A	335	GLN	2.6
1	A	42	ASN	2.6
1	A	6	ILE	2.6
1	B	300	ARG	2.5
1	A	145	GLU	2.5
1	A	311	ARG	2.5
1	B	44	ARG	2.5
1	B	111	GLU	2.5
1	A	338	GLU	2.4
1	A	28	GLU	2.4
1	A	48	VAL	2.4
1	A	315	TYR	2.4
1	A	220	GLU	2.3
1	B	97	PRO	2.3
1	A	97	PRO	2.2
1	B	128	PRO	2.2
1	A	222	PHE	2.2
1	B	291	ARG	2.2
1	B	147	GLU	2.1
1	B	338	GLU	2.1
1	B	224	VAL	2.1
1	A	304	ASP	2.1
1	B	114	SER	2.1
1	A	223	ASP	2.1
1	B	10	GLU	2.0
1	B	251	GLU	2.0
1	A	148	ALA	2.0
1	A	140	LYS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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($\text{\AA}^2$)	Q<0.9
2	SO4	B	600	5/5	0.95	0.11	22,22,23,24	0
2	SO4	B	500	5/5	0.97	0.07	13,14,16,17	0
2	SO4	A	400	5/5	0.98	0.05	13,13,16,18	0
3	PR	A	522	1/1	1.00	0.04	19,19,19,19	0
3	PR	B	422	1/1	1.00	0.04	15,15,15,15	0

6.5 Other polymers [i](#)

There are no such residues in this entry.