



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:05 AM UTC

PDB ID : 6TIM / pdb_00006tim
Title : THE ADAPTABILITY OF THE ACTIVE SITE OF TRYPA NOSOMAL
TRIOSEPHOSPHATE ISOMERASE AS OBSERVED IN THE CRYSTAL
STRUCTURES OF THREE DIFFERENT COMPLEXES
Authors : Noble, M.E.M.; Wierenga, R.K.; Hol, W.G.J.
Deposited on : 1991-04-23
Resolution : 2.20 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

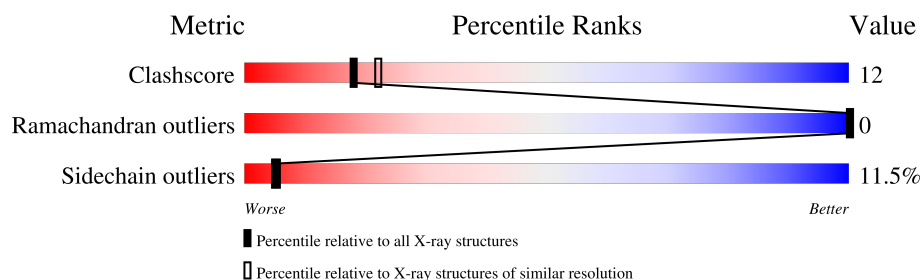
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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))
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	250	
1	B	250	

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
2	G3P	B	300	X	-	X	-

2 Entry composition [i](#)

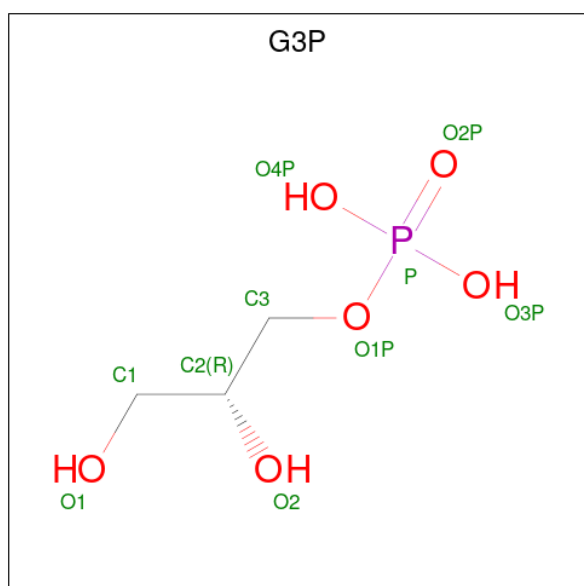
There are 3 unique types of molecules in this entry. The entry contains 3867 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	249	Total	C	N	O	S	0	0	0
			1883	1197	331	350	5			
1	B	249	Total	C	N	O	S	0	0	0
			1883	1197	331	350	5			

- Molecule 2 is SN-GLYCEROL-3-PHOSPHATE (CCD ID: G3P) (formula: $C_3H_9O_6P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	O	P	0	0
			10	3	6	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	53	Total	O	0	0
			53	53		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	38	Total	O	0	0
			38	38		

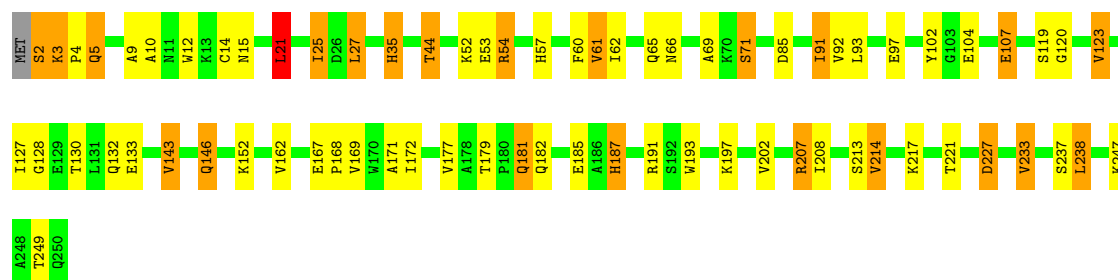
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

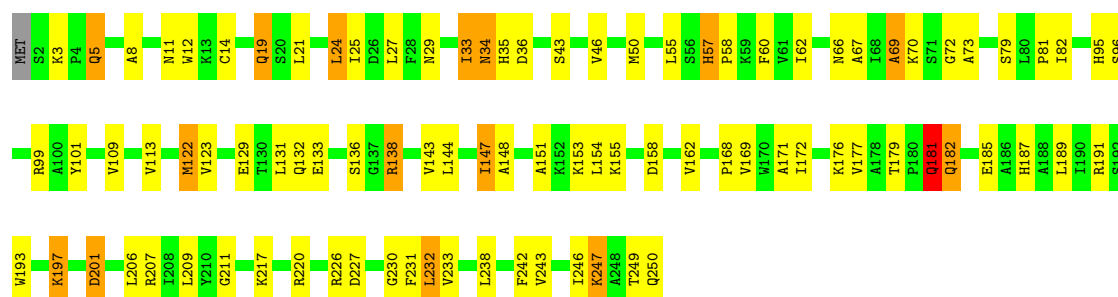
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain A: 



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	112.36Å 97.59Å 46.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.20	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	TNT	Depositor
R, R_{free}	0.370 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3867	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G3P

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	1.09	1/1917 (0.1%)	1.76	29/2599 (1.1%)
1	B	1.08	0/1917	1.72	26/2599 (1.0%)
All	All	1.08	1/3834 (0.0%)	1.74	55/5198 (1.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	104	GLU	CD-OE2	5.88	1.36	1.25

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	VAL	N-CA-CB	9.77	122.69	110.47
1	A	214	VAL	CB-CA-C	7.97	121.97	110.33
1	B	19	GLN	CB-CA-C	7.17	122.14	110.88
1	A	61	VAL	CA-C-O	-6.84	114.48	121.67
1	A	171	ALA	CA-C-N	-6.59	114.13	122.37
1	A	171	ALA	C-N-CA	-6.59	114.13	122.37
1	A	69	ALA	N-CA-C	6.54	119.22	111.71
1	A	162	VAL	N-CA-C	6.45	117.20	108.17
1	A	233	VAL	N-CA-C	6.33	117.03	108.17
1	A	21	LEU	N-CA-CB	6.08	118.99	109.94
1	A	187	HIS	N-CA-C	6.07	117.89	111.28
1	A	177	VAL	CA-C-N	-6.01	113.71	122.19
1	A	177	VAL	C-N-CA	-6.01	113.71	122.19
1	B	69	ALA	N-CA-C	5.88	118.48	111.71
1	B	8	ALA	N-CA-CB	5.87	119.93	110.65
1	A	120	GLY	N-CA-C	5.83	122.79	115.21
1	B	217	LYS	N-CA-C	5.83	117.43	111.14
1	A	15	ASN	CA-C-N	-5.75	114.35	121.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	15	ASN	C-N-CA	-5.75	114.35	121.83
1	B	36	ASP	CA-C-N	5.73	131.24	122.25
1	B	36	ASP	C-N-CA	5.73	131.24	122.25
1	B	172	ILE	CA-C-N	5.70	128.72	120.11
1	B	172	ILE	C-N-CA	5.70	128.72	120.11
1	A	2	SER	N-CA-CB	5.69	120.18	110.50
1	B	209	LEU	CA-C-N	-5.63	114.77	122.93
1	B	209	LEU	C-N-CA	-5.63	114.77	122.93
1	A	227	ASP	N-CA-CB	5.62	119.08	110.70
1	A	54	ARG	N-CA-C	5.61	118.59	111.69
1	A	35	HIS	CA-CB-CG	-5.57	108.23	113.80
1	B	57	HIS	CA-C-N	5.56	125.23	119.56
1	B	57	HIS	C-N-CA	5.56	125.23	119.56
1	B	181	GLN	CA-C-N	5.56	127.67	120.44
1	B	181	GLN	C-N-CA	5.56	127.67	120.44
1	A	102	TYR	N-CA-C	5.50	119.56	112.41
1	A	169	VAL	N-CA-C	5.49	116.22	110.62
1	B	19	GLN	N-CA-CB	5.45	117.91	110.01
1	B	72	GLY	N-CA-C	5.45	117.26	110.29
1	B	96	SER	N-CA-CB	5.43	118.59	110.22
1	B	3	LYS	N-CA-C	-5.40	101.83	110.10
1	B	151	ALA	O-C-N	5.38	127.83	122.12
1	A	3	LYS	O-C-N	5.37	125.14	121.71
1	A	107	GLU	CB-CA-C	5.37	119.31	110.88
1	B	101	TYR	N-CA-C	5.34	118.25	111.69
1	A	107	GLU	CA-C-N	5.26	127.67	120.46
1	A	107	GLU	C-N-CA	5.26	127.67	120.46
1	A	44	THR	CA-CB-OG1	5.22	117.43	109.60
1	A	146	GLN	CB-CG-CD	-5.21	103.74	112.60
1	B	169	VAL	N-CA-C	5.09	116.43	110.62
1	B	162	VAL	N-CA-C	5.09	116.30	108.71
1	B	29	ASN	CA-CB-CG	5.09	117.69	112.60
1	A	5	GLN	CA-C-N	-5.08	115.33	120.21
1	A	5	GLN	C-N-CA	-5.08	115.33	120.21
1	B	187	HIS	N-CA-CB	5.07	117.58	110.12
1	B	123	VAL	N-CA-C	5.04	115.17	108.11
1	B	143	VAL	N-CA-C	5.03	117.37	111.09

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	1883	0	1917	40	0
1	B	1883	0	1917	56	0
2	B	10	0	7	4	0
3	A	53	0	0	0	0
3	B	38	0	0	0	0
All	All	3867	0	3841	93	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 12.

All (93) 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:132:GLN:HE22	1:B:138:ARG:NH2	1.53	1.06
1:A:179:THR:H	1:A:182:GLN:HE21	1.21	0.84
1:A:52:LYS:HG3	1:A:62:ILE:HD13	1.59	0.84
1:A:10:ALA:HB1	1:A:237:SER:HB2	1.67	0.76
1:A:179:THR:H	1:A:182:GLN:NE2	1.85	0.75
1:A:52:LYS:HG3	1:A:62:ILE:CD1	2.20	0.72
1:B:226:ARG:O	1:B:226:ARG:HD2	1.89	0.72
1:B:79:SER:HB2	1:B:81:PRO:HD2	1.72	0.71
1:B:132:GLN:HE22	1:B:138:ARG:HH21	1.38	0.69
1:B:5:GLN:HE21	1:B:207:ARG:HH12	1.41	0.69
1:B:21:LEU:O	1:B:25:ILE:HG13	1.93	0.68
1:B:168:PRO:HD2	1:B:211:GLY:O	1.93	0.67
1:A:10:ALA:CB	1:A:237:SER:HB2	2.27	0.63
1:B:11:ASN:HB2	1:B:232:LEU:HD21	1.80	0.62
1:B:133:GLU:HG2	1:B:138:ARG:NH1	2.14	0.62
1:A:191:ARG:HH21	1:A:227:ASP:HB3	1.66	0.60
1:B:226:ARG:HD2	1:B:226:ARG:C	2.26	0.60
1:B:133:GLU:HG2	1:B:138:ARG:HH12	1.69	0.58
1:B:181:GLN:O	1:B:185:GLU:HG2	2.03	0.58
1:B:24:LEU:HD21	1:B:238:LEU:O	2.05	0.57
1:A:25:ILE:HG21	1:A:54:ARG:HB3	1.88	0.54
1:A:132:GLN:OE1	1:A:132:GLN:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:55:LEU:HD11	1:B:60:PHE:CB	2.38	0.53
1:A:181:GLN:O	1:A:185:GLU:HG3	2.07	0.53
1:A:71:SER:HB3	1:B:14:CYS:O	2.08	0.53
1:B:154:LEU:HD22	1:B:158:ASP:HB3	1.91	0.53
1:B:168:PRO:HG2	1:B:171:ALA:HB3	1.91	0.53
1:B:179:THR:H	1:B:182:GLN:NE2	2.06	0.53
1:A:57:HIS:HB3	1:A:60:PHE:HD1	1.73	0.52
1:A:168:PRO:O	1:A:172:ILE:HD12	2.09	0.52
1:A:57:HIS:HB3	1:A:60:PHE:CD1	2.45	0.52
1:B:201:ASP:OD1	1:B:201:ASP:N	2.42	0.51
1:B:95:HIS:HE2	2:B:300:G3P:H11	1.75	0.51
1:B:193:TRP:CE2	1:B:197:LYS:HD3	2.46	0.51
1:B:11:ASN:HD22	2:B:300:G3P:H11	1.76	0.51
1:B:55:LEU:HD11	1:B:60:PHE:HB2	1.93	0.50
1:A:35:HIS:H	1:A:35:HIS:CD2	2.30	0.49
1:B:21:LEU:HB2	1:B:50:MET:HE1	1.94	0.49
1:A:181:GLN:H	1:A:181:GLN:CD	2.21	0.49
1:A:3:LYS:HB3	1:A:4:PRO:HD2	1.94	0.49
1:A:127:ILE:HB	1:A:146:GLN:OE1	2.12	0.48
1:A:217:LYS:N	1:A:217:LYS:HD2	2.29	0.47
1:B:155:LYS:O	1:B:158:ASP:HB2	2.13	0.47
1:A:12:TRP:CE3	1:A:21:LEU:HD22	2.49	0.47
1:B:136:SER:HB2	1:B:138:ARG:HG3	1.96	0.47
1:A:91:ILE:HG23	1:A:123:VAL:HG13	1.96	0.47
1:B:11:ASN:HD22	2:B:300:G3P:C1	2.27	0.47
1:B:57:HIS:ND1	1:B:58:PRO:HD2	2.30	0.47
1:B:147:ILE:CG2	1:B:148:ALA:N	2.78	0.47
1:B:79:SER:CB	1:B:81:PRO:HD2	2.42	0.47
1:A:130:THR:OG1	1:A:133:GLU:HG3	2.15	0.47
1:A:193:TRP:CZ2	1:A:197:LYS:HG3	2.50	0.47
1:B:11:ASN:HB2	1:B:232:LEU:CD2	2.44	0.46
1:A:65:GLN:O	1:A:66:ASN:HB2	2.14	0.46
1:A:187:HIS:CE1	1:A:208:ILE:HG22	2.51	0.46
1:B:249:THR:O	1:B:249:THR:OG1	2.29	0.46
1:B:191:ARG:HD2	1:B:227:ASP:OD1	2.15	0.46
1:B:12:TRP:CE3	1:B:43:SER:HB3	2.52	0.45
1:B:132:GLN:NE2	1:B:138:ARG:NH2	2.39	0.45
1:A:27:LEU:C	1:A:27:LEU:HD22	2.42	0.45
1:B:69:ALA:O	1:B:70:LYS:HG2	2.16	0.45
1:A:12:TRP:CD1	1:A:238:LEU:HD13	2.52	0.45
1:B:50:MET:HE2	1:B:50:MET:HB3	1.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:66:ASN:CG	1:B:67:ALA:H	2.25	0.44
1:B:147:ILE:HG22	1:B:148:ALA:N	2.32	0.44
1:B:191:ARG:NH2	1:B:206:LEU:O	2.51	0.44
1:B:242:PHE:O	1:B:246:ILE:HG13	2.18	0.44
1:A:97:GLU:OE2	1:B:73:ALA:HB1	2.18	0.43
1:B:34:ASN:HD22	1:B:35:HIS:N	2.16	0.43
1:A:91:ILE:HG12	1:A:93:LEU:HG	2.00	0.43
1:B:247:LYS:HE3	1:B:247:LYS:HB2	1.68	0.43
1:B:122:MET:HE2	1:B:122:MET:HB3	1.85	0.43
1:B:144:LEU:HD11	1:B:189:LEU:HD11	2.00	0.43
1:B:232:LEU:HD22	2:B:300:G3P:O1	2.20	0.42
1:A:5:GLN:OE1	1:A:207:ARG:NH2	2.53	0.42
1:A:66:ASN:C	1:A:91:ILE:HD11	2.45	0.42
1:B:243:VAL:HG12	1:B:247:LYS:HE2	2.02	0.42
1:A:14:CYS:O	1:A:14:CYS:SG	2.77	0.42
1:A:128:GLY:HA3	1:A:167:GLU:O	2.20	0.42
1:A:91:ILE:HG13	1:A:92:VAL:N	2.34	0.42
1:A:197:LYS:HD2	1:A:197:LYS:HA	1.93	0.42
1:A:44:THR:HG21	1:B:82:ILE:HD13	2.00	0.41
1:B:129:GLU:OE1	1:B:129:GLU:N	2.52	0.41
1:A:133:GLU:HG3	1:A:133:GLU:H	1.48	0.41
1:B:99:ARG:HH11	1:B:99:ARG:HD3	1.62	0.41
1:B:109:VAL:O	1:B:113:VAL:HG23	2.20	0.41
1:A:9:ALA:O	1:A:233:VAL:N	2.38	0.41
1:B:250:GLN:N	1:B:250:GLN:CD	2.77	0.41
1:A:35:HIS:HE1	1:A:249:THR:OG1	2.04	0.40
1:A:193:TRP:CE2	1:A:197:LYS:HG3	2.55	0.40
1:B:230:GLY:C	1:B:231:PHE:CG	2.99	0.40
1:B:33:ILE:HD13	1:B:33:ILE:HG21	1.81	0.40
1:B:69:ALA:C	1:B:70:LYS:HG2	2.46	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	247/250 (99%)	232 (94%)	15 (6%)	0	100	100
1	B	247/250 (99%)	238 (96%)	9 (4%)	0	100	100
All	All	494/500 (99%)	470 (95%)	24 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	196/197 (100%)	174 (89%)	22 (11%)	6	5
1	B	196/197 (100%)	173 (88%)	23 (12%)	5	5
All	All	392/394 (100%)	347 (88%)	45 (12%)	5	5

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	21	LEU
1	A	25	ILE
1	A	27	LEU
1	A	53	GLU
1	A	61	VAL
1	A	71	SER
1	A	85	ASP
1	A	91	ILE
1	A	107	GLU
1	A	119	SER
1	A	123	VAL
1	A	143	VAL
1	A	152	LYS
1	A	181	GLN

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Mol	Chain	Res	Type
1	A	202	VAL
1	A	207	ARG
1	A	213	SER
1	A	214	VAL
1	A	221	THR
1	A	238	LEU
1	A	247	LYS
1	B	5	GLN
1	B	19	GLN
1	B	24	LEU
1	B	27	LEU
1	B	33	ILE
1	B	34	ASN
1	B	46	VAL
1	B	62	ILE
1	B	122	MET
1	B	131	LEU
1	B	138	ARG
1	B	147	ILE
1	B	153	LYS
1	B	176	LYS
1	B	177	VAL
1	B	181	GLN
1	B	182	GLN
1	B	197	LYS
1	B	201	ASP
1	B	220	ARG
1	B	232	LEU
1	B	233	VAL
1	B	247	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	19	GLN
1	A	34	ASN
1	A	35	HIS
1	A	182	GLN
1	B	5	GLN
1	B	34	ASN
1	B	66	ASN
1	B	132	GLN

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Mol	Chain	Res	Type
1	B	181	GLN
1	B	182	GLN
1	B	224	GLN
1	B	250	GLN

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](#)

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	G3P	B	300	-	9,9,9	0.50	0	10,12,12	1.20	1 (10%)

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	G3P	B	300	-	1/1/2/2	4/8/8/8	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
2	B	300	G3P	O3P-P-O1P	-2.51	100.12	106.67

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	300	G3P	C2

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	300	G3P	O1-C1-C2-C3
2	B	300	G3P	O2-C2-C3-O1P
2	B	300	G3P	C1-C2-C3-O1P
2	B	300	G3P	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	300	G3P	4	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.