



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:08 PM UTC

PDB ID : 1BTM / pdb_00001btm
Title : TRIOSEPHOSPHATE ISOMERASE (TIM) COMPLEXED WITH 2-PHOSPHOGLYCOLIC ACID
Authors : Delboni, L.F.; Mande, S.C.; Hol, W.G.J.
Deposited on : 1995-11-11
Resolution : 2.80 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

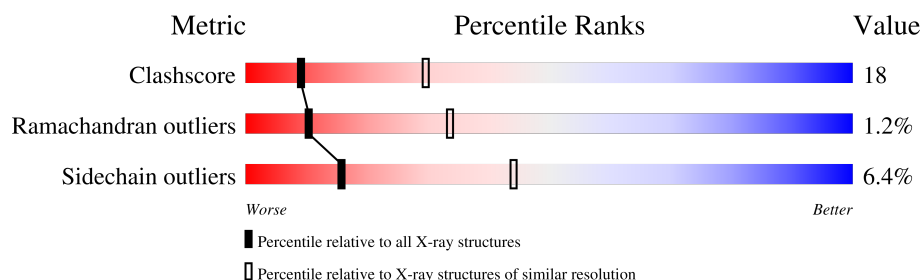
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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	252	
1	B	252	

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	PGA	B	570	-	X	-	-

2 Entry composition [i](#)

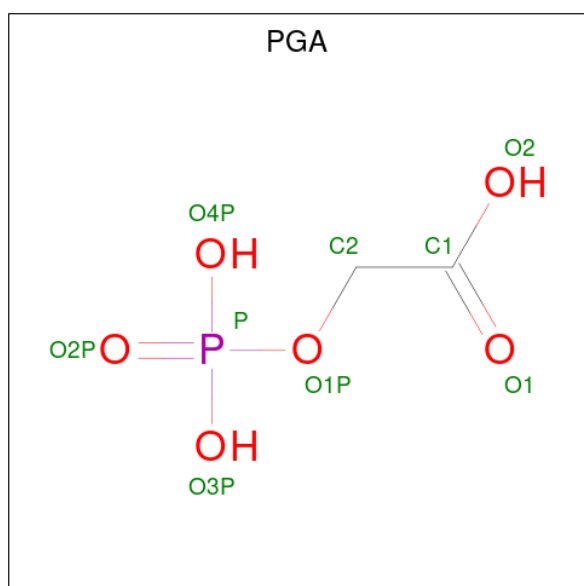
There are 2 unique types of molecules in this entry. The entry contains 3781 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	251	Total	C	N	O	S	0	0	0
			1879	1186	325	360	8			
1	B	251	Total	C	N	O	S	0	0	0
			1884	1190	328	358	8			

- Molecule 2 is 2-PHOSPHOGLYCOLIC ACID (CCD ID: PGA) (formula: C₂H₅O₆P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			9	2	6	1		
2	B	1	Total	C	O	P	0	0
			9	2	6	1		

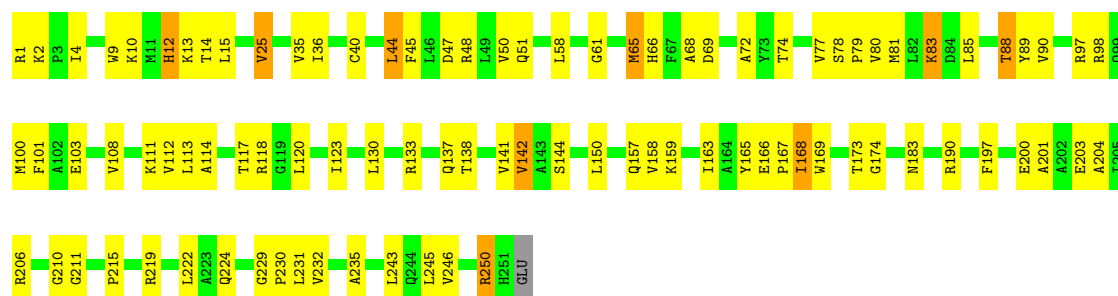
3 Residue-property plots

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.

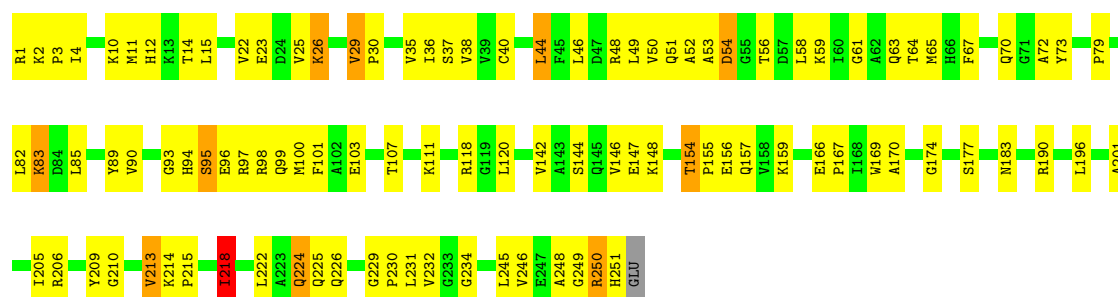
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

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 2	Depositor
Cell constants a, b, c, α , β , γ	78.61Å 108.42Å 71.21Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.80	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.80)	Depositor
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.176 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3781	wwPDB-VP
Average B, all atoms (Å ²)	19.0	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: PGA

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	0.57	0/1912	1.05	6/2596 (0.2%)
1	B	0.60	0/1918	1.07	11/2603 (0.4%)
All	All	0.59	0/3830	1.06	17/5199 (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

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	12	HIS	N-CA-C	10.22	129.21	114.39
1	B	12	HIS	N-CA-C	10.04	127.31	114.56
1	B	25	VAL	N-CA-C	8.16	118.20	110.53
1	B	177	SER	N-CA-C	-7.78	100.04	110.55
1	B	225	GLN	N-CA-C	6.85	118.82	111.36
1	A	25	VAL	N-CA-C	6.51	118.49	111.58
1	A	231	LEU	N-CA-C	-6.29	96.86	107.99
1	A	174	GLY	N-CA-C	-6.19	106.21	114.25
1	B	53	ALA	N-CA-C	-5.61	105.09	112.72
1	A	13	LYS	N-CA-C	5.48	116.96	109.18
1	B	213	VAL	N-CA-C	-5.47	102.53	109.80
1	B	14	THR	N-CA-C	-5.24	101.63	109.95
1	B	234	GLY	N-CA-C	5.23	118.97	112.64
1	A	123	ILE	N-CA-C	-5.17	98.59	109.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	174	GLY	N-CA-C	-5.12	108.55	115.21
1	B	154	THR	N-CA-C	-5.08	103.75	110.40
1	B	218	ILE	CB-CA-C	-5.08	105.47	111.97

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	209	TYR	Sidechain

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	1879	0	1873	74	0
1	B	1884	0	1885	78	0
2	A	9	0	2	0	0
2	B	9	0	2	0	0
All	All	3781	0	3762	138	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 18.

All (138) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:65:MET:HE2	1:A:79:PRO:HB3	1.40	1.03
1:B:65:MET:HE3	1:B:90:VAL:HG11	1.42	1.01
1:A:15:LEU:HD11	1:A:48:ARG:HD2	1.56	0.87
1:A:159:LYS:HG2	1:A:204:ALA:HB3	1.59	0.83
1:A:36:ILE:HD12	1:A:206:ARG:HH12	1.44	0.81
1:B:26:LYS:HD2	1:B:56:THR:HG21	1.67	0.77
1:A:250:ARG:HG2	1:A:250:ARG:HH11	1.48	0.76
1:A:98:ARG:HA	1:A:103:GLU:HB3	1.70	0.73
1:B:83:LYS:HG3	1:B:118:ARG:O	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:LEU:HD21	1:B:82:LEU:HD23	1.71	0.72
1:B:215:PRO:HA	1:B:218:ILE:HD11	1.72	0.72
1:A:222:LEU:HD21	1:A:229:GLY:HA2	1.72	0.71
1:B:250:ARG:O	1:B:250:ARG:HD2	1.92	0.69
1:B:36:ILE:HD12	1:B:206:ARG:HH12	1.58	0.67
1:A:36:ILE:HD12	1:A:206:ARG:NH1	2.09	0.67
1:B:65:MET:HG2	1:B:90:VAL:HG21	1.76	0.65
1:A:85:LEU:HD12	1:B:44:LEU:HD22	1.78	0.65
1:B:218:ILE:HG22	1:B:222:LEU:HD13	1.79	0.64
1:A:15:LEU:HD21	1:A:48:ARG:NE	2.13	0.64
1:B:107:THR:O	1:B:111:LYS:HG3	2.00	0.62
1:B:3:PRO:HG2	1:B:35:VAL:HG22	1.82	0.61
1:A:44:LEU:HG	1:B:85:LEU:HD11	1.83	0.61
1:B:50:VAL:HG11	1:B:85:LEU:O	2.00	0.61
1:A:250:ARG:HG2	1:A:250:ARG:NH1	2.11	0.60
1:A:2:LYS:HE3	1:A:36:ILE:HG13	1.83	0.60
1:A:83:LYS:HG3	1:A:118:ARG:O	2.02	0.59
1:B:167:PRO:HB2	1:B:169:TRP:CE2	2.36	0.59
1:B:98:ARG:HA	1:B:103:GLU:HB3	1.83	0.59
1:A:100:MET:HE1	1:B:73:TYR:HD1	1.67	0.58
1:B:218:ILE:HG22	1:B:222:LEU:CD1	2.33	0.58
1:B:218:ILE:HG12	1:B:245:LEU:HD23	1.85	0.58
1:B:1:ARG:NH1	1:B:190:ARG:NH2	2.51	0.58
1:B:65:MET:HE1	1:B:120:LEU:HD13	1.85	0.58
1:B:93:GLY:O	1:B:98:ARG:HD2	2.04	0.58
1:A:25:VAL:HG13	1:A:243:LEU:HD21	1.85	0.57
1:A:66:HIS:ND1	1:B:11:MET:HE1	2.19	0.57
1:A:138:THR:O	1:A:142:VAL:HB	2.05	0.57
1:A:77:VAL:HG13	1:B:44:LEU:HD11	1.85	0.57
1:B:95:SER:O	1:B:99:GLN:HG2	2.04	0.57
1:B:154:THR:OG1	1:B:157:GLN:HG3	2.05	0.56
1:A:25:VAL:HG13	1:A:243:LEU:CD2	2.36	0.55
1:B:96:GLU:O	1:B:100:MET:HB2	2.06	0.55
1:A:113:LEU:O	1:A:117:THR:HG23	2.06	0.55
1:A:159:LYS:HG3	1:A:201:ALA:HA	1.88	0.55
1:B:30:PRO:HD3	1:B:246:VAL:HG13	1.88	0.54
1:A:97:ARG:HA	1:A:101:PHE:HD2	1.72	0.54
1:B:159:LYS:HG2	1:B:201:ALA:HA	1.89	0.54
1:A:108:VAL:O	1:A:112:VAL:HG23	2.08	0.54
1:A:130:LEU:O	1:A:133:ARG:HB3	2.09	0.53
1:B:166:GLU:HG2	1:B:210:GLY:HA3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:114:ALA:O	1:A:118:ARG:HB2	2.08	0.53
1:B:142:VAL:O	1:B:146:VAL:HG23	2.10	0.52
1:A:159:LYS:CG	1:A:201:ALA:HA	2.39	0.52
1:B:65:MET:CE	1:B:120:LEU:HD13	2.39	0.52
1:B:65:MET:CE	1:B:90:VAL:HG11	2.30	0.51
1:A:44:LEU:HG	1:B:85:LEU:CD1	2.40	0.51
1:B:2:LYS:HE3	1:B:36:ILE:CG1	2.40	0.51
1:B:214:LYS:O	1:B:218:ILE:HG13	2.09	0.51
1:A:69:ASP:HB3	1:A:80:VAL:HG21	1.92	0.51
1:A:47:ASP:O	1:A:51:GLN:HG3	2.11	0.51
1:B:37:SER:OG	1:B:246:VAL:HG21	2.10	0.51
1:A:40:CYS:HA	1:A:61:GLY:O	2.11	0.50
1:A:158:VAL:HG21	1:A:197:PHE:CD1	2.46	0.50
1:A:65:MET:HG2	1:A:66:HIS:N	2.25	0.50
1:B:248:ALA:C	1:B:250:ARG:H	2.19	0.50
1:A:166:GLU:HG2	1:A:210:GLY:HA3	1.93	0.50
1:B:218:ILE:HD13	1:B:248:ALA:HB2	1.94	0.50
1:A:45:PHE:CD1	1:A:45:PHE:N	2.77	0.50
1:A:4:ILE:HB	1:A:206:ARG:NH1	2.27	0.49
1:B:29:VAL:HG21	1:B:58:LEU:HD23	1.94	0.49
1:B:213:VAL:O	1:B:214:LYS:HD2	2.12	0.49
1:B:40:CYS:HA	1:B:61:GLY:O	2.12	0.49
1:A:66:HIS:CE1	1:A:68:ALA:HB3	2.48	0.49
1:B:46:LEU:O	1:B:50:VAL:HG23	2.13	0.48
1:B:2:LYS:O	1:B:206:ARG:HD2	2.13	0.48
1:B:96:GLU:O	1:B:100:MET:HE3	2.14	0.48
1:B:97:ARG:HA	1:B:101:PHE:CD2	2.48	0.48
1:B:4:ILE:O	1:B:229:GLY:HA3	2.14	0.48
1:A:72:ALA:HA	1:B:10:LYS:HD3	1.96	0.48
1:B:2:LYS:HE3	1:B:36:ILE:HD11	1.96	0.48
1:B:155:PRO:O	1:B:159:LYS:HG3	2.14	0.48
1:A:215:PRO:HD3	1:A:235:ALA:HB1	1.95	0.47
1:B:36:ILE:HG21	1:B:89:TYR:OH	2.14	0.47
1:A:9:TRP:O	1:A:12:HIS:HB2	2.14	0.47
1:A:10:LYS:HD3	1:B:72:ALA:HA	1.97	0.47
1:A:65:MET:O	1:A:111:LYS:HD3	2.14	0.47
1:A:65:MET:HE2	1:A:79:PRO:CB	2.29	0.47
1:A:137:GLN:HB3	1:A:141:VAL:HG23	1.96	0.46
1:B:147:GLU:HG2	1:B:196:LEU:HD11	1.98	0.46
1:B:52:ALA:C	1:B:54:ASP:H	2.23	0.46
1:A:74:THR:HG23	1:B:63:GLN:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:218:ILE:HG12	1:B:245:LEU:CD2	2.44	0.46
1:A:1:ARG:NH1	1:A:190:ARG:CZ	2.79	0.46
1:A:100:MET:HE1	1:B:73:TYR:CD1	2.50	0.46
1:A:12:HIS:CD2	1:B:70:GLN:HE21	2.35	0.45
1:A:35:VAL:CG2	1:A:250:ARG:HA	2.46	0.45
1:A:183:ASN:HB2	1:A:224:GLN:HB3	1.98	0.45
1:B:169:TRP:H	1:B:169:TRP:CD1	2.34	0.45
1:A:232:VAL:CG1	1:A:235:ALA:HB3	2.46	0.45
1:A:1:ARG:NH1	1:A:190:ARG:NH2	2.65	0.45
1:B:15:LEU:HD11	1:B:48:ARG:HG3	1.98	0.45
1:B:94:HIS:O	1:B:98:ARG:HG3	2.17	0.45
1:B:232:VAL:HG11	1:B:245:LEU:HD11	1.99	0.45
1:A:44:LEU:HD11	1:B:46:LEU:HD12	1.98	0.44
1:B:35:VAL:HG21	1:B:249:GLY:HA3	1.99	0.44
1:A:78:SER:OG	1:A:81:MET:HG3	2.18	0.44
1:B:1:ARG:HD3	1:B:205:ILE:O	2.17	0.44
1:B:226:GLN:HA	1:B:226:GLN:OE1	2.18	0.44
1:A:78:SER:HB3	1:B:11:MET:SD	2.57	0.44
1:A:150:LEU:HD11	1:A:163:ILE:HD11	1.98	0.44
1:A:166:GLU:HA	1:A:210:GLY:O	2.18	0.43
1:B:79:PRO:HB2	1:B:118:ARG:HG3	2.00	0.43
1:B:30:PRO:HB3	1:B:251:HIS:C	2.43	0.43
1:A:65:MET:HG2	1:A:66:HIS:O	2.19	0.43
1:B:22:VAL:O	1:B:26:LYS:HG2	2.19	0.43
1:A:65:MET:CE	1:A:120:LEU:HD13	2.48	0.42
1:B:144:SER:O	1:B:148:LYS:HG3	2.19	0.42
1:A:165:TYR:CZ	1:A:167:PRO:HG3	2.55	0.42
1:B:38:VAL:HG22	1:B:59:LYS:HB2	2.01	0.42
1:A:167:PRO:O	1:A:168:ILE:C	2.62	0.42
1:A:66:HIS:HA	1:A:111:LYS:NZ	2.35	0.42
1:B:167:PRO:HG2	1:B:170:ALA:HB3	2.01	0.41
1:A:2:LYS:CE	1:A:36:ILE:HG13	2.50	0.41
1:B:67:PHE:HB3	1:B:111:LYS:HG2	2.02	0.41
1:A:65:MET:HB3	1:A:90:VAL:HG21	2.02	0.41
1:A:88:THR:OG1	1:A:89:TYR:CD1	2.73	0.41
1:A:50:VAL:HG11	1:A:85:LEU:O	2.20	0.41
1:A:243:LEU:HA	1:A:246:VAL:HG12	2.02	0.41
1:A:66:HIS:HA	1:A:111:LYS:HZ2	1.86	0.41
1:B:251:HIS:O	1:B:251:HIS:CG	2.73	0.41
1:A:14:THR:O	1:A:15:LEU:C	2.63	0.40
1:A:169:TRP:O	1:A:173:THR:HG21	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:232:VAL:HG11	1:B:245:LEU:CD1	2.52	0.40
1:A:215:PRO:HA	1:A:245:LEU:HD23	2.03	0.40
1:A:222:LEU:CD2	1:A:229:GLY:HA2	2.49	0.40
1:B:183:ASN:HB2	1:B:224:GLN:HG2	2.03	0.40
1:A:232:VAL:HG21	1:A:245:LEU:HD13	2.02	0.40
1:B:26:LYS:NZ	1:B:54:ASP:OD1	2.53	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	249/252 (99%)	232 (93%)	14 (6%)	3 (1%)	10	34
1	B	249/252 (99%)	230 (92%)	16 (6%)	3 (1%)	10	34
All	All	498/504 (99%)	462 (93%)	30 (6%)	6 (1%)	10	34

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	230	PRO
1	B	230	PRO
1	A	168	ILE
1	B	54	ASP
1	B	26	LYS
1	A	211	GLY

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	196/201 (98%)	184 (94%)	12 (6%)	17	46
1	B	197/201 (98%)	184 (93%)	13 (7%)	15	43
All	All	393/402 (98%)	368 (94%)	25 (6%)	16	44

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LEU
1	A	58	LEU
1	A	65	MET
1	A	83	LYS
1	A	88	THR
1	A	142	VAL
1	A	144	SER
1	A	157	GLN
1	A	200	GLU
1	A	203	GLU
1	A	219	ARG
1	A	250	ARG
1	B	23	GLU
1	B	29	VAL
1	B	44	LEU
1	B	49	LEU
1	B	51	GLN
1	B	64	THR
1	B	83	LYS
1	B	95	SER
1	B	156	GLU
1	B	218	ILE
1	B	224	GLN
1	B	231	LEU
1	B	250	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	HIS
1	A	208	GLN

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Mol	Chain	Res	Type
1	B	8	ASN
1	B	70	GLN
1	B	224	GLN
1	B	244	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](#)

2 ligands are 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	PGA	B	570	-	8,8,8	1.92	2 (25%)	10,11,11	2.50	3 (30%)
2	PGA	A	560	-	8,8,8	1.65	1 (12%)	10,11,11	2.76	3 (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
2	PGA	B	570	-	-	5/6/6/6	-
2	PGA	A	560	-	-	2/6/6/6	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	570	PGA	O1-C1	3.85	1.34	1.22
2	A	560	PGA	O1-C1	3.11	1.32	1.22
2	B	570	PGA	C2-C1	-2.02	1.44	1.50

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	560	PGA	O2-C1-O1	-5.90	108.17	123.33
2	B	570	PGA	O2-C1-O1	-5.75	108.54	123.33
2	A	560	PGA	O2-C1-C2	4.12	133.13	113.66
2	A	560	PGA	O1P-C2-C1	-3.77	104.86	110.54
2	B	570	PGA	O1P-C2-C1	-3.71	104.95	110.54
2	B	570	PGA	O2-C1-C2	3.17	128.60	113.66

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	570	PGA	C2-O1P-P-O2P
2	B	570	PGA	C2-O1P-P-O3P
2	B	570	PGA	C2-O1P-P-O4P
2	B	570	PGA	O2-C1-C2-O1P
2	A	560	PGA	O2-C1-C2-O1P
2	B	570	PGA	O1-C1-C2-O1P
2	A	560	PGA	O1-C1-C2-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates [i](#)

EDS was not executed - this section is therefore empty.

6.4 Ligands [i](#)

EDS was not executed - this section is therefore empty.

6.5 Other polymers [i](#)

EDS was not executed - this section is therefore empty.