Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 05:11 PM EDT

PDB ID	:	1DC4
Title	:	STRUCTURAL ANALYSIS OF GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE FROM ESCHERICHIA COLI: DIRECT EVIDENCE FOR SUBSTRATE BINDING AND COFACTOR-INDUCED CONFORMATIONAL CHANGES
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Deposited on	:	1999-11-04
Resolution	:	2.50 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 (i) 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 (i)) were used in the production of this report:

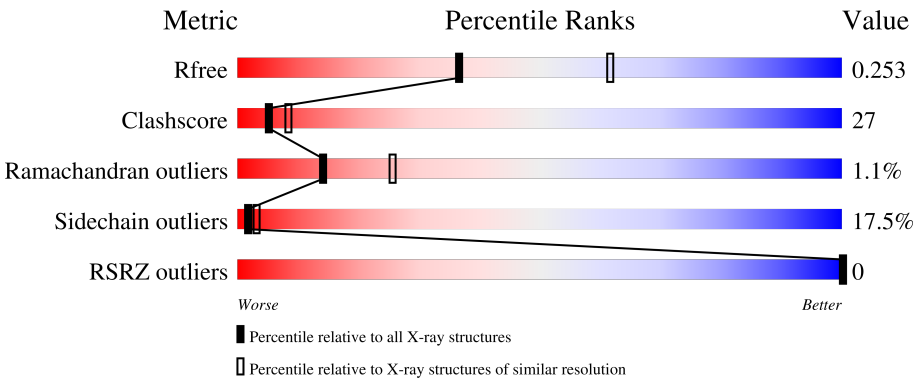
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.50 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}	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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 <=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	330	52% 38% 11%
1	B	330	52% 38% 10%

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	A	350	X	-	-	-
2	G3P	B	350	X	-	-	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5237 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.

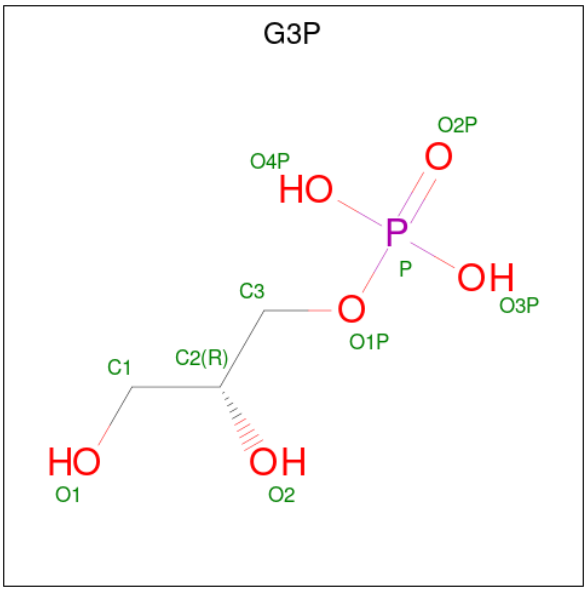
- Molecule 1 is a protein called GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	330	2488	1563	431	484	3	7	0	0	0
1	B	330	2488	1563	431	484	3	7	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	43	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	118	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	127	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	172	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	228	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
A	267	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	40	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	43	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	118	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	127	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	172	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	228	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2
B	267	MSE	MET	MODIFIED RESIDUE	UNP P0A9B2

- Molecule 2 is SN-GLYCEROL-3-PHOSPHATE (three-letter code: G3P) (formula: $C_3H_9O_6P$).



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

- Molecule 3 is water.

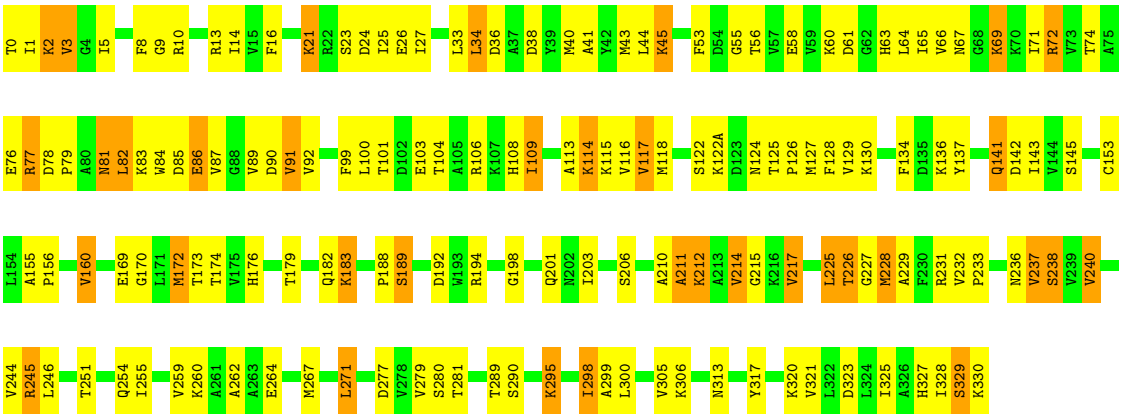
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	118	118	118	0	0
			Total	O		
3	B	123	123	123	0	0

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.

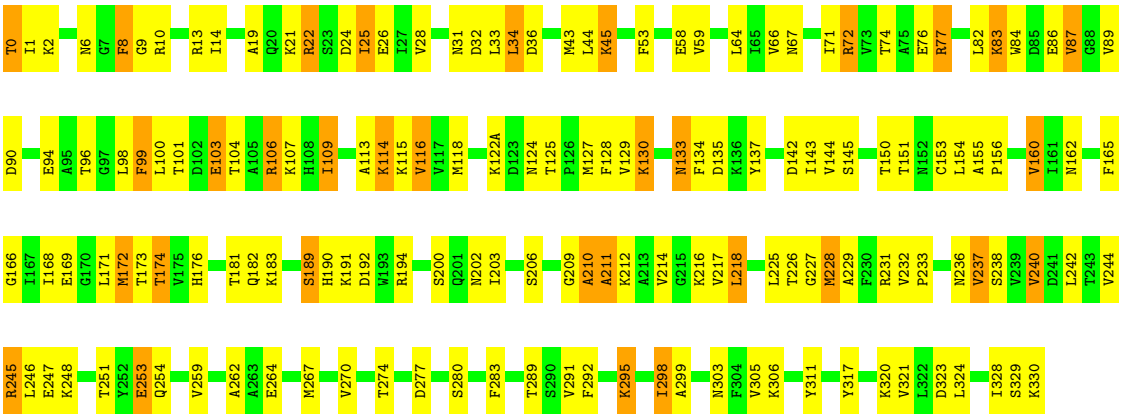
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

Chain A: 52% 38% 11%



• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

Chain B: 52% 38% 10%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 41	Depositor
Cell constants a, b, c, α, β, γ	120.82Å 120.82Å 157.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.83 – 2.50	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.50) 89.1 (19.83-2.50)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.66 (at 2.50Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.198 , 0.258 0.197 , 0.253	Depositor DCC
R_{free} test set	1899 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å^2)	36.9	Xtriage
Anisotropy	0.004	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 32.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.479 for -h,k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	5237	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	0.52	2/2520 (0.1%)	0.69	1/3400 (0.0%)
1	B	0.51	2/2520 (0.1%)	0.68	1/3400 (0.0%)
All	All	0.52	4/5040 (0.1%)	0.68	2/6800 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	228	MSE	CG-SE	-6.65	1.72	1.95
1	B	228	MSE	CG-SE	-6.60	1.73	1.95
1	A	172	MSE	CG-SE	-6.24	1.74	1.95
1	B	172	MSE	CG-SE	-6.13	1.74	1.95

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	203	ILE	N-CA-C	-6.84	92.53	111.00
1	A	203	ILE	N-CA-C	-6.64	93.07	111.00

There are no chirality outliers.

There are no planarity outliers.

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	2488	0	2505	131	0
1	B	2488	0	2505	152	1
2	A	10	0	6	1	0
2	B	10	0	6	2	0
3	A	118	0	0	7	1
3	B	123	0	0	14	0
All	All	5237	0	5022	267	1

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 27.

All (267) 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:34:LEU:HD13	1:A:43:MSE:HE1	1.21	1.15
1:B:34:LEU:HD13	1:B:43:MSE:HE1	1.35	1.05
1:B:228:MSE:HG3	1:B:229:ALA:N	1.72	1.03
1:A:115:LYS:HG2	1:A:142:ASP:HA	1.42	1.01
1:A:109:ILE:HD11	1:A:143:ILE:HD11	1.48	0.95
1:A:118:MSE:HE3	1:A:145:SER:HB2	1.49	0.95
1:B:115:LYS:HD3	1:B:142:ASP:HA	1.49	0.94
1:B:77:ARG:HH11	1:B:77:ARG:HB3	1.38	0.88
1:B:172:MSE:HG3	1:B:173:THR:N	1.88	0.87
1:A:262:ALA:HB1	1:A:267:MSE:HE3	1.56	0.87
1:A:91:VAL:HG11	1:A:325:ILE:HG12	1.57	0.84
1:B:236:ASN:O	1:B:237:VAL:HG22	1.77	0.84
1:A:228:MSE:HG3	1:A:229:ALA:N	1.91	0.84
1:A:172:MSE:HG2	1:A:227:GLY:HA3	1.60	0.84
1:A:172:MSE:HG3	1:A:173:THR:N	1.94	0.82
1:A:137:TYR:CE2	1:A:328:ILE:HA	2.14	0.82
1:B:189:SER:HB3	1:B:192:ASP:O	1.80	0.81
1:A:237:VAL:HG21	1:A:280:SER:O	1.84	0.78
1:A:117:VAL:HG11	1:A:325:ILE:HG13	1.66	0.78
1:B:172:MSE:HG2	1:B:227:GLY:HA3	1.65	0.78
1:A:38:ASP:HB3	3:A:2150:HOH:O	1.83	0.77
1:A:109:ILE:CD1	1:A:143:ILE:HD11	2.14	0.77
1:A:143:ILE:HG13	3:A:2192:HOH:O	1.84	0.77
1:B:251:THR:H	1:B:254:GLN:HE21	1.30	0.76
1:B:109:ILE:HD11	1:B:143:ILE:HD11	1.67	0.76
1:A:79:PRO:HA	1:A:82:LEU:HD23	1.67	0.76
1:B:115:LYS:CD	1:B:142:ASP:HA	2.16	0.76
1:B:58:GLU:HB2	3:B:2206:HOH:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:MSE:CE	1:B:216:LYS:HD2	2.17	0.74
1:A:155:ALA:HB3	1:A:156:PRO:HD3	1.71	0.73
1:B:83:LYS:HB3	1:B:86:GLU:HG3	1.71	0.72
1:B:154:LEU:HD23	1:B:214:VAL:HG21	1.71	0.72
1:B:106:ARG:O	1:B:109:ILE:HG12	1.90	0.72
1:A:82:LEU:HD23	3:A:2199:HOH:O	1.91	0.70
1:A:91:VAL:CG1	1:A:325:ILE:HG12	2.21	0.70
1:A:172:MSE:O	1:B:306:LYS:HE3	1.91	0.70
1:A:115:LYS:HG2	1:A:142:ASP:CA	2.19	0.69
1:A:245:ARG:HG3	1:A:245:ARG:HH11	1.56	0.69
1:B:176:HIS:NE2	2:B:350:G3P:H32	2.07	0.69
1:A:118:MSE:HE1	1:A:122:SER:HB3	1.74	0.69
1:A:16:PHE:HZ	1:A:66:VAL:HG21	1.57	0.69
1:B:45:LYS:HZ3	1:B:45:LYS:HB2	1.58	0.68
1:A:169:GLU:OE2	1:A:245:ARG:NH1	2.27	0.68
1:B:34:LEU:HD13	1:B:43:MSE:CE	2.17	0.68
1:A:172:MSE:HE3	1:A:240:VAL:HB	1.76	0.67
1:A:91:VAL:HG21	1:A:328:ILE:HD11	1.75	0.67
1:A:281:THR:H	1:B:202:ASN:ND2	1.92	0.67
1:B:237:VAL:HG23	1:B:280:SER:HB2	1.74	0.67
1:B:116:VAL:HG13	1:B:143:ILE:HG12	1.76	0.67
1:B:8:PHE:HZ	3:B:2241:HOH:O	1.77	0.67
1:B:1:ILE:HD12	1:B:24:ASP:O	1.97	0.65
1:B:44:LEU:O	1:B:53:PHE:HB2	1.95	0.65
1:B:77:ARG:HB3	1:B:77:ARG:NH1	2.10	0.65
1:B:87:VAL:HG12	3:B:2197:HOH:O	1.95	0.65
1:B:84:TRP:HB3	1:B:89:VAL:HG22	1.79	0.64
1:A:298:ILE:HD11	1:B:228:MSE:HB3	1.77	0.64
1:A:109:ILE:HA	1:A:113:ALA:O	1.97	0.64
1:A:236:ASN:O	1:A:237:VAL:HG22	1.98	0.64
1:B:209:GLY:O	1:B:211:ALA:N	2.31	0.64
1:A:176:HIS:NE2	2:A:350:G3P:H32	2.12	0.64
1:B:66:VAL:HG23	1:B:71:ILE:HD13	1.80	0.64
1:B:137:TYR:CE2	1:B:328:ILE:HA	2.34	0.63
1:A:40:MSE:HA	1:A:43:MSE:HE3	1.80	0.63
1:B:155:ALA:HB3	1:B:156:PRO:HD3	1.81	0.62
1:B:151:THR:OG1	1:B:210:ALA:HA	2.00	0.62
1:A:9:GLY:O	1:A:13:ARG:HG3	2.00	0.62
1:B:190:HIS:H	1:B:190:HIS:CD2	2.16	0.62
1:A:77:ARG:HG2	1:A:77:ARG:HH11	1.64	0.62
1:B:237:VAL:CG2	1:B:280:SER:HB2	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:ALA:O	1:A:214:VAL:HG12	1.99	0.62
1:B:210:ALA:O	1:B:214:VAL:HG23	2.00	0.62
1:A:87:VAL:HG13	1:A:89:VAL:HG23	1.82	0.61
1:B:237:VAL:HG21	1:B:280:SER:O	2.00	0.61
1:A:90:ASP:HA	1:A:114:LYS:HE3	1.81	0.61
1:B:262:ALA:HB1	1:B:267:MSE:HE3	1.83	0.61
1:A:198:GLY:HA3	1:A:201:GLN:HE21	1.65	0.61
1:B:228:MSE:HE2	1:B:229:ALA:O	2.01	0.60
1:A:172:MSE:HE2	1:A:174:THR:HB	1.84	0.60
1:A:72:ARG:HD3	1:A:74:THR:HG23	1.84	0.60
1:A:189:SER:HB3	1:A:192:ASP:O	2.02	0.59
1:A:211:ALA:HB1	1:A:226:THR:HG22	1.85	0.59
1:A:41:ALA:O	1:A:45:LYS:HG3	2.03	0.58
1:B:0:THR:HG21	1:B:26:GLU:OE1	2.02	0.58
1:A:176:HIS:HA	1:A:238:SER:HB3	1.85	0.58
1:A:3:VAL:HG12	1:A:91:VAL:O	2.04	0.58
1:A:182:GLN:OE1	1:A:231:ARG:HD2	2.03	0.58
1:B:76:GLU:HB3	3:B:2211:HOH:O	2.02	0.58
1:B:118:MSE:HB2	1:B:144:VAL:O	2.04	0.58
1:A:3:VAL:HG12	1:A:91:VAL:HG12	1.86	0.57
1:A:306:LYS:HE3	1:B:172:MSE:O	2.04	0.57
1:A:251:THR:OG1	1:A:254:GLN:HG3	2.05	0.57
1:A:118:MSE:HE3	1:A:145:SER:CB	2.30	0.57
1:A:100:LEU:HB2	1:A:122(A):LYS:HG3	1.87	0.57
1:B:9:GLY:O	1:B:13:ARG:HG3	2.04	0.57
1:B:118:MSE:HE1	1:B:125:THR:HG21	1.87	0.57
1:A:160:VAL:HG12	1:A:267:MSE:HE1	1.86	0.57
1:A:118:MSE:HE2	1:A:125:THR:HG21	1.86	0.57
1:B:99:PHE:HB3	1:B:104:THR:HB	1.87	0.56
1:A:142:ASP:O	1:A:143:ILE:HD13	2.06	0.56
1:A:182:GLN:HB3	3:A:2006:HOH:O	2.05	0.56
1:B:34:LEU:CD1	1:B:43:MSE:HE1	2.24	0.56
1:B:129:VAL:H	1:B:133:ASN:ND2	2.04	0.55
1:B:169:GLU:OE2	1:B:245:ARG:HD3	2.06	0.55
1:B:109:ILE:HG22	1:B:113:ALA:O	2.06	0.55
1:B:160:VAL:HG12	1:B:267:MSE:HE1	1.89	0.55
1:A:118:MSE:CE	1:A:145:SER:HB2	2.31	0.55
1:A:228:MSE:HE2	1:A:229:ALA:O	2.07	0.54
1:B:137:TYR:CE2	1:B:328:ILE:HG22	2.42	0.54
1:B:176:HIS:HB3	1:B:231:ARG:HD3	1.88	0.54
1:A:198:GLY:HA3	1:A:201:GLN:NE2	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:99:PHE:HB3	1:B:104:THR:CB	2.39	0.53
1:B:169:GLU:HG2	1:B:245:ARG:HD3	1.90	0.53
1:B:127:MSE:HE2	1:B:216:LYS:HD2	1.89	0.53
1:B:84:TRP:O	1:B:87:VAL:HG23	2.09	0.53
1:A:5:ILE:HD11	1:A:27:ILE:HD12	1.90	0.53
1:A:91:VAL:HG23	1:A:115:LYS:HB2	1.90	0.53
1:B:127:MSE:HG2	1:B:145:SER:HB3	1.91	0.52
1:A:69:LYS:H	1:A:69:LYS:HD2	1.74	0.52
1:A:92:VAL:HG22	3:A:2194:HOH:O	2.08	0.52
1:B:172:MSE:HE3	1:B:240:VAL:HB	1.92	0.52
1:B:44:LEU:HB2	3:B:2241:HOH:O	2.10	0.52
1:B:106:ARG:HG3	1:B:106:ARG:HH11	1.74	0.52
1:B:10:ARG:O	1:B:14:ILE:HG12	2.10	0.51
1:B:66:VAL:CG2	1:B:71:ILE:HD13	2.40	0.51
1:B:128:PHE:HA	1:B:133:ASN:HD21	1.76	0.51
1:A:89:VAL:HB	3:A:2194:HOH:O	2.10	0.51
1:B:101:THR:OG1	1:B:104:THR:HG23	2.11	0.51
1:A:56:THR:O	1:A:66:VAL:HA	2.09	0.51
1:B:90:ASP:HA	1:B:114:LYS:HE3	1.92	0.50
1:A:91:VAL:CG2	1:A:115:LYS:HB2	2.41	0.50
1:B:19:ALA:HA	1:B:22:ARG:HG3	1.94	0.50
1:B:72:ARG:HD3	3:B:2093:HOH:O	2.11	0.50
1:B:104:THR:O	1:B:107:LYS:HG3	2.11	0.50
1:A:108:HIS:HB2	1:A:116:VAL:HG21	1.93	0.50
1:B:106:ARG:HG3	1:B:106:ARG:NH1	2.25	0.50
1:B:118:MSE:CE	1:B:125:THR:HG21	2.40	0.50
1:B:172:MSE:HE2	1:B:174:THR:HB	1.93	0.50
1:A:106:ARG:O	1:A:109:ILE:HG13	2.12	0.50
1:B:129:VAL:H	1:B:133:ASN:HD21	1.59	0.50
1:B:109:ILE:HA	1:B:113:ALA:O	2.12	0.50
1:A:170:GLY:O	1:A:225:LEU:HB2	2.11	0.49
1:A:101:THR:OG1	1:A:104:THR:HG23	2.11	0.49
1:B:154:LEU:CD2	1:B:214:VAL:HG21	2.40	0.49
1:B:274:THR:HG22	1:B:292:PHE:O	2.12	0.49
1:A:44:LEU:O	1:A:53:PHE:HB2	2.12	0.49
1:B:2:LYS:HG3	1:B:28:VAL:HG11	1.93	0.49
1:A:262:ALA:CB	1:A:267:MSE:HE3	2.35	0.49
1:A:300:LEU:CD2	1:B:169:GLU:HB2	2.43	0.49
1:A:64:LEU:O	1:A:65:ILE:HD13	2.13	0.48
1:A:277:ASP:HB3	1:B:194:ARG:HG2	1.95	0.48
1:A:82:LEU:HG	1:A:84:TRP:CZ2	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:LEU:HD13	1:B:84:TRP:CZ2	2.48	0.48
1:B:209:GLY:O	1:B:210:ALA:C	2.51	0.48
1:A:1:ILE:HD13	1:A:329:SER:CB	2.43	0.48
1:B:169:GLU:CG	1:B:245:ARG:HD3	2.44	0.48
1:A:76:GLU:HA	1:A:76:GLU:OE1	2.14	0.47
1:A:2:LYS:HD3	1:A:2:LYS:HA	1.61	0.47
1:B:259:VAL:HG11	1:B:292:PHE:CG	2.50	0.47
1:A:245:ARG:HG3	1:A:245:ARG:NH1	2.24	0.47
1:A:78:ASP:HB3	1:A:81:ASN:HD21	1.78	0.47
1:A:126:PRO:HB2	1:A:128:PHE:CE2	2.49	0.47
1:A:295:LYS:HB2	1:B:194:ARG:HH21	1.80	0.47
1:B:283:PHE:CE1	1:B:291:VAL:HG11	2.49	0.47
1:A:305:VAL:HG22	1:A:306:LYS:N	2.30	0.47
1:B:305:VAL:HG22	1:B:306:LYS:N	2.29	0.47
1:A:232:VAL:HG11	1:B:232:VAL:HG11	1.95	0.47
1:A:281:THR:H	1:B:202:ASN:HD21	1.58	0.47
1:B:130:LYS:HG2	1:B:270:VAL:CG2	2.45	0.47
1:B:210:ALA:O	1:B:211:ALA:C	2.53	0.47
1:A:160:VAL:CG1	1:A:267:MSE:HE1	2.45	0.46
1:A:194:ARG:HG2	1:B:277:ASP:HB3	1.97	0.46
1:A:72:ARG:NH2	1:A:83:LYS:O	2.48	0.46
1:B:28:VAL:CG2	1:B:89:VAL:HG12	2.45	0.46
1:A:78:ASP:HA	1:A:79:PRO:HD2	1.76	0.46
1:A:179:THR:OG1	1:A:231:ARG:NH1	2.48	0.46
1:A:172:MSE:CE	1:A:240:VAL:HB	2.43	0.46
1:B:162:ASN:O	1:B:166:GLY:N	2.49	0.46
1:B:83:LYS:O	1:B:86:GLU:HG3	2.16	0.46
1:B:299:ALA:HA	1:B:305:VAL:HG23	1.97	0.46
1:A:77:ARG:HG2	1:A:77:ARG:NH1	2.30	0.46
1:B:77:ARG:HH11	1:B:77:ARG:CB	2.19	0.46
1:B:109:ILE:HG12	1:B:109:ILE:H	1.35	0.46
1:B:137:TYR:CZ	1:B:328:ILE:HG22	2.51	0.46
1:B:153:CYS:SG	1:B:240:VAL:HG13	2.56	0.45
1:A:320:LYS:HA	1:A:323:ASP:HB2	1.98	0.45
1:B:6:ASN:O	1:B:96:THR:HG23	2.16	0.45
1:A:183:LYS:HE3	1:A:188:PRO:O	2.17	0.45
1:B:182:GLN:HB3	3:B:2004:HOH:O	2.17	0.45
1:A:109:ILE:H	1:A:109:ILE:HG12	1.38	0.45
1:A:271:LEU:HD23	1:A:290:SER:O	2.16	0.45
1:B:106:ARG:O	1:B:109:ILE:CG1	2.63	0.45
1:B:153:CYS:HA	1:B:289:THR:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:ALA:HA	1:A:305:VAL:HG23	1.99	0.45
1:B:245:ARG:HA	1:B:303:ASN:O	2.17	0.45
1:A:34:LEU:CD1	1:A:43:MSE:HE1	2.16	0.45
1:A:55:GLY:HA3	1:A:67:ASN:OD1	2.17	0.45
1:A:267:MSE:HE2	3:A:2174:HOH:O	2.16	0.45
1:B:45:LYS:HB2	1:B:45:LYS:NZ	2.30	0.45
1:A:63:HIS:HB3	1:A:71:ILE:O	2.17	0.44
1:B:96:THR:OG1	1:B:98:LEU:HB2	2.18	0.44
1:A:3:VAL:HA	1:A:89:VAL:HG13	1.98	0.44
1:A:317:TYR:O	1:A:321:VAL:HG23	2.18	0.44
1:B:283:PHE:HE1	1:B:291:VAL:HG11	1.82	0.44
1:A:115:LYS:HE2	1:A:141:GLN:O	2.18	0.44
1:A:279:VAL:HG23	1:B:202:ASN:ND2	2.32	0.44
1:B:200:SER:HA	1:B:233:PRO:HB3	1.98	0.44
1:A:90:ASP:O	1:A:114:LYS:HB2	2.18	0.44
1:B:317:TYR:O	1:B:321:VAL:HG23	2.18	0.44
1:A:194:ARG:HH21	1:B:295:LYS:HB2	1.84	0.43
1:B:44:LEU:HD22	3:B:2241:HOH:O	2.17	0.43
1:B:142:ASP:OD1	1:B:142:ASP:N	2.48	0.43
1:A:0:THR:HG23	1:A:2:LYS:NZ	2.33	0.43
1:B:67:ASN:HA	3:B:2214:HOH:O	2.18	0.43
1:B:99:PHE:N	3:B:2121:HOH:O	2.51	0.43
1:A:153:CYS:HA	1:A:289:THR:O	2.18	0.43
1:A:24:ASP:OD2	1:A:24:ASP:N	2.52	0.43
1:A:295:LYS:HB2	1:B:194:ARG:NH2	2.33	0.43
1:B:212:LYS:HE3	1:B:226:THR:HB	2.00	0.43
1:B:168:ILE:HD11	1:B:247:GLU:HA	1.99	0.43
1:A:174:THR:HG23	1:A:174:THR:O	2.19	0.43
1:B:253:GLU:HB2	3:B:2186:HOH:O	2.18	0.43
1:B:324:LEU:HD12	1:B:324:LEU:O	2.18	0.42
1:B:103:GLU:HG2	3:B:2144:HOH:O	2.20	0.42
1:A:212:LYS:O	1:A:215:GLY:N	2.50	0.42
1:A:327:HIS:O	1:A:330:LYS:HB2	2.19	0.42
1:B:2:LYS:N	1:B:2:LYS:HD2	2.35	0.42
1:A:33:LEU:HD12	1:A:33:LEU:N	2.35	0.42
1:A:127:MSE:HG2	1:A:145:SER:HB3	2.02	0.42
1:B:1:ILE:HD12	1:B:1:ILE:H	1.84	0.42
1:B:176:HIS:NE2	2:B:350:G3P:C3	2.79	0.42
1:B:72:ARG:HD3	1:B:74:THR:HG23	2.01	0.42
1:B:218:LEU:HD12	1:B:218:LEU:HA	1.92	0.42
1:A:194:ARG:NH2	1:B:295:LYS:HB2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:255:ILE:O	1:A:259:VAL:HG13	2.19	0.42
1:B:33:LEU:C	1:B:34:LEU:HG	2.40	0.42
1:A:137:TYR:HE2	1:A:328:ILE:HA	1.77	0.41
1:B:228:MSE:HG3	1:B:229:ALA:H	1.73	0.41
1:B:101:THR:HG1	1:B:104:THR:HG23	1.84	0.41
1:B:320:LYS:HA	1:B:323:ASP:HB2	2.01	0.41
1:B:22:ARG:HH21	1:B:25:ILE:HD11	1.84	0.41
1:B:59:VAL:O	1:B:59:VAL:HG22	2.19	0.41
1:B:127:MSE:HE2	3:B:2234:HOH:O	2.19	0.41
1:A:69:LYS:HD2	1:A:69:LYS:N	2.34	0.41
1:A:118:MSE:HE1	1:A:125:THR:HB	2.03	0.41
1:A:129:VAL:HG23	1:A:217:VAL:HG21	2.03	0.41
1:A:306:LYS:HB2	1:B:171:LEU:HD13	2.01	0.41
1:B:172:MSE:CE	1:B:174:THR:HB	2.51	0.41
1:B:150:THR:HG22	1:B:210:ALA:CB	2.51	0.41
1:B:212:LYS:C	1:B:214:VAL:N	2.73	0.41
1:B:209:GLY:C	1:B:211:ALA:N	2.74	0.41
1:B:242:LEU:HG	1:B:244:VAL:HG13	2.02	0.41
1:B:72:ARG:NH2	1:B:83:LYS:O	2.54	0.41
1:B:84:TRP:HB3	1:B:89:VAL:CG2	2.48	0.41
1:B:165:PHE:HA	1:B:248:LYS:HD2	2.03	0.41
1:B:267:MSE:HE2	3:B:2140:HOH:O	2.20	0.41
1:A:91:VAL:HA	1:A:115:LYS:O	2.21	0.41
1:A:10:ARG:O	1:A:14:ILE:HG12	2.21	0.40
1:B:124:ASN:O	1:B:125:THR:C	2.60	0.40
1:B:238:SER:HB2	1:B:311:TYR:CZ	2.56	0.40
1:A:25:ILE:CG2	1:A:26:GLU:N	2.84	0.40
1:A:279:VAL:CG2	1:B:202:ASN:ND2	2.84	0.40
1:A:21:LYS:H	1:A:21:LYS:HG2	1.51	0.40
1:A:82:LEU:HD13	1:A:82:LEU:HA	1.89	0.40
1:A:85:ASP:OD1	1:A:86:GLU:N	2.54	0.40
1:B:31:ASN:O	1:B:32:ASP:HB2	2.21	0.40
1:B:99:PHE:HB3	1:B:104:THR:OG1	2.21	0.40
1:B:298:ILE:HG13	1:B:299:ALA:N	2.36	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:ASN:OD1	3:A:2230:HOH:O[6_665]	2.16	0.04

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	328/330 (99%)	283 (86%)	41 (12%)	4 (1%)	13 24
1	B	328/330 (99%)	290 (88%)	35 (11%)	3 (1%)	17 31
All	All	656/660 (99%)	573 (87%)	76 (12%)	7 (1%)	14 26

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	211	ALA
1	B	210	ALA
1	B	211	ALA
1	A	141	GLN
1	B	237	VAL
1	A	237	VAL
1	A	233	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	265/258 (103%)	217 (82%)	48 (18%)	1 3
1	B	265/258 (103%)	220 (83%)	45 (17%)	2 3
All	All	530/516 (103%)	437 (82%)	93 (18%)	2 3

All (93) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	LYS
1	A	3	VAL
1	A	8	PHE
1	A	21	LYS
1	A	23	SER
1	A	34	LEU
1	A	36	ASP
1	A	45	LYS
1	A	58	GLU
1	A	60	LYS
1	A	61	ASP
1	A	69	LYS
1	A	72	ARG
1	A	77	ARG
1	A	81	ASN
1	A	82	LEU
1	A	86	GLU
1	A	91	VAL
1	A	99	PHE
1	A	103	GLU
1	A	109	ILE
1	A	114	LYS
1	A	117	VAL
1	A	124	ASN
1	A	130	LYS
1	A	134	PHE
1	A	136	LYS
1	A	160	VAL
1	A	183	LYS
1	A	189	SER
1	A	206	SER
1	A	212	LYS
1	A	214	VAL
1	A	217	VAL
1	A	225	LEU
1	A	226	THR
1	A	238	SER
1	A	240	VAL
1	A	244	VAL
1	A	245	ARG
1	A	246	LEU
1	A	260	LYS
1	A	264	GLU

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Mol	Chain	Res	Type
1	A	271	LEU
1	A	295	LYS
1	A	298	ILE
1	A	313	ASN
1	A	329	SER
1	B	0	THR
1	B	8	PHE
1	B	21	LYS
1	B	22	ARG
1	B	25	ILE
1	B	34	LEU
1	B	36	ASP
1	B	45	LYS
1	B	64	LEU
1	B	72	ARG
1	B	77	ARG
1	B	83	LYS
1	B	87	VAL
1	B	94	GLU
1	B	99	PHE
1	B	100	LEU
1	B	103	GLU
1	B	106	ARG
1	B	109	ILE
1	B	114	LYS
1	B	116	VAL
1	B	122(A)	LYS
1	B	130	LYS
1	B	133	ASN
1	B	134	PHE
1	B	135	ASP
1	B	160	VAL
1	B	174	THR
1	B	181	THR
1	B	183	LYS
1	B	189	SER
1	B	191	LYS
1	B	206	SER
1	B	217	VAL
1	B	218	LEU
1	B	225	LEU
1	B	240	VAL

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Mol	Chain	Res	Type
1	B	245	ARG
1	B	246	LEU
1	B	253	GLU
1	B	264	GLU
1	B	295	LYS
1	B	298	ILE
1	B	329	SER
1	B	330	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	81	ASN
1	A	201	GLN
1	A	222	ASN
1	B	133	ASN
1	B	146	ASN
1	B	190	HIS
1	B	202	ASN
1	B	254	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 monosaccharides 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	G3P	A	350	1	9,9,9	0.79	0	11,12,12	1.23	2 (18%)
2	G3P	B	350	1	9,9,9	0.97	0	11,12,12	1.27	2 (18%)

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	A	350	1	1/1/2/2	2/8/8/8	-
2	G3P	B	350	1	1/1/2/2	2/8/8/8	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	350	G3P	P-O1P-C3	2.72	125.79	118.30
2	A	350	G3P	P-O1P-C3	2.54	125.30	118.30
2	B	350	G3P	O4P-P-O1P	2.31	112.87	106.73
2	A	350	G3P	O4P-P-O1P	2.20	112.59	106.73

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	350	G3P	C2
2	B	350	G3P	C2

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	350	G3P	O1-C1-C2-O2
2	B	350	G3P	O1-C1-C2-O2
2	A	350	G3P	O1-C1-C2-C3
2	B	350	G3P	O1-C1-C2-C3

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	350	G3P	1	0
2	B	350	G3P	2	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	323/330 (97%)	-0.07	0	100	100	23, 35, 49, 56	0
1	B	323/330 (97%)	-0.03	0	100	100	20, 35, 50, 58	0
All	All	646/660 (97%)	-0.05	0	100	100	20, 35, 50, 58	0

There are no RSRZ outliers to report.

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 monosaccharides 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
2	G3P	B	350	10/10	0.95	0.18	43,52,58,59	0
2	G3P	A	350	10/10	0.96	0.16	43,52,57,57	0

6.5 Other polymers (i)

There are no such residues in this entry.