



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 05:10 am GMT

PDB ID : 1UP7
Title : Structure of the 6-phospho-beta glucosidase from *Thermotoga maritima* at 2.4 Angstrom resolution in the tetragonal form with NAD and glucose-6-phosphate
Authors : Varrot, A.; Yip, V.L.; Withers, S.G.; Davies, G.J.
Deposited on : 2003-09-29
Resolution : 2.40 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

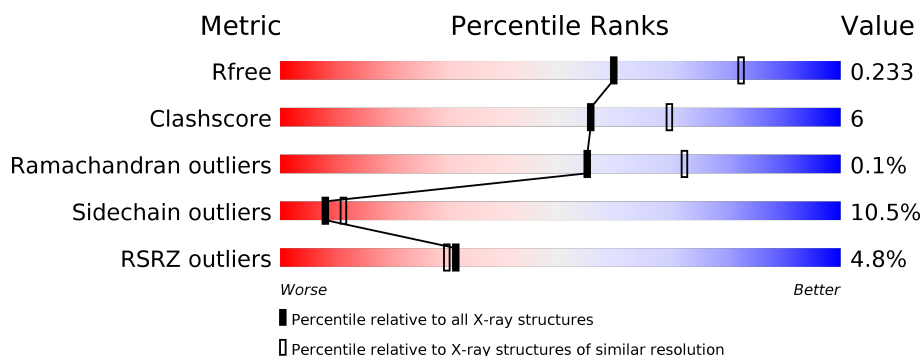
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	100719	3166 (2.40-2.40)
Clashscore	112137	3674 (2.40-2.40)
Ramachandran outliers	110173	3616 (2.40-2.40)
Sidechain outliers	110143	3617 (2.40-2.40)
RSRZ outliers	101464	3195 (2.40-2.40)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	417	<div> <div>4%</div> <div> <div></div> <div>77%</div> <div>18%</div> <div>..</div> </div> </div>
1	B	417	<div> <div>5%</div> <div> <div></div> <div>78%</div> <div>16%</div> <div>..</div> </div> </div>
1	C	417	<div> <div>2%</div> <div> <div></div> <div>76%</div> <div>19%</div> <div>..</div> </div> </div>
1	D	417	<div> <div>4%</div> <div> <div></div> <div>75%</div> <div>20%</div> <div>..</div> </div> </div>
1	E	417	<div> <div>8%</div> <div> <div></div> <div>76%</div> <div>18%</div> <div>..</div> </div> </div>
1	F	417	<div> <div>6%</div> <div> <div></div> <div>77%</div> <div>19%</div> <div>..</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	417	
1	H	417	

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	NAD	F	1416	-	-	-	X
2	NAD	H	1416	-	-	-	X
3	G6P	A	1417	X	-	-	-
3	G6P	B	1417	X	-	-	-
3	G6P	C	1417	X	-	-	X
3	G6P	D	1417	X	-	-	-
3	G6P	E	1417	X	-	-	-
3	G6P	F	1417	X	-	-	-
3	G6P	G	1417	X	-	-	-
3	G6P	H	1417	X	-	-	-
4	SO4	A	1418	-	-	-	X
4	SO4	C	1418	-	-	-	X

2 Entry composition

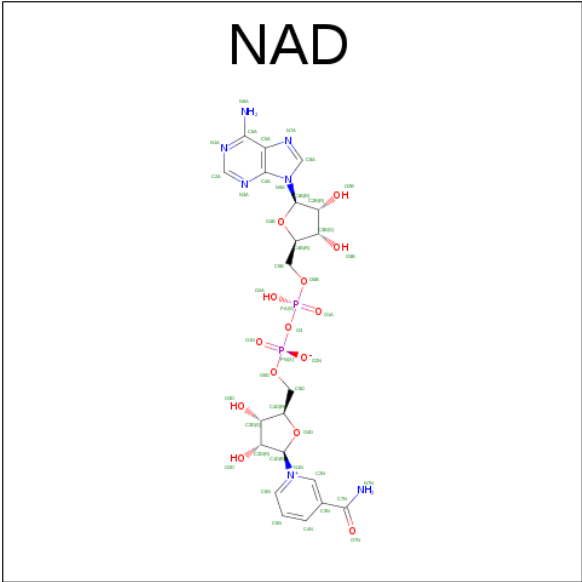
There are 5 unique types of molecules in this entry. The entry contains 27816 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 6-PHOSPHO-BETA-GLUCOSIDASE.

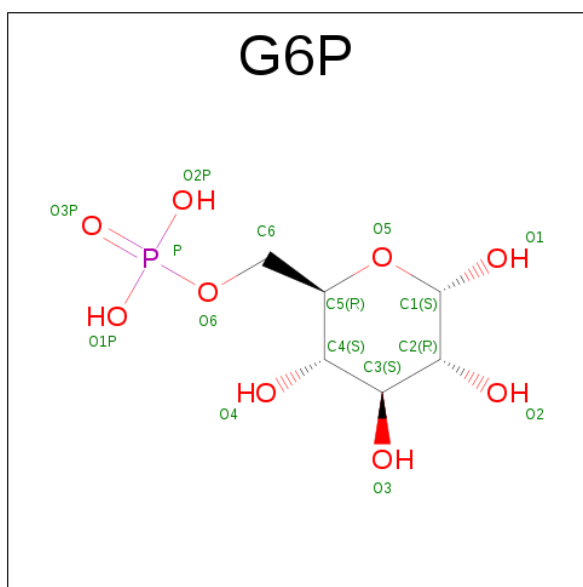
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	414	Total	C	N	O	S	10	0	0
			3362	2166	563	624	9			
1	B	409	Total	C	N	O	S	74	0	0
			3318	2139	553	617	9			
1	C	409	Total	C	N	O	S	26	1	0
			3325	2144	553	618	10			
1	D	409	Total	C	N	O	S	51	0	0
			3317	2137	552	619	9			
1	E	406	Total	C	N	O	S	154	0	0
			3294	2124	548	613	9			
1	F	411	Total	C	N	O	S	116	0	0
			3333	2148	555	621	9			
1	G	409	Total	C	N	O	S	77	0	0
			3318	2139	553	617	9			
1	H	407	Total	C	N	O	S	86	0	0
			3300	2127	549	615	9			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



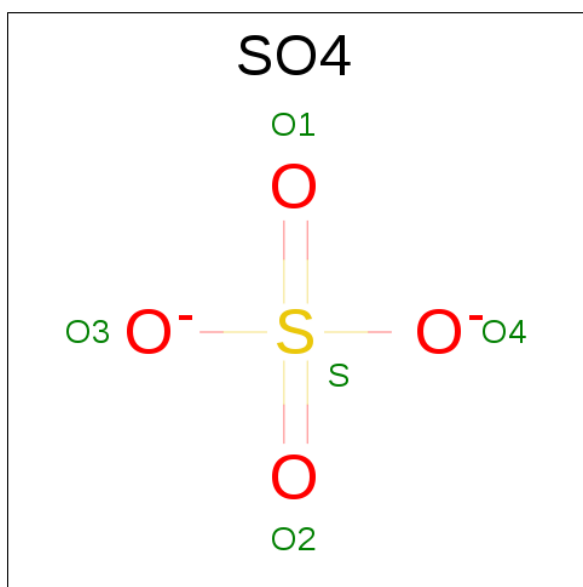
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is SUGAR (ALPHA-D-GLUCOSE-6-PHOSPHATE) (three-letter code: G6P) (formula: C₆H₁₃O₉P).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	6	9	1		
3	B	1	Total	C	O	P	0	0
			16	6	9	1		
3	C	1	Total	C	O	P	0	0
			16	6	9	1		
3	D	1	Total	C	O	P	0	0
			16	6	9	1		
3	E	1	Total	C	O	P	0	0
			16	6	9	1		
3	F	1	Total	C	O	P	0	0
			16	6	9	1		
3	G	1	Total	C	O	P	0	0
			16	6	9	1		
3	H	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

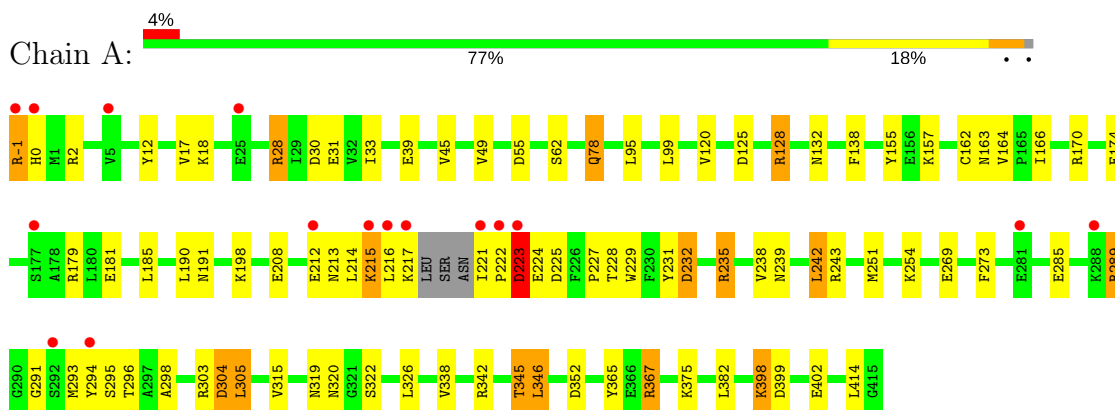
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	149	Total	O	0	0
			149	149		
5	B	103	Total	O	0	0
			103	103		
5	C	108	Total	O	0	0
			108	108		
5	D	91	Total	O	0	0
			91	91		
5	E	78	Total	O	0	0
			78	78		
5	F	83	Total	O	0	0
			83	83		
5	G	81	Total	O	0	0
			81	81		
5	H	66	Total	O	0	0
			66	66		

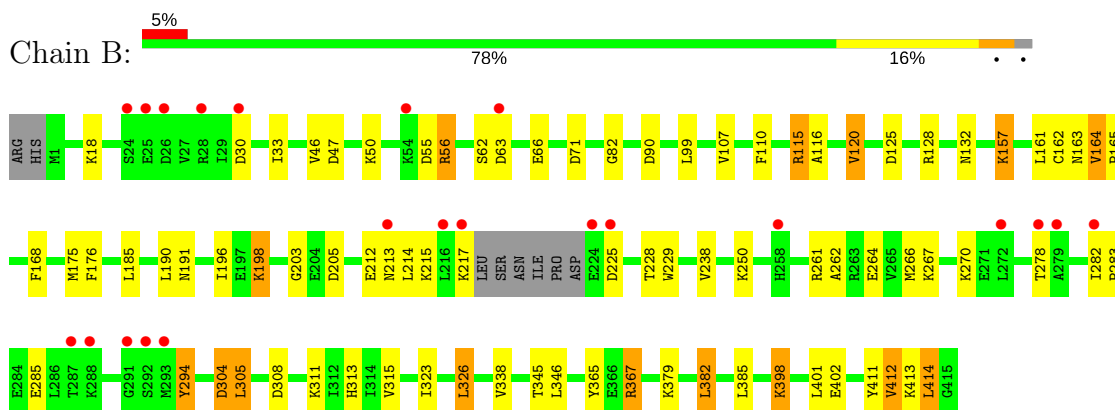
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

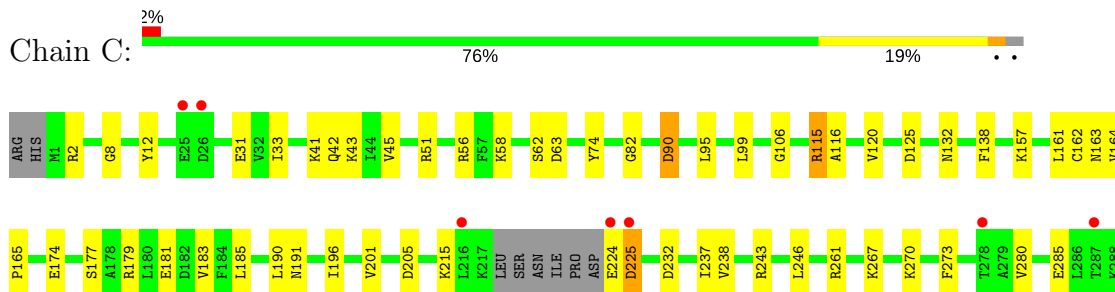
• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE

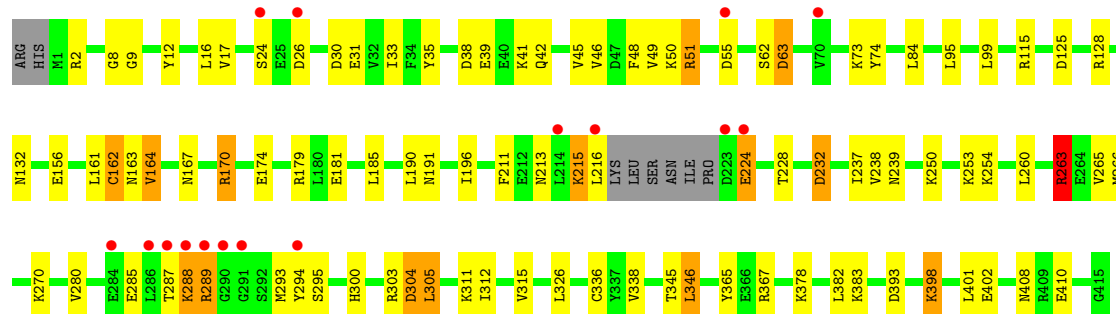
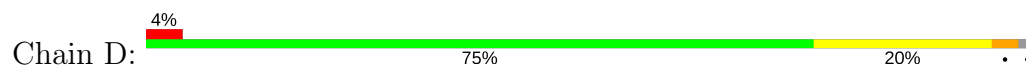


• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE

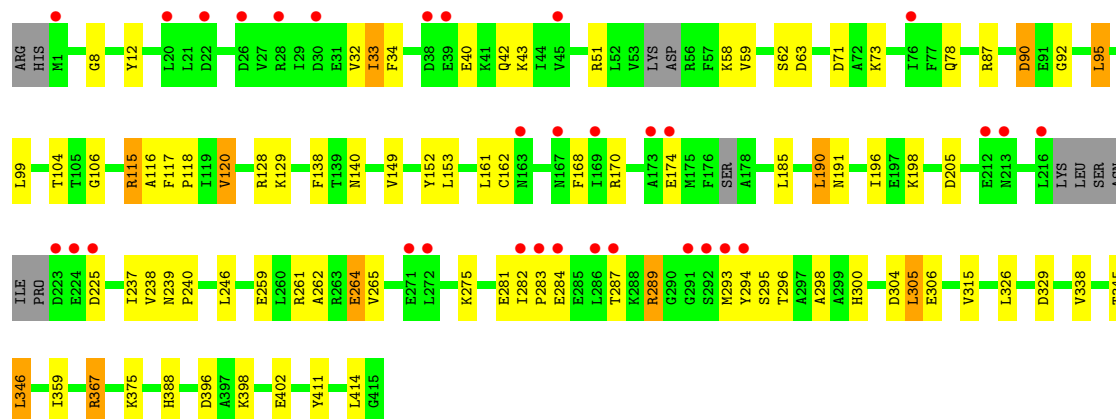




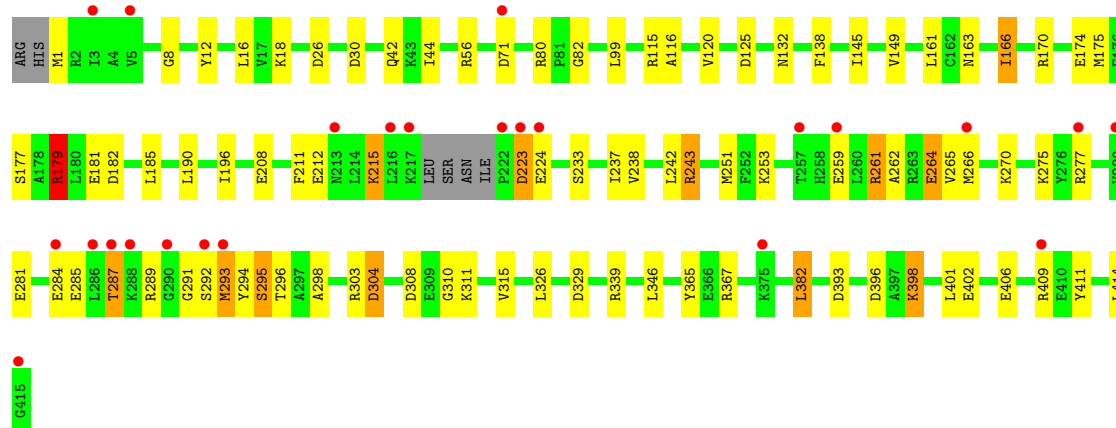
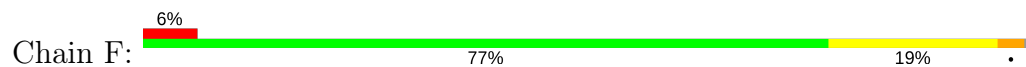
• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



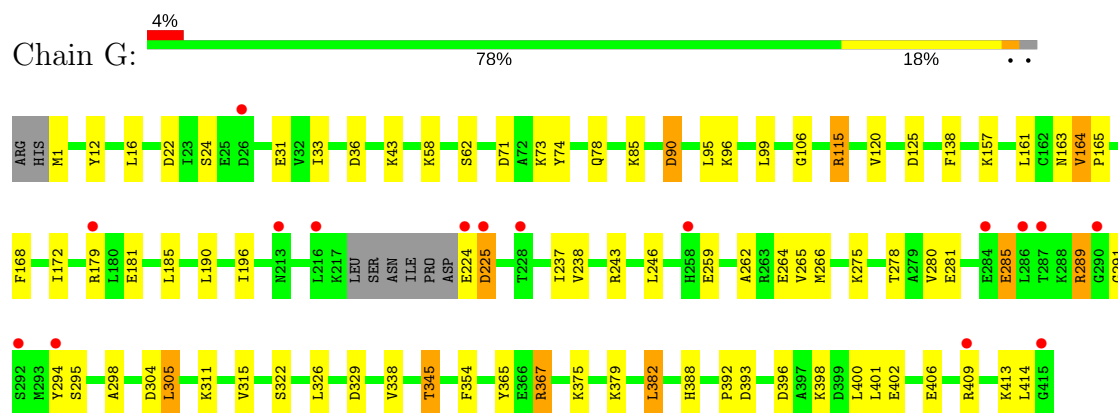
• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



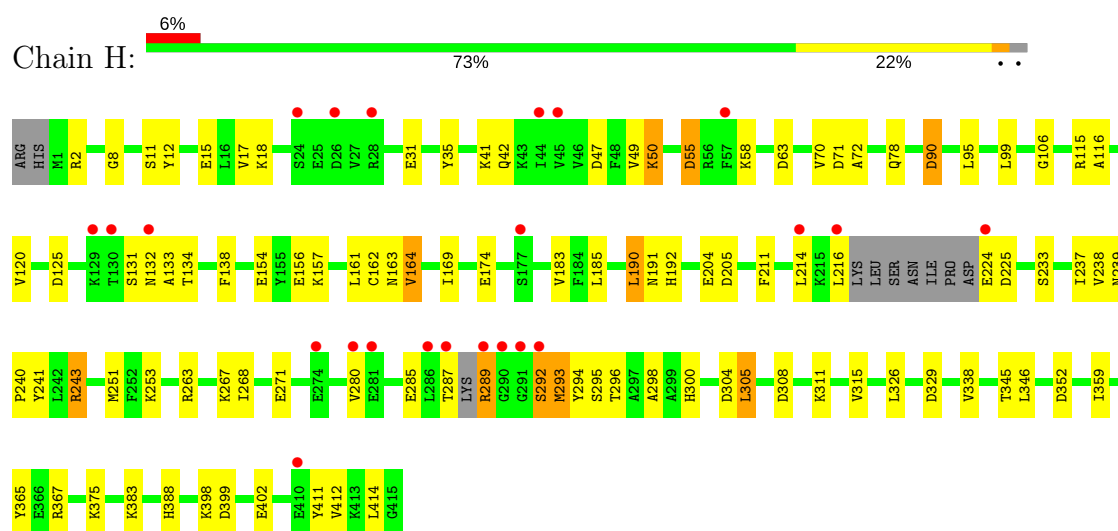
• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



• Molecule 1: 6-PHOSPHO-BETA-GLUCOSIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	178.13Å 178.13Å 278.93Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.40 19.96 – 2.40	Depositor EDS
% Data completeness (in resolution range)	98.3 (19.96-2.40) 98.3 (19.96-2.40)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.47 (at 2.41Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.199 , 0.240 0.196 , 0.233	Depositor DCC
R_{free} test set	8549 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	34.6	Xtriage
Anisotropy	0.222	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	27816	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.65% 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: G6P, SO4, NAD

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	0.74	0/3429	0.88	10/4620 (0.2%)
1	B	0.65	0/3383	0.86	12/4557 (0.3%)
1	C	0.68	0/3391	0.90	15/4567 (0.3%)
1	D	0.74	1/3382 (0.0%)	0.87	11/4557 (0.2%)
1	E	0.68	4/3357 (0.1%)	0.85	12/4521 (0.3%)
1	F	0.53	0/3399	0.79	11/4579 (0.2%)
1	G	0.60	0/3383	0.83	13/4557 (0.3%)
1	H	0.57	1/3364 (0.0%)	0.78	12/4532 (0.3%)
All	All	0.65	6/27088 (0.0%)	0.85	96/36490 (0.3%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	51	ARG	CZ-NH1	23.24	1.63	1.33
1	D	51	ARG	NE-CZ	8.03	1.43	1.33
1	E	51	ARG	NE-CZ	7.98	1.43	1.33
1	E	59	VAL	CB-CG2	6.38	1.66	1.52
1	H	50	LYS	CB-CG	5.79	1.68	1.52
1	E	51	ARG	CZ-NH2	5.72	1.40	1.33

All (96) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	51	ARG	NE-CZ-NH2	-21.85	109.37	120.30
1	C	115	ARG	NE-CZ-NH2	-12.57	114.02	120.30
1	E	51	ARG	NE-CZ-NH1	12.39	126.50	120.30
1	C	225	ASP	CB-CG-OD2	8.93	126.34	118.30
1	G	115	ARG	NE-CZ-NH2	-8.58	116.01	120.30
1	F	304	ASP	CB-CG-OD2	8.35	125.81	118.30
1	B	115	ARG	NE-CZ-NH2	-7.66	116.47	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	304	ASP	CB-CG-OD2	7.45	125.01	118.30
1	C	115	ARG	NE-CZ-NH1	7.28	123.94	120.30
1	A	304	ASP	CB-CG-OD2	7.19	124.77	118.30
1	C	90	ASP	CB-CG-OD2	7.18	124.76	118.30
1	D	304	ASP	CB-CG-OD2	7.06	124.65	118.30
1	B	225	ASP	CB-CG-OD2	7.03	124.62	118.30
1	B	308	ASP	CB-CG-OD2	6.95	124.56	118.30
1	H	225	ASP	CB-CG-OD2	6.83	124.45	118.30
1	D	263	ARG	NE-CZ-NH2	-6.82	116.89	120.30
1	G	329	ASP	CB-CG-OD1	6.70	124.33	118.30
1	B	304	ASP	CB-CG-OD2	6.66	124.29	118.30
1	G	22	ASP	CB-CG-OD2	6.57	124.21	118.30
1	B	115	ARG	NE-CZ-NH1	6.49	123.55	120.30
1	D	30	ASP	CB-CG-OD2	6.44	124.10	118.30
1	A	352	ASP	CB-CG-OD2	6.37	124.03	118.30
1	G	125	ASP	CB-CG-OD2	6.34	124.01	118.30
1	G	396	ASP	CB-CG-OD2	6.24	123.92	118.30
1	C	367	ARG	NE-CZ-NH2	-6.23	117.18	120.30
1	E	51	ARG	CD-NE-CZ	-6.16	114.97	123.60
1	G	367	ARG	NE-CZ-NH1	6.15	123.37	120.30
1	H	63	ASP	CB-CG-OD2	6.12	123.81	118.30
1	G	304	ASP	CB-CG-OD2	6.09	123.78	118.30
1	E	115	ARG	NE-CZ-NH2	-6.07	117.27	120.30
1	H	304	ASP	CB-CG-OD2	6.07	123.76	118.30
1	B	47	ASP	CB-CG-OD2	6.01	123.71	118.30
1	E	225	ASP	CB-CG-OD2	5.99	123.69	118.30
1	D	63	ASP	CB-CG-OD2	5.98	123.68	118.30
1	B	367	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	C	63	ASP	CB-CG-OD2	5.93	123.64	118.30
1	B	63	ASP	CB-CG-OD2	5.93	123.64	118.30
1	D	125	ASP	CB-CG-OD2	5.89	123.60	118.30
1	C	367	ARG	NE-CZ-NH1	5.88	123.24	120.30
1	G	90	ASP	CB-CG-OD2	5.84	123.55	118.30
1	C	396	ASP	CB-CG-OD2	5.84	123.55	118.30
1	D	393	ASP	CB-CG-OD2	5.81	123.53	118.30
1	F	396	ASP	CB-CG-OD2	5.78	123.50	118.30
1	C	328	ASP	CB-CG-OD2	5.74	123.47	118.30
1	D	55	ASP	CB-CG-OD2	5.72	123.45	118.30
1	F	329	ASP	CB-CG-OD2	5.68	123.41	118.30
1	F	308	ASP	CB-CG-OD2	5.64	123.37	118.30
1	B	55	ASP	CB-CG-OD2	5.63	123.37	118.30
1	E	396	ASP	CB-CG-OD2	5.63	123.37	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	179	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	H	308	ASP	CB-CG-OD2	5.61	123.35	118.30
1	H	352	ASP	CB-CG-OD2	5.60	123.34	118.30
1	A	232	ASP	CB-CG-OD2	5.60	123.34	118.30
1	G	115	ARG	NE-CZ-NH1	5.60	123.10	120.30
1	F	125	ASP	CB-CG-OD2	5.57	123.31	118.30
1	F	393	ASP	CB-CG-OD2	5.53	123.28	118.30
1	C	232	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	225	ASP	CB-CG-OD2	5.49	123.24	118.30
1	F	30	ASP	CB-CG-OD2	5.48	123.23	118.30
1	B	125	ASP	CB-CG-OD2	5.47	123.22	118.30
1	H	90	ASP	CB-CG-OD2	5.47	123.22	118.30
1	D	38	ASP	CB-CG-OD2	5.45	123.21	118.30
1	E	329	ASP	CB-CG-OD1	5.45	123.20	118.30
1	D	263	ARG	NE-CZ-NH1	5.43	123.01	120.30
1	H	329	ASP	CB-CG-OD2	5.42	123.17	118.30
1	F	71	ASP	CB-CG-OD2	5.42	123.17	118.30
1	A	55	ASP	CB-CG-OD2	5.41	123.17	118.30
1	C	308	ASP	CB-CG-OD2	5.40	123.16	118.30
1	A	399	ASP	CB-CG-OD2	5.37	123.13	118.30
1	H	205	ASP	CB-CG-OD2	5.33	123.10	118.30
1	A	125	ASP	CB-CG-OD2	5.32	123.09	118.30
1	H	125	ASP	CB-CG-OD2	5.31	123.08	118.30
1	G	71	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	367	ARG	NE-CZ-NH1	5.28	122.94	120.30
1	B	30	ASP	CB-CG-OD2	5.27	123.04	118.30
1	C	205	ASP	CB-CG-OD2	5.26	123.03	118.30
1	E	304	ASP	CB-CG-OD2	5.25	123.02	118.30
1	A	223	ASP	CB-CG-OD2	5.23	123.01	118.30
1	E	205	ASP	CB-CG-OD2	5.19	122.97	118.30
1	C	125	ASP	CB-CG-OD2	5.18	122.96	118.30
1	H	55	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	399	ASP	CB-CG-OD2	5.16	122.94	118.30
1	G	36	ASP	CB-CG-OD2	5.15	122.94	118.30
1	F	223	ASP	CB-CG-OD2	5.14	122.93	118.30
1	F	26	ASP	CB-CG-OD2	5.14	122.92	118.30
1	G	393	ASP	CB-CG-OD2	5.14	122.92	118.30
1	A	367	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	B	71	ASP	CB-CG-OD2	5.13	122.91	118.30
1	E	90	ASP	CB-CG-OD2	5.10	122.89	118.30
1	D	232	ASP	CB-CG-OD2	5.06	122.86	118.30
1	E	71	ASP	CB-CG-OD2	5.06	122.85	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	63	ASP	CB-CG-OD2	5.05	122.85	118.30
1	G	225	ASP	CB-CG-OD2	5.04	122.84	118.30
1	H	47	ASP	CB-CG-OD2	5.03	122.83	118.30
1	H	71	ASP	CB-CG-OD2	5.03	122.82	118.30
1	D	26	ASP	CB-CG-OD2	5.00	122.80	118.30

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	3362	0	3397	53	0
1	B	3318	0	3355	38	0
1	C	3325	0	3363	40	0
1	D	3317	0	3346	51	0
1	E	3294	0	3322	43	0
1	F	3333	0	3367	35	0
1	G	3318	0	3355	29	0
1	H	3300	0	3328	48	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
2	C	44	0	26	0	0
2	D	44	0	26	0	0
2	E	44	0	26	1	0
2	F	44	0	26	2	0
2	G	44	0	26	0	0
2	H	44	0	26	0	0
3	A	16	0	11	0	0
3	B	16	0	11	0	0
3	C	16	0	11	0	0
3	D	16	0	11	2	0
3	E	16	0	11	0	0
3	F	16	0	11	0	0
3	G	16	0	11	0	0
3	H	16	0	11	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	5	0	0	0	0
4	C	5	0	0	0	0
5	A	149	0	0	2	0
5	B	103	0	0	1	0
5	C	108	0	0	0	0
5	D	91	0	0	1	0
5	E	78	0	0	0	0
5	F	83	0	0	1	0
5	G	81	0	0	1	0
5	H	66	0	0	0	0
All	All	27816	0	27129	313	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 6.

All (313) 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:235:ARG:HH11	1:A:235:ARG:HG2	0.97	1.07
1:H:162:CYS:HB2	1:H:191:ASN:ND2	1.80	0.96
1:A:235:ARG:NH1	1:A:235:ARG:HG2	1.76	0.92
1:E:162:CYS:HB2	1:E:191:ASN:HD21	1.34	0.91
1:B:398:LYS:O	1:B:402:GLU:HG3	1.72	0.87
1:H:162:CYS:HB2	1:H:191:ASN:HD21	1.34	0.87
1:B:305:LEU:HD13	1:B:338:VAL:HG13	1.58	0.83
1:A:346:LEU:HD12	1:D:346:LEU:CD1	2.08	0.82
1:D:48:PHE:HA	1:D:51:ARG:CZ	2.10	0.81
1:A:346:LEU:CD1	1:D:346:LEU:CD1	2.59	0.80
1:D:162:CYS:CB	1:D:191:ASN:HD21	1.97	0.77
1:E:346:LEU:HD12	1:H:346:LEU:HD12	1.66	0.77
1:H:162:CYS:CB	1:H:191:ASN:ND2	2.48	0.76
1:H:162:CYS:CB	1:H:191:ASN:HD21	1.99	0.75
1:A:345:THR:HG22	5:A:2106:HOH:O	1.85	0.75
1:C:8:GLY:HA3	1:C:42:GLN:HE21	1.51	0.75
1:A:162:CYS:CB	1:A:191:ASN:HD21	2.01	0.74
1:A:235:ARG:HH11	1:A:235:ARG:CG	1.89	0.73
1:A:162:CYS:HB2	1:A:191:ASN:HD21	1.54	0.73
1:G:90:ASP:OD1	1:G:115:ARG:NH2	2.22	0.72
1:E:162:CYS:HB2	1:E:191:ASN:ND2	2.05	0.72
1:D:2:ARG:HG3	1:D:31:GLU:HG3	1.70	0.71
1:E:33:ILE:HD11	1:E:62:SER:HB2	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:56:ARG:HG2	1:B:56:ARG:HH11	1.54	0.70
1:B:346:LEU:HD23	1:C:346:LEU:HD12	1.73	0.70
1:D:162:CYS:HB2	1:D:191:ASN:HD21	1.56	0.70
1:F:138:PHE:HZ	1:F:298:ALA:HB2	1.57	0.70
1:E:162:CYS:CB	1:E:191:ASN:HD21	2.05	0.69
1:C:2:ARG:HG3	1:C:31:GLU:HG3	1.75	0.69
1:F:8:GLY:HA3	1:F:42:GLN:HE21	1.58	0.68
1:A:212:GLU:HA	1:A:215:LYS:HD3	1.77	0.67
1:A:295:SER:OG	1:A:296:THR:N	2.26	0.67
1:G:179:ARG:NH1	1:G:181:GLU:OE2	2.28	0.67
1:D:8:GLY:HA3	1:D:42:GLN:HE21	1.60	0.67
1:G:90:ASP:CG	1:G:115:ARG:HH22	1.98	0.67
1:D:163:ASN:HB3	1:D:294:TYR:CD1	2.30	0.66
1:C:90:ASP:CG	1:C:115:ARG:HH22	1.98	0.66
1:C:90:ASP:OD1	1:C:115:ARG:NH2	2.24	0.66
1:E:346:LEU:CD1	1:H:346:LEU:HD12	2.26	0.66
1:D:48:PHE:HA	1:D:51:ARG:NH2	2.11	0.65
1:E:259:GLU:OE1	1:E:264:GLU:HG2	1.97	0.65
1:H:70:VAL:O	1:H:131:SER:HB3	1.97	0.64
1:A:166:ILE:HG12	1:A:293:MET:HE3	1.78	0.64
1:A:346:LEU:HD12	1:D:346:LEU:HD13	1.78	0.64
1:F:289:ARG:NH2	2:F:1416:NAD:O1N	2.29	0.64
1:D:16:LEU:HA	1:D:295:SER:HB3	1.78	0.64
1:H:138:PHE:HZ	1:H:298:ALA:HB2	1.64	0.63
1:A:179:ARG:NH1	1:A:181:GLU:OE2	2.33	0.62
1:B:90:ASP:OD1	1:B:115:ARG:NH2	2.33	0.61
1:H:90:ASP:OD1	1:H:115:ARG:NH2	2.33	0.61
1:D:162:CYS:CB	1:D:191:ASN:ND2	2.64	0.61
1:E:87:ARG:NH1	1:E:265:VAL:HG21	2.16	0.61
1:H:163:ASN:HB3	1:H:294:TYR:CD1	2.36	0.61
1:A:269:GLU:O	1:A:273:PHE:HD2	1.84	0.60
1:H:296:THR:HG22	1:H:300:HIS:CE1	2.36	0.60
1:E:90:ASP:OD1	1:E:115:ARG:NH2	2.34	0.60
1:B:262:ALA:O	1:B:266:MET:HG3	2.01	0.60
1:F:138:PHE:CZ	1:F:298:ALA:HB2	2.35	0.60
1:H:138:PHE:CZ	1:H:298:ALA:HB2	2.36	0.60
1:E:296:THR:HG23	1:E:300:HIS:CE1	2.36	0.60
1:A:215:LYS:HG2	1:A:228:THR:HG23	1.83	0.59
1:E:87:ARG:HD3	1:E:262:ALA:CB	2.32	0.59
1:D:12:TYR:OH	1:D:289:ARG:HB3	2.02	0.59
1:B:164:VAL:HG22	1:B:165:PRO:HD3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:17:VAL:HG11	1:H:49:VAL:HG13	1.85	0.59
1:E:87:ARG:HD3	1:E:262:ALA:HB2	1.84	0.59
1:C:163:ASN:HB3	1:C:294:TYR:CD1	2.38	0.59
1:F:12:TYR:OH	1:F:289:ARG:HB3	2.03	0.59
1:D:263:ARG:HD3	5:D:2049:HOH:O	2.01	0.59
1:A:162:CYS:CB	1:A:191:ASN:ND2	2.66	0.59
1:B:162:CYS:HB2	1:B:191:ASN:ND2	2.17	0.59
1:G:259:GLU:OE1	1:G:264:GLU:HG2	2.03	0.59
1:D:33:ILE:HD11	1:D:62:SER:HB2	1.86	0.58
1:E:346:LEU:CD1	1:H:346:LEU:CD1	2.82	0.58
1:B:82:GLY:HA2	1:B:411:TYR:CZ	2.39	0.58
1:H:305:LEU:HD13	1:H:338:VAL:HG13	1.86	0.57
1:H:292:SER:O	1:H:293:MET:HB2	2.03	0.57
1:C:305:LEU:HD13	1:C:338:VAL:HG13	1.86	0.57
1:D:300:HIS:HD2	1:D:303:ARG:NH2	2.02	0.57
1:D:48:PHE:HA	1:D:51:ARG:NH1	2.19	0.57
1:A:305:LEU:HD13	1:A:338:VAL:HG13	1.85	0.57
1:D:303:ARG:HD2	1:D:304:ASP:OD1	2.05	0.57
1:D:46:VAL:HG12	1:D:50:LYS:HE3	1.87	0.57
1:C:319:ASN:O	1:C:345:THR:HG21	2.06	0.56
1:B:56:ARG:NH1	1:B:56:ARG:HG2	2.18	0.56
1:G:33:ILE:HD11	1:G:62:SER:HB2	1.87	0.56
1:A:45:VAL:CG2	1:A:273:PHE:HE1	2.18	0.56
1:C:322:SER:HB2	1:C:345:THR:HG23	1.87	0.56
1:H:240:PRO:O	1:H:243:ARG:HG2	2.06	0.55
1:D:164:VAL:HG21	1:D:239:ASN:ND2	2.22	0.55
1:E:90:ASP:CG	1:E:115:ARG:HH22	2.10	0.55
1:E:170:ARG:O	1:E:174:GLU:HG3	2.06	0.55
1:C:382:LEU:HD13	1:C:401:LEU:HD22	1.89	0.55
1:E:116:ALA:O	1:E:120:VAL:HG13	2.07	0.55
1:F:82:GLY:HA3	1:F:115:ARG:HD3	1.89	0.55
1:B:305:LEU:HD13	1:B:338:VAL:CG1	2.35	0.54
1:C:179:ARG:NH1	1:C:181:GLU:OE2	2.39	0.54
1:F:262:ALA:O	1:F:266:MET:HG3	2.07	0.54
1:D:305:LEU:HD13	1:D:338:VAL:HG13	1.90	0.54
1:C:295:SER:OG	1:C:296:THR:N	2.40	0.54
1:B:132:ASN:O	1:B:157:LYS:NZ	2.42	0.53
1:H:12:TYR:OH	1:H:289:ARG:HB3	2.07	0.53
1:A:17:VAL:HG11	1:A:49:VAL:HG13	1.91	0.53
1:F:382:LEU:HD13	1:F:401:LEU:HD22	1.90	0.53
1:B:90:ASP:CG	1:B:115:ARG:HH22	2.11	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:382:LEU:HD13	1:C:401:LEU:CD2	2.38	0.53
1:D:224:GLU:OE2	1:D:254:LYS:HE3	2.09	0.53
1:G:305:LEU:HD13	1:G:338:VAL:HG13	1.91	0.53
1:D:294:TYR:HE1	3:D:1417:G6P:H3	1.73	0.53
1:D:382:LEU:HD21	1:D:398:LYS:HA	1.90	0.53
1:E:8:GLY:HA3	1:E:42:GLN:HE21	1.73	0.53
1:F:224:GLU:HB3	1:F:243:ARG:HH11	1.74	0.52
1:F:80:ARG:NH2	2:F:1416:NAD:O1N	2.40	0.52
1:F:292:SER:O	1:F:293:MET:HB2	2.09	0.52
1:F:163:ASN:HB3	1:F:294:TYR:CD1	2.45	0.52
1:H:240:PRO:O	1:H:243:ARG:CG	2.58	0.52
1:H:268:ILE:HG21	1:H:289:ARG:HG2	1.92	0.52
1:F:82:GLY:HA2	1:F:411:TYR:CZ	2.45	0.52
1:G:73:LYS:HG2	1:G:74:TYR:CE2	2.44	0.52
1:A:303:ARG:HD2	1:A:304:ASP:OD1	2.10	0.51
1:H:78:GLN:O	1:H:78:GLN:HG2	2.11	0.51
1:F:211:PHE:O	1:F:215:LYS:HD2	2.09	0.51
1:A:398:LYS:HD2	1:B:229:TRP:CD1	2.45	0.51
1:E:78:GLN:O	1:E:78:GLN:HG2	2.10	0.51
1:F:179:ARG:NH2	1:F:181:GLU:OE2	2.44	0.51
1:G:1:MET:N	5:G:2001:HOH:O	2.43	0.51
1:A:319:ASN:O	1:A:345:THR:HG21	2.10	0.51
1:E:115:ARG:HG2	1:E:411:TYR:CB	2.41	0.51
1:G:168:PHE:CZ	1:G:172:ILE:HD11	2.46	0.50
1:G:16:LEU:HD22	1:G:78:GLN:OE1	2.11	0.50
1:H:90:ASP:CG	1:H:115:ARG:HH22	2.12	0.50
1:A:162:CYS:HB2	1:A:191:ASN:ND2	2.24	0.50
1:C:12:TYR:OH	1:C:289:ARG:HB3	2.12	0.50
1:G:16:LEU:HA	1:G:295:SER:HB2	1.93	0.50
1:C:162:CYS:HB2	1:C:191:ASN:ND2	2.27	0.50
1:E:12:TYR:OH	1:E:289:ARG:HB3	2.12	0.50
1:A:346:LEU:HD12	1:D:346:LEU:HD12	1.92	0.50
1:A:346:LEU:CD1	1:D:346:LEU:HD11	2.40	0.49
1:B:323:ILE:HG21	1:B:326:LEU:HD22	1.94	0.49
1:F:196:ILE:HB	1:F:237:ILE:HB	1.94	0.49
1:F:262:ALA:O	1:F:265:VAL:HG22	2.13	0.49
1:F:303:ARG:HD2	1:F:304:ASP:OD1	2.13	0.49
1:E:346:LEU:HD12	1:H:346:LEU:CD1	2.41	0.49
1:F:224:GLU:OE1	1:F:243:ARG:NH1	2.45	0.49
1:H:72:ALA:O	1:H:133:ALA:HB2	2.12	0.49
1:B:412:VAL:HG23	1:B:414:LEU:HD13	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:305:LEU:HD13	1:C:338:VAL:CG1	2.42	0.49
1:E:190:LEU:HD13	1:E:359:ILE:HG23	1.93	0.49
1:A:2:ARG:HG3	1:A:31:GLU:HG3	1.94	0.49
1:A:208:GLU:OE2	1:A:235:ARG:NH2	2.45	0.49
1:E:305:LEU:HD13	1:E:338:VAL:HG13	1.94	0.49
1:F:224:GLU:O	1:F:243:ARG:HD2	2.12	0.49
1:H:294:TYR:HE1	3:H:1417:G6P:H3	1.77	0.49
1:A:45:VAL:CG2	1:A:273:PHE:CE1	2.96	0.48
1:B:198:LYS:NZ	1:B:205:ASP:OD2	2.46	0.48
1:B:46:VAL:O	1:B:50:LYS:HG3	2.13	0.48
1:E:117:PHE:N	1:E:118:PRO:HD2	2.28	0.48
1:A:224:GLU:OE2	1:A:254:LYS:HE3	2.13	0.48
1:C:183:VAL:HG22	1:C:201:VAL:HG22	1.95	0.48
1:G:406:GLU:OE1	1:G:406:GLU:HA	2.13	0.48
1:F:284:GLU:O	1:F:287:THR:OG1	2.31	0.48
1:A:322:SER:HB2	1:A:345:THR:HG23	1.96	0.48
1:B:66:GLU:HB2	5:B:2008:HOH:O	2.13	0.48
1:A:138:PHE:CZ	1:A:298:ALA:HB2	2.48	0.48
1:F:295:SER:OG	1:F:296:THR:N	2.45	0.48
1:H:164:VAL:HG11	1:H:239:ASN:HD21	1.79	0.48
1:D:35:TYR:C	1:D:42:GLN:HE22	2.17	0.48
1:B:175:MET:HE2	1:B:176:PHE:CE2	2.48	0.48
1:C:164:VAL:HB	1:C:165:PRO:HD3	1.96	0.48
1:B:168:PHE:CE2	1:B:196:ILE:HD13	2.49	0.48
1:A:291:GLY:O	1:A:294:TYR:HD1	1.96	0.47
1:H:190:LEU:HD13	1:H:359:ILE:HG23	1.95	0.47
1:C:33:ILE:HD11	1:C:62:SER:HB2	1.96	0.47
1:G:291:GLY:O	1:G:294:TYR:HD2	1.97	0.47
1:F:310:GLY:HA2	1:F:339:ARG:HB2	1.96	0.47
1:C:41:LYS:HE2	1:C:273:PHE:CZ	2.49	0.47
1:E:162:CYS:CB	1:E:191:ASN:ND2	2.73	0.47
1:E:346:LEU:HD11	1:H:346:LEU:CD1	2.45	0.47
1:H:8:GLY:HA3	1:H:42:GLN:HE21	1.80	0.47
1:C:116:ALA:O	1:C:120:VAL:HG13	2.15	0.47
1:C:31:GLU:HB3	1:C:58:LYS:HB2	1.97	0.46
1:G:382:LEU:HD13	1:G:401:LEU:HD22	1.97	0.46
1:H:224:GLU:CG	1:H:251:MET:HE1	2.45	0.46
1:G:379:LYS:HB3	1:H:233:SER:HA	1.97	0.46
1:E:104:THR:HG22	1:E:140:ASN:HB3	1.96	0.46
1:A:164:VAL:HG21	1:A:239:ASN:ND2	2.31	0.46
1:B:285:GLU:HG3	1:B:285:GLU:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:162:CYS:HB2	1:D:191:ASN:ND2	2.25	0.46
1:D:179:ARG:HH12	1:D:181:GLU:CD	2.19	0.46
1:A:320:ASN:ND2	5:A:2107:HOH:O	2.49	0.46
1:E:152:TYR:OH	1:E:367:ARG:HD2	2.14	0.46
1:A:78:GLN:O	1:A:78:GLN:CG	2.64	0.46
1:C:224:GLU:OE2	1:C:243:ARG:NH1	2.48	0.46
1:F:145:ILE:O	1:F:149:VAL:HG23	2.15	0.46
1:D:115:ARG:HD3	1:D:408:ASN:OD1	2.16	0.46
1:E:73:LYS:NZ	1:E:306:GLU:OE2	2.38	0.46
1:F:295:SER:HB3	5:F:2041:HOH:O	2.15	0.46
1:G:196:ILE:HB	1:G:237:ILE:HB	1.98	0.45
1:G:224:GLU:OE2	1:G:243:ARG:NH1	2.49	0.45
1:B:304:ASP:OD2	1:B:313:HIS:NE2	2.42	0.45
1:C:352:ASP:OD2	1:D:383:LYS:NZ	2.45	0.45
1:B:162:CYS:SG	1:B:191:ASN:ND2	2.90	0.45
1:D:398:LYS:HE3	1:D:398:LYS:HB2	1.40	0.45
1:F:161:LEU:HD12	1:F:161:LEU:HA	1.74	0.45
1:H:116:ALA:O	1:H:120:VAL:HG13	2.17	0.45
1:E:168:PHE:CE2	1:E:196:ILE:HD13	2.52	0.45
1:B:163:ASN:HB3	1:B:294:TYR:CD2	2.52	0.45
1:D:16:LEU:CA	1:D:295:SER:HB3	2.46	0.45
1:A:33:ILE:HD11	1:A:62:SER:HB2	1.99	0.45
1:F:382:LEU:HD21	1:F:398:LYS:HG3	1.99	0.45
1:G:12:TYR:OH	1:G:289:ARG:HB3	2.16	0.45
1:B:346:LEU:CD2	1:C:346:LEU:HD12	2.46	0.45
1:D:294:TYR:CE1	3:D:1417:G6P:H3	2.52	0.45
1:A:346:LEU:HD11	1:D:346:LEU:HD11	1.97	0.45
1:E:32:VAL:HG12	1:E:34:PHE:CE1	2.51	0.45
1:A:216:LEU:O	1:A:217:LYS:O	2.34	0.44
1:C:106:GLY:HA2	1:C:388:HIS:CE1	2.52	0.44
1:G:285:GLU:O	1:G:285:GLU:HG3	2.17	0.44
1:C:138:PHE:CZ	1:C:298:ALA:HB2	2.53	0.44
1:A:0:HIS:HA	1:A:30:ASP:OD2	2.18	0.44
1:A:238:VAL:HG22	1:A:242:LEU:HD23	2.00	0.44
1:B:346:LEU:HD23	1:C:346:LEU:CD1	2.46	0.44
1:D:73:LYS:HG2	1:D:74:TYR:CE2	2.52	0.44
1:B:116:ALA:O	1:B:120:VAL:HG13	2.18	0.44
1:D:287:THR:C	1:D:289:ARG:H	2.20	0.44
1:A:285:GLU:O	1:A:285:GLU:CG	2.65	0.44
1:D:287:THR:C	1:D:289:ARG:N	2.72	0.44
1:B:346:LEU:CD2	1:C:346:LEU:CD1	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:106:GLY:HA2	1:H:388:HIS:CE1	2.53	0.43
1:A:-1:ARG:HD3	1:A:28:ARG:HD3	1.99	0.43
1:B:33:ILE:HD11	1:B:62:SER:HB2	2.01	0.43
1:G:164:VAL:N	1:G:165:PRO:CD	2.81	0.43
1:H:115:ARG:HG2	1:H:411:TYR:HB3	2.00	0.43
1:H:211:PHE:CE1	1:H:237:ILE:HG13	2.53	0.43
1:E:282:ILE:HA	1:E:283:PRO:HD3	1.89	0.43
1:D:211:PHE:O	1:D:215:LYS:HD2	2.19	0.43
1:H:11:SER:OG	1:H:289:ARG:NH1	2.51	0.43
1:E:138:PHE:CZ	1:E:298:ALA:HB2	2.53	0.43
1:H:162:CYS:SG	1:H:164:VAL:HG12	2.59	0.43
1:D:196:ILE:HB	1:D:237:ILE:HB	2.01	0.43
1:F:179:ARG:HG2	1:F:182:ASP:OD2	2.18	0.43
1:A:138:PHE:HZ	1:A:298:ALA:HB2	1.84	0.43
1:D:17:VAL:HG11	1:D:49:VAL:HG13	2.01	0.43
1:E:284:GLU:O	1:E:287:THR:OG1	2.34	0.43
1:G:392:PRO:HG3	1:G:400:LEU:HD23	2.00	0.43
1:C:196:ILE:HB	1:C:237:ILE:HB	1.99	0.43
1:F:224:GLU:HG2	1:F:251:MET:CE	2.48	0.43
1:B:107:VAL:O	1:B:110:PHE:HB3	2.19	0.42
1:E:261:ARG:HA	1:E:264:GLU:HG3	2.01	0.42
1:G:163:ASN:HB3	1:G:294:TYR:CD2	2.53	0.42
1:H:169:ILE:HG23	1:H:183:VAL:HB	2.01	0.42
1:A:163:ASN:HB3	1:A:294:TYR:CD1	2.54	0.42
1:E:296:THR:CG2	1:E:300:HIS:CE1	3.02	0.42
1:F:116:ALA:O	1:F:120:VAL:HG13	2.20	0.42
1:A:224:GLU:HG2	1:A:251:MET:CE	2.48	0.42
1:E:149:VAL:HG22	1:E:153:LEU:HD12	2.02	0.42
1:H:224:GLU:HG3	1:H:251:MET:HE1	2.01	0.42
1:B:382:LEU:HD13	1:B:401:LEU:HD22	2.02	0.42
1:B:215:LYS:HD3	1:B:228:THR:HG23	2.00	0.42
1:A:214:LEU:HD23	1:A:231:TYR:CZ	2.55	0.42
1:A:285:GLU:HG3	1:A:285:GLU:O	2.20	0.42
1:C:74:TYR:OH	1:C:306:GLU:OE2	2.25	0.42
1:D:167:ASN:OD1	1:D:170:ARG:NH2	2.53	0.42
1:H:305:LEU:HD13	1:H:338:VAL:CG1	2.49	0.42
1:B:282:ILE:HA	1:B:283:PRO:HD3	1.86	0.42
1:E:78:GLN:HG3	2:E:1416:NAD:N7N	2.35	0.42
1:H:192:HIS:CD2	1:H:241:TYR:CE2	3.07	0.42
1:A:346:LEU:CD1	1:D:346:LEU:HD12	2.48	0.42
1:A:224:GLU:OE1	1:A:243:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:PHE:HB2	1:D:51:ARG:HH22	1.85	0.42
1:E:161:LEU:HA	1:E:161:LEU:HD12	1.90	0.42
1:A:128:ARG:HB2	1:A:155:TYR:CE1	2.55	0.42
1:C:379:LYS:HE3	1:D:232:ASP:HB3	2.02	0.41
1:B:215:LYS:HG2	1:B:228:THR:HG23	2.01	0.41
1:H:35:TYR:C	1:H:42:GLN:HE22	2.23	0.41
1:E:92:GLY:HA2	1:E:95:LEU:HD22	2.01	0.41
1:G:31:GLU:HB3	1:G:58:LYS:HB2	2.02	0.41
1:H:162:CYS:SG	1:H:163:ASN:N	2.93	0.41
1:B:203:GLY:HA3	1:C:340:SER:HB3	2.02	0.41
1:E:239:ASN:OD1	1:E:240:PRO:HD2	2.20	0.41
1:A:12:TYR:OH	1:A:289:ARG:HB3	2.21	0.41
1:C:323:ILE:HG21	1:C:326:LEU:HD22	2.02	0.41
1:E:106:GLY:HA2	1:E:388:HIS:CE1	2.55	0.41
1:F:291:GLY:O	1:F:294:TYR:HD1	2.02	0.41
1:G:106:GLY:HA2	1:G:388:HIS:CE1	2.55	0.41
1:B:261:ARG:HA	1:B:264:GLU:HG3	2.03	0.41
1:C:45:VAL:CG2	1:C:273:PHE:CE1	3.03	0.41
1:H:2:ARG:HG3	1:H:31:GLU:HG3	2.02	0.41
1:G:354:PHE:HB2	1:H:383:LYS:HE2	2.02	0.41
1:A:232:ASP:HB3	1:B:379:LYS:HE2	2.03	0.41
1:E:196:ILE:HB	1:E:237:ILE:HB	2.02	0.41
1:F:166:ILE:HD13	1:F:293:MET:SD	2.61	0.41
1:G:322:SER:HB2	1:G:345:THR:HG23	2.02	0.41
1:D:305:LEU:HD13	1:D:338:VAL:CG1	2.51	0.41
1:D:9:GLY:HA2	1:D:45:VAL:HG21	2.03	0.41
1:F:409:ARG:HE	1:F:409:ARG:HB2	1.56	0.41
1:G:138:PHE:CZ	1:G:298:ALA:HB2	2.56	0.41
1:H:134:THR:HA	1:H:157:LYS:HB3	2.01	0.41
1:H:294:TYR:CE1	3:H:1417:G6P:H3	2.55	0.41
1:A:227:PRO:HG2	1:A:229:TRP:CE2	2.56	0.40
1:C:162:CYS:HB2	1:C:191:ASN:HD21	1.86	0.40
1:C:82:GLY:HA2	1:C:411:TYR:CZ	2.56	0.40
1:D:312:ILE:HA	1:D:336:CYS:O	2.21	0.40
1:D:84:LEU:HB2	1:D:266:MET:HE2	2.04	0.40
1:G:262:ALA:O	1:G:266:MET:HG3	2.21	0.40
1:C:285:GLU:O	1:C:285:GLU:HG2	2.22	0.40
1:C:82:GLY:HA3	1:C:115:ARG:HD3	2.04	0.40
1:D:260:LEU:O	1:D:263:ARG:HB2	2.22	0.40
1:F:16:LEU:HA	1:F:295:SER:HB2	2.02	0.40
1:G:379:LYS:O	1:H:233:SER:HB3	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:161:LEU:HA	1:C:161:LEU:HD12	1.96	0.40
1:D:382:LEU:HG	1:D:401:LEU:HD22	2.04	0.40
1:F:261:ARG:HA	1:F:264:GLU:HG3	2.01	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	410/417 (98%)	402 (98%)	6 (2%)	2 (0%)	32	46
1	B	405/417 (97%)	400 (99%)	5 (1%)	0	100	100
1	C	406/417 (97%)	399 (98%)	7 (2%)	0	100	100
1	D	405/417 (97%)	397 (98%)	6 (2%)	2 (0%)	32	46
1	E	398/417 (95%)	392 (98%)	6 (2%)	0	100	100
1	F	407/417 (98%)	399 (98%)	8 (2%)	0	100	100
1	G	405/417 (97%)	397 (98%)	8 (2%)	0	100	100
1	H	401/417 (96%)	391 (98%)	10 (2%)	0	100	100
All	All	3237/3336 (97%)	3177 (98%)	56 (2%)	4 (0%)	55	72

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	PRO
1	A	223	ASP
1	D	288	LYS
1	D	285	GLU

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	366/369 (99%)	330 (90%)	36 (10%)	9	14
1	B	361/369 (98%)	327 (91%)	34 (9%)	10	15
1	C	362/369 (98%)	329 (91%)	33 (9%)	11	16
1	D	361/369 (98%)	318 (88%)	43 (12%)	6	8
1	E	358/369 (97%)	327 (91%)	31 (9%)	12	18
1	F	363/369 (98%)	318 (88%)	45 (12%)	5	6
1	G	361/369 (98%)	325 (90%)	36 (10%)	9	13
1	H	359/369 (97%)	314 (88%)	45 (12%)	5	6
All	All	2891/2952 (98%)	2588 (90%)	303 (10%)	8	11

All (303) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-1	ARG
1	A	18	LYS
1	A	28	ARG
1	A	39	GLU
1	A	78	GLN
1	A	95	LEU
1	A	99	LEU
1	A	120	VAL
1	A	128	ARG
1	A	132	ASN
1	A	157	LYS
1	A	170	ARG
1	A	174	GLU
1	A	185	LEU
1	A	190	LEU
1	A	198	LYS
1	A	213	ASN
1	A	215	LYS
1	A	221	ILE

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Mol	Chain	Res	Type
1	A	223	ASP
1	A	235	ARG
1	A	242	LEU
1	A	289	ARG
1	A	305	LEU
1	A	315	VAL
1	A	326	LEU
1	A	342	ARG
1	A	345	THR
1	A	346	LEU
1	A	365	TYR
1	A	367	ARG
1	A	375	LYS
1	A	382	LEU
1	A	398	LYS
1	A	402	GLU
1	A	414	LEU
1	B	18	LYS
1	B	56	ARG
1	B	99	LEU
1	B	120	VAL
1	B	128	ARG
1	B	157	LYS
1	B	161	LEU
1	B	164	VAL
1	B	185	LEU
1	B	190	LEU
1	B	198	LYS
1	B	212	GLU
1	B	213	ASN
1	B	214	LEU
1	B	217	LYS
1	B	238	VAL
1	B	250	LYS
1	B	267	LYS
1	B	270	LYS
1	B	278	THR
1	B	294	TYR
1	B	305	LEU
1	B	311	LYS
1	B	315	VAL
1	B	326	LEU

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Mol	Chain	Res	Type
1	B	345	THR
1	B	365	TYR
1	B	367	ARG
1	B	382	LEU
1	B	385	LEU
1	B	398	LYS
1	B	412	VAL
1	B	413	LYS
1	B	414	LEU
1	C	43	LYS
1	C	51	ARG
1	C	56	ARG
1	C	95	LEU
1	C	99	LEU
1	C	132	ASN
1	C	157	LYS
1	C	174	GLU
1	C	177	SER
1	C	185	LEU
1	C	190	LEU
1	C	215	LYS
1	C	225	ASP
1	C	238	VAL
1	C	246	LEU
1	C	261	ARG
1	C	267	LYS
1	C	270	LYS
1	C	280	VAL
1	C	294	TYR
1	C	305	LEU
1	C	309	GLU
1	C	315	VAL
1	C	326	LEU
1	C	345	THR
1	C	346	LEU
1	C	347	SER
1	C	365	TYR
1	C	367	ARG
1	C	375	LYS
1	C	382	LEU
1	C	402	GLU
1	C	414	LEU

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Mol	Chain	Res	Type
1	D	24	SER
1	D	39	GLU
1	D	41	LYS
1	D	63	ASP
1	D	95	LEU
1	D	99	LEU
1	D	128	ARG
1	D	132	ASN
1	D	156	GLU
1	D	161	LEU
1	D	162	CYS
1	D	164	VAL
1	D	170	ARG
1	D	174	GLU
1	D	185	LEU
1	D	190	LEU
1	D	213	ASN
1	D	215	LYS
1	D	216	LEU
1	D	224	GLU
1	D	228	THR
1	D	238	VAL
1	D	250	LYS
1	D	253	LYS
1	D	263	ARG
1	D	265	VAL
1	D	270	LYS
1	D	280	VAL
1	D	288	LYS
1	D	289	ARG
1	D	293	MET
1	D	305	LEU
1	D	311	LYS
1	D	315	VAL
1	D	326	LEU
1	D	345	THR
1	D	346	LEU
1	D	365	TYR
1	D	367	ARG
1	D	378	LYS
1	D	398	LYS
1	D	402	GLU

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Mol	Chain	Res	Type
1	D	410	GLU
1	E	33	ILE
1	E	40	GLU
1	E	43	LYS
1	E	58	LYS
1	E	95	LEU
1	E	99	LEU
1	E	120	VAL
1	E	128	ARG
1	E	129	LYS
1	E	185	LEU
1	E	190	LEU
1	E	198	LYS
1	E	238	VAL
1	E	246	LEU
1	E	264	GLU
1	E	275	LYS
1	E	281	GLU
1	E	289	ARG
1	E	293	MET
1	E	294	TYR
1	E	295	SER
1	E	305	LEU
1	E	315	VAL
1	E	326	LEU
1	E	345	THR
1	E	346	LEU
1	E	367	ARG
1	E	375	LYS
1	E	398	LYS
1	E	402	GLU
1	E	414	LEU
1	F	1	MET
1	F	18	LYS
1	F	44	ILE
1	F	56	ARG
1	F	99	LEU
1	F	132	ASN
1	F	166	ILE
1	F	170	ARG
1	F	174	GLU
1	F	175	MET

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Mol	Chain	Res	Type
1	F	177	SER
1	F	179	ARG
1	F	185	LEU
1	F	190	LEU
1	F	208	GLU
1	F	212	GLU
1	F	215	LYS
1	F	223	ASP
1	F	233	SER
1	F	238	VAL
1	F	242	LEU
1	F	243	ARG
1	F	253	LYS
1	F	259	GLU
1	F	261	ARG
1	F	264	GLU
1	F	270	LYS
1	F	275	LYS
1	F	277	ARG
1	F	281	GLU
1	F	285	GLU
1	F	287	THR
1	F	293	MET
1	F	295	SER
1	F	311	LYS
1	F	315	VAL
1	F	326	LEU
1	F	346	LEU
1	F	365	TYR
1	F	367	ARG
1	F	382	LEU
1	F	398	LYS
1	F	402	GLU
1	F	406	GLU
1	F	414	LEU
1	G	24	SER
1	G	43	LYS
1	G	85	LYS
1	G	95	LEU
1	G	96	LYS
1	G	99	LEU
1	G	120	VAL

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Mol	Chain	Res	Type
1	G	157	LYS
1	G	161	LEU
1	G	164	VAL
1	G	185	LEU
1	G	190	LEU
1	G	225	ASP
1	G	238	VAL
1	G	246	LEU
1	G	265	VAL
1	G	275	LYS
1	G	278	THR
1	G	280	VAL
1	G	281	GLU
1	G	285	GLU
1	G	289	ARG
1	G	305	LEU
1	G	311	LYS
1	G	315	VAL
1	G	326	LEU
1	G	345	THR
1	G	365	TYR
1	G	367	ARG
1	G	375	LYS
1	G	382	LEU
1	G	398	LYS
1	G	402	GLU
1	G	409	ARG
1	G	413	LYS
1	G	414	LEU
1	H	15	GLU
1	H	18	LYS
1	H	41	LYS
1	H	50	LYS
1	H	55	ASP
1	H	58	LYS
1	H	95	LEU
1	H	99	LEU
1	H	132	ASN
1	H	154	GLU
1	H	156	GLU
1	H	161	LEU
1	H	164	VAL

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Mol	Chain	Res	Type
1	H	174	GLU
1	H	185	LEU
1	H	190	LEU
1	H	204	GLU
1	H	214	LEU
1	H	216	LEU
1	H	238	VAL
1	H	243	ARG
1	H	253	LYS
1	H	263	ARG
1	H	267	LYS
1	H	271	GLU
1	H	280	VAL
1	H	285	GLU
1	H	287	THR
1	H	289	ARG
1	H	292	SER
1	H	293	MET
1	H	295	SER
1	H	305	LEU
1	H	311	LYS
1	H	315	VAL
1	H	326	LEU
1	H	345	THR
1	H	365	TYR
1	H	367	ARG
1	H	375	LYS
1	H	398	LYS
1	H	399	ASP
1	H	402	GLU
1	H	412	VAL
1	H	414	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	0	HIS
1	A	191	ASN
1	A	300	HIS
1	A	320	ASN
1	B	132	ASN
1	B	320	ASN

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Mol	Chain	Res	Type
1	C	42	GLN
1	C	213	ASN
1	D	42	GLN
1	D	191	ASN
1	D	300	HIS
1	D	320	ASN
1	E	42	GLN
1	E	191	ASN
1	E	300	HIS
1	E	320	ASN
1	F	42	GLN
1	F	213	ASN
1	F	320	ASN
1	G	320	ASN
1	H	42	GLN
1	H	300	HIS
1	H	320	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

18 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	NAD	A	1416	-	41,48,48	1.72	3 (7%)	43,73,73	2.04	7 (16%)
3	G6P	A	1417	-	16,16,16	0.71	0	24,24,24	1.21	2 (8%)
4	SO4	A	1418	-	4,4,4	0.46	0	6,6,6	0.51	0
2	NAD	B	1416	-	41,48,48	1.74	3 (7%)	43,73,73	1.81	3 (6%)
3	G6P	B	1417	-	16,16,16	0.43	0	24,24,24	0.70	0
2	NAD	C	1416	-	41,48,48	1.71	3 (7%)	43,73,73	1.99	4 (9%)
3	G6P	C	1417	-	16,16,16	0.70	0	24,24,24	1.14	1 (4%)
4	SO4	C	1418	-	4,4,4	0.68	0	6,6,6	0.39	0
2	NAD	D	1416	-	41,48,48	1.71	3 (7%)	43,73,73	1.79	3 (6%)
3	G6P	D	1417	-	16,16,16	0.41	0	24,24,24	0.96	1 (4%)
2	NAD	E	1416	-	41,48,48	1.68	3 (7%)	43,73,73	1.85	3 (6%)
3	G6P	E	1417	-	16,16,16	0.55	0	24,24,24	0.85	0
2	NAD	F	1416	-	41,48,48	1.65	3 (7%)	43,73,73	1.87	1 (2%)
3	G6P	F	1417	-	16,16,16	0.48	0	24,24,24	1.00	2 (8%)
2	NAD	G	1416	-	41,48,48	1.70	3 (7%)	43,73,73	1.94	5 (11%)
3	G6P	G	1417	-	16,16,16	0.62	0	24,24,24	1.02	2 (8%)
2	NAD	H	1416	-	41,48,48	1.60	3 (7%)	43,73,73	1.88	3 (6%)
3	G6P	H	1417	-	16,16,16	0.43	0	24,24,24	1.00	1 (4%)

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	NAD	A	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	A	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
4	SO4	A	1418	-	-	0/0/0/0	0/0/0/0
2	NAD	B	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	B	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
2	NAD	C	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	C	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
4	SO4	C	1418	-	-	0/0/0/0	0/0/0/0
2	NAD	D	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	D	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
2	NAD	E	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	E	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
2	NAD	F	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	F	1417	-	1/1/6/6	0/6/26/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAD	G	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	G	1417	-	1/1/6/6	0/6/26/26	0/1/1/1
2	NAD	H	1416	-	-	0/22/62/62	0/5/5/5
3	G6P	H	1417	-	1/1/6/6	0/6/26/26	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1416	NAD	C2A-N1A	2.26	1.38	1.33
2	G	1416	NAD	C2A-N1A	2.44	1.38	1.33
2	F	1416	NAD	C2A-N1A	2.55	1.38	1.33
2	D	1416	NAD	C2A-N1A	2.66	1.38	1.33
2	A	1416	NAD	C2A-N1A	2.67	1.38	1.33
2	C	1416	NAD	C2A-N1A	2.72	1.39	1.33
2	E	1416	NAD	C2A-N1A	2.84	1.39	1.33
2	B	1416	NAD	C2A-N1A	2.96	1.39	1.33
2	H	1416	NAD	C2A-N3A	3.17	1.37	1.32
2	F	1416	NAD	C2A-N3A	3.39	1.37	1.32
2	A	1416	NAD	C2A-N3A	3.40	1.37	1.32
2	D	1416	NAD	C2A-N3A	3.57	1.38	1.32
2	G	1416	NAD	C2A-N3A	3.60	1.38	1.32
2	B	1416	NAD	C2A-N3A	3.73	1.38	1.32
2	E	1416	NAD	C2A-N3A	3.76	1.38	1.32
2	C	1416	NAD	C2A-N3A	3.98	1.38	1.32
2	H	1416	NAD	O7N-C7N	8.24	1.41	1.24
2	F	1416	NAD	O7N-C7N	8.42	1.41	1.24
2	E	1416	NAD	O7N-C7N	8.44	1.41	1.24
2	C	1416	NAD	O7N-C7N	8.50	1.41	1.24
2	A	1416	NAD	O7N-C7N	8.62	1.42	1.24
2	D	1416	NAD	O7N-C7N	8.79	1.42	1.24
2	G	1416	NAD	O7N-C7N	8.80	1.42	1.24
2	B	1416	NAD	O7N-C7N	8.99	1.42	1.24

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1416	NAD	N3A-C2A-N1A	-11.24	119.07	128.86
2	F	1416	NAD	N3A-C2A-N1A	-10.89	119.37	128.86
2	G	1416	NAD	N3A-C2A-N1A	-10.81	119.44	128.86
2	H	1416	NAD	N3A-C2A-N1A	-10.56	119.66	128.86
2	E	1416	NAD	N3A-C2A-N1A	-10.47	119.74	128.86
2	A	1416	NAD	N3A-C2A-N1A	-10.45	119.76	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1416	NAD	N3A-C2A-N1A	-10.34	119.86	128.86
2	D	1416	NAD	N3A-C2A-N1A	-9.74	120.38	128.86
2	H	1416	NAD	C4B-O4B-C1B	-3.65	105.88	109.77
2	A	1416	NAD	C4B-O4B-C1B	-3.60	105.94	109.77
2	D	1416	NAD	C4B-O4B-C1B	-2.96	106.62	109.77
2	A	1416	NAD	C1B-N9A-C4A	-2.94	121.56	126.64
2	C	1416	NAD	C4B-O4B-C1B	-2.85	106.74	109.77
2	C	1416	NAD	C1B-N9A-C4A	-2.55	122.23	126.64
3	D	1417	G6P	C1-C2-C3	-2.44	106.25	110.65
2	D	1416	NAD	C4A-C5A-N7A	-2.41	107.08	109.41
2	A	1416	NAD	C4A-C5A-N7A	-2.35	107.14	109.41
2	G	1416	NAD	C4B-O4B-C1B	-2.33	107.28	109.77
2	B	1416	NAD	C4B-O4B-C1B	-2.31	107.31	109.77
2	A	1416	NAD	O7N-C7N-N7N	-2.20	119.45	122.58
2	G	1416	NAD	O3B-C3B-C4B	-2.11	104.93	111.09
2	E	1416	NAD	C4B-O4B-C1B	-2.05	107.59	109.77
2	G	1416	NAD	C1B-N9A-C4A	-2.01	123.17	126.64
3	A	1417	G6P	C4-C3-C2	-2.00	107.31	110.84
3	G	1417	G6P	O2P-P-O6	2.04	112.15	106.73
3	F	1417	G6P	C3-C4-C5	2.07	113.86	110.22
3	F	1417	G6P	O5-C5-C4	2.07	113.47	109.66
2	B	1416	NAD	O7N-C7N-C3N	2.16	122.15	119.62
2	H	1416	NAD	O5D-C5D-C4D	2.18	116.74	109.00
3	G	1417	G6P	P-O6-C6	2.19	124.34	118.30
3	C	1417	G6P	O2-C2-C1	2.28	114.48	109.75
2	C	1416	NAD	C3N-C7N-N7N	2.31	120.41	117.77
2	E	1416	NAD	C4D-O4D-C1D	2.51	112.44	109.77
2	G	1416	NAD	O7N-C7N-C3N	2.57	122.64	119.62
2	A	1416	NAD	O7N-C7N-C3N	2.60	122.66	119.62
3	H	1417	G6P	O5-C5-C4	2.62	114.48	109.66
2	A	1416	NAD	C4D-O4D-C1D	2.78	112.73	109.77
3	A	1417	G6P	O2P-P-O6	3.14	115.09	106.73

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	H	1417	G6P	C1
3	A	1417	G6P	C1
3	G	1417	G6P	C1
3	D	1417	G6P	C1
3	F	1417	G6P	C1
3	C	1417	G6P	C1

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Mol	Chain	Res	Type	Atom
3	E	1417	G6P	C1
3	B	1417	G6P	C1

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	1417	G6P	2	0
2	E	1416	NAD	1	0
2	F	1416	NAD	2	0
3	H	1417	G6P	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 ⓘ

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	414/417 (99%)	-0.16	16 (3%)	40	39	13, 19, 26, 58	3 (0%)
1	B	409/417 (98%)	-0.01	22 (5%)	26	25	12, 19, 25, 31	22 (5%)
1	C	409/417 (98%)	-0.22	7 (1%)	70	68	13, 19, 25, 31	13 (3%)
1	D	409/417 (98%)	-0.16	16 (3%)	40	39	13, 19, 27, 39	18 (4%)
1	E	406/417 (97%)	0.24	32 (7%)	13	12	13, 19, 24, 30	41 (10%)
1	F	411/417 (98%)	0.09	24 (5%)	24	22	13, 19, 25, 36	31 (7%)
1	G	409/417 (98%)	-0.15	16 (3%)	40	39	13, 19, 25, 30	22 (5%)
1	H	407/417 (97%)	0.00	23 (5%)	24	23	13, 19, 26, 36	25 (6%)
All	All	3274/3336 (98%)	-0.05	156 (4%)	31	30	12, 19, 25, 58	175 (5%)

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	221	ILE	6.7
1	F	216	LEU	5.9
1	A	222	PRO	5.8
1	F	222	PRO	5.3
1	A	223	ASP	5.3
1	D	223	ASP	5.3
1	B	216	LEU	5.0
1	E	223	ASP	4.9
1	E	287	THR	4.8
1	E	293	MET	4.7
1	E	292	SER	4.5
1	H	291	GLY	4.3
1	B	278	THR	4.3
1	C	216	LEU	4.2
1	D	287	THR	4.1
1	H	177	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	E	213	ASN	4.1
1	F	224	GLU	4.0
1	F	292	SER	4.0
1	A	216	LEU	4.0
1	E	294	TYR	4.0
1	E	224	GLU	4.0
1	G	224	GLU	3.9
1	B	287	THR	3.9
1	C	278	THR	3.8
1	B	292	SER	3.8
1	F	284	GLU	3.7
1	H	280	VAL	3.6
1	F	293	MET	3.6
1	B	217	LYS	3.6
1	G	287	THR	3.5
1	B	213	ASN	3.5
1	E	272	LEU	3.5
1	A	-1	ARG	3.4
1	B	224	GLU	3.4
1	H	286	LEU	3.4
1	E	45	VAL	3.3
1	D	290	GLY	3.3
1	G	415	GLY	3.3
1	F	287	THR	3.3
1	A	0	HIS	3.2
1	E	38	ASP	3.2
1	H	26	ASP	3.2
1	B	225	ASP	3.2
1	C	25	GLU	3.1
1	D	291	GLY	3.1
1	D	286	LEU	3.1
1	D	294	TYR	3.1
1	F	290	GLY	3.1
1	G	26	ASP	3.1
1	G	216	LEU	3.1
1	D	288	LYS	3.0
1	F	217	LYS	3.0
1	D	26	ASP	3.0
1	E	30	ASP	3.0
1	H	24	SER	3.0
1	H	287	THR	3.0
1	F	213	ASN	3.0

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Mol	Chain	Res	Type	RSRZ
1	H	290	GLY	3.0
1	G	409	ARG	3.0
1	E	282	ILE	2.9
1	G	292	SER	2.9
1	H	214	LEU	2.9
1	H	224	GLU	2.9
1	F	288	LYS	2.9
1	G	286	LEU	2.8
1	B	24	SER	2.8
1	H	410	GLU	2.8
1	D	55	ASP	2.8
1	H	130	THR	2.8
1	E	216	LEU	2.8
1	E	169	ILE	2.8
1	B	279	ALA	2.7
1	F	223	ASP	2.7
1	A	288	LYS	2.7
1	F	266	MET	2.7
1	E	39	GLU	2.6
1	F	409	ARG	2.6
1	E	286	LEU	2.6
1	H	289	ARG	2.6
1	E	26	ASP	2.6
1	A	294	TYR	2.6
1	G	290	GLY	2.6
1	E	163	ASN	2.6
1	B	30	ASP	2.6
1	F	259	GLU	2.6
1	B	25	GLU	2.5
1	C	224	GLU	2.5
1	E	173	ALA	2.5
1	F	415	GLY	2.5
1	B	291	GLY	2.5
1	B	54	LYS	2.5
1	D	214	LEU	2.5
1	H	45	VAL	2.5
1	F	277	ARG	2.5
1	A	217	LYS	2.5
1	C	225	ASP	2.5
1	F	286	LEU	2.5
1	B	293	MET	2.5
1	E	225	ASP	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	63	ASP	2.4
1	C	26	ASP	2.4
1	G	294	TYR	2.4
1	E	167	ASN	2.4
1	E	28	ARG	2.4
1	B	28	ARG	2.4
1	A	25	GLU	2.4
1	E	174	GLU	2.4
1	H	44	ILE	2.4
1	G	284	GLU	2.4
1	H	132	ASN	2.4
1	G	179	ARG	2.4
1	E	212	GLU	2.3
1	H	281	GLU	2.3
1	G	213	ASN	2.3
1	D	289	ARG	2.3
1	D	224	GLU	2.3
1	A	5	VAL	2.3
1	D	216	LEU	2.3
1	E	283	PRO	2.2
1	H	28	ARG	2.2
1	A	281	GLU	2.2
1	B	258	HIS	2.2
1	E	22	ASP	2.2
1	G	225	ASP	2.2
1	A	215	LYS	2.2
1	A	212	GLU	2.2
1	B	282	ILE	2.2
1	H	274	GLU	2.2
1	H	216	LEU	2.2
1	A	177	SER	2.2
1	F	5	VAL	2.2
1	A	292	SER	2.2
1	H	129	LYS	2.1
1	G	228	THR	2.1
1	H	57	PHE	2.1
1	C	287	THR	2.1
1	E	271	GLU	2.1
1	E	284	GLU	2.1
1	D	70	VAL	2.1
1	F	280	VAL	2.1
1	E	76	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	291	GLY	2.1
1	F	257	THR	2.1
1	F	3	ILE	2.1
1	G	258	HIS	2.1
1	B	272	LEU	2.1
1	E	20	LEU	2.1
1	B	26	ASP	2.0
1	D	24	SER	2.0
1	D	284	GLU	2.0
1	H	292	SER	2.0
1	B	288	LYS	2.0
1	E	1	MET	2.0
1	F	375	LYS	2.0
1	F	71	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	SO4	A	1418	5/5	0.81	0.25	9.06	57,59,61,62	0
4	SO4	C	1418	5/5	0.83	0.20	5.09	53,54,61,63	0
2	NAD	F	1416	44/44	0.92	0.37	3.68	21,35,41,45	44
2	NAD	H	1416	44/44	0.93	0.44	3.22	24,28,35,39	44
3	G6P	C	1417	16/16	0.93	0.31	2.08	58,69,71,71	0
3	G6P	B	1417	16/16	0.91	0.31	1.53	37,42,45,45	16
2	NAD	E	1416	44/44	0.87	0.31	1.51	31,33,39,41	44

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	G6P	G	1417	16/16	0.88	0.30	1.49	62,70,71,71	0
3	G6P	F	1417	16/16	0.83	0.30	1.23	47,52,54,55	16
3	G6P	A	1417	16/16	0.90	0.25	1.20	46,58,60,60	0
3	G6P	E	1417	16/16	0.82	0.31	1.16	36,39,40,40	16
3	G6P	H	1417	16/16	0.85	0.28	0.95	43,48,49,51	16
3	G6P	D	1417	16/16	0.86	0.26	0.56	43,47,48,49	16
2	NAD	D	1416	44/44	0.96	0.11	-0.78	31,44,54,55	0
2	NAD	B	1416	44/44	0.96	0.12	-0.86	34,52,64,69	0
2	NAD	G	1416	44/44	0.97	0.10	-0.95	30,48,59,62	0
2	NAD	C	1416	44/44	0.97	0.10	-1.00	24,41,53,59	0
2	NAD	A	1416	44/44	0.98	0.09	-1.14	21,35,49,52	0

6.5 Other polymers [i](#)

There are no such residues in this entry.