



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:18 PM UTC

PDB ID : 1H8F / pdb_00001h8f
Title : Glycogen Synthase Kinase 3 beta.
Authors : Dajani, R.; Pearl, L.H.; Roe, S.M.
Deposited on : 2001-02-05
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

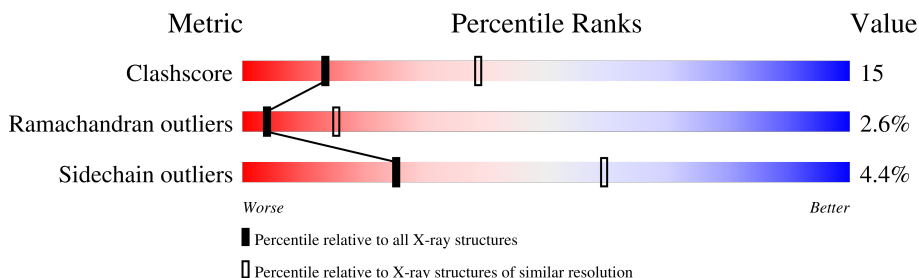
1 Overall quality at a glance

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	352	 74% 22% . .
1	B	352	 71% 24% . ..

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	EPE	A	400	-	-	X	-
2	EPE	B	400	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 5786 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.

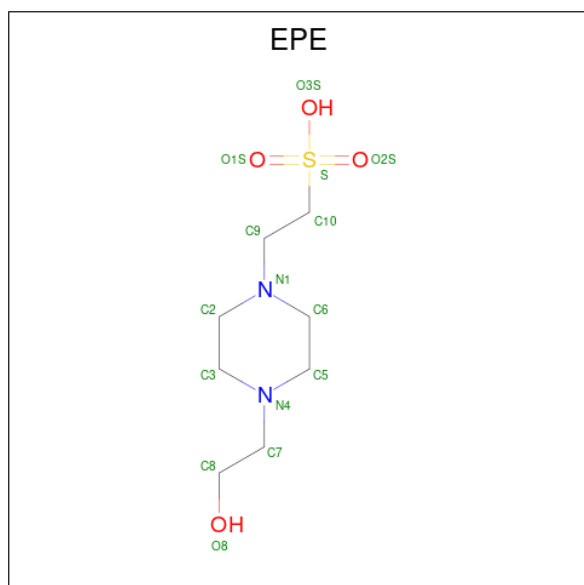
- Molecule 1 is a protein called GLYCOGEN SYNTHASE KINASE-3 BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	352	Total	C	N	O	S	0	0	0
			2805	1804	480	510	11			
1	B	350	Total	C	N	O	S	0	0	0
			2790	1796	477	506	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	292	ALA	LYS	conflict	UNP P49841
A	350	LEU	HIS	conflict	UNP P49841
B	292	ALA	LYS	conflict	UNP P49841
B	350	LEU	HIS	conflict	UNP P49841

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	82	Total	O	0	0
			82	82		
3	B	79	Total	O	0	0
			79	79		

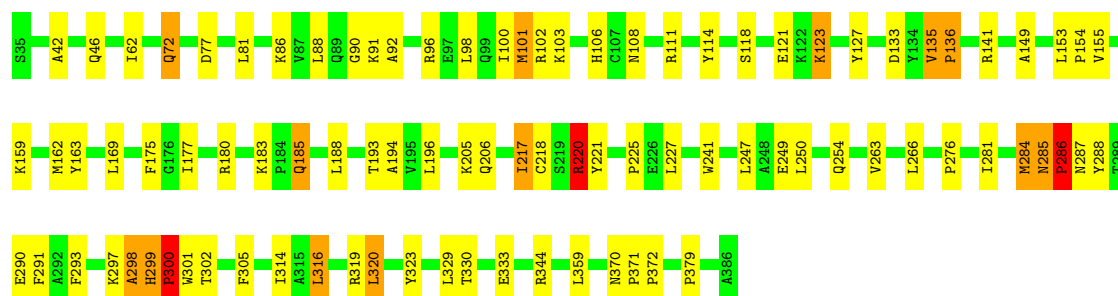
3 Residue-property plots

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.

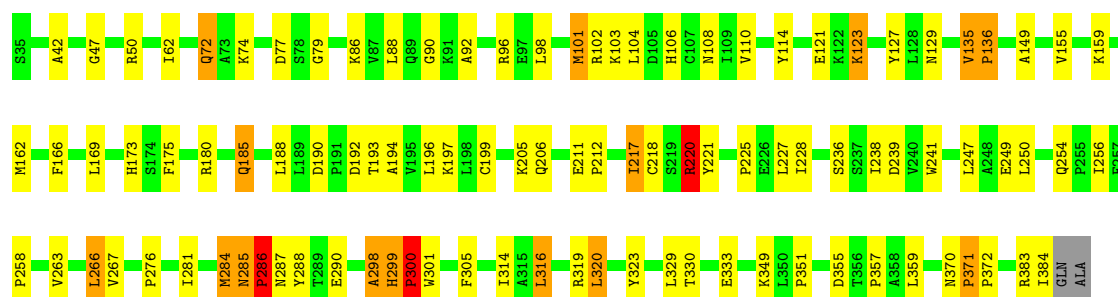
• Molecule 1: GLYCOGEN SYNTHASE KINASE-3 BETA

Chain A: 



• Molecule 1: GLYCOGEN SYNTHASE KINASE-3 BETA

Chain B: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.20Å 86.06Å 178.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.12 – 2.80	Depositor
% Data completeness (in resolution range)	99.9 (35.12-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.220 , 0.256	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5786	wwPDB-VP
Average B, all atoms (Å ²)	58.0	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: EPE

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	0.49	0/2876	0.95	8/3913 (0.2%)
1	B	0.50	0/2861	0.94	15/3894 (0.4%)
All	All	0.49	0/5737	0.94	23/7807 (0.3%)

There are no bond length outliers.

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	299	HIS	CA-C-N	7.78	129.56	119.84
1	B	299	HIS	C-N-CA	7.78	129.56	119.84
1	A	299	HIS	CA-C-N	7.56	129.29	119.84
1	A	299	HIS	C-N-CA	7.56	129.29	119.84
1	B	284	MET	N-CA-C	-6.90	104.73	113.01
1	A	284	MET	N-CA-C	-6.77	104.89	113.01
1	B	149	ALA	N-CA-C	-6.07	103.48	113.50
1	A	149	ALA	N-CA-C	-5.98	103.64	113.50
1	B	220	ARG	N-CA-C	5.94	123.45	110.80
1	A	220	ARG	N-CA-C	5.70	122.93	110.80
1	B	135	VAL	CA-C-N	5.60	126.84	119.84
1	B	135	VAL	C-N-CA	5.60	126.84	119.84
1	A	135	VAL	CA-C-N	5.36	126.54	119.84
1	A	135	VAL	C-N-CA	5.36	126.54	119.84
1	B	298	ALA	N-CA-C	5.27	117.86	109.96
1	B	104	LEU	N-CA-C	5.26	117.54	109.07
1	B	371	PRO	N-CA-C	5.19	117.03	110.70
1	B	192	ASP	N-CA-C	5.18	116.73	111.14
1	B	190	ASP	CA-C-N	5.17	124.62	119.24
1	B	190	ASP	C-N-CA	5.17	124.62	119.24
1	A	298	ALA	N-CA-C	5.17	117.71	109.96
1	B	50	ARG	CA-C-N	5.06	125.06	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	50	ARG	C-N-CA	5.06	125.06	119.90

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2805	0	2829	78	0
1	B	2790	0	2816	89	0
2	A	15	0	18	7	0
2	B	15	0	18	7	0
3	A	82	0	0	4	0
3	B	79	0	0	2	0
All	All	5786	0	5681	165	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 15.

All (165) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:185:GLN:HE21	1:B:185:GLN:H	0.98	0.96
1:A:185:GLN:H	1:A:185:GLN:HE21	1.03	0.96
1:A:220:ARG:CD	1:A:221:TYR:H	1.83	0.90
1:B:220:ARG:CD	1:B:221:TYR:H	1.88	0.87
1:A:220:ARG:HD3	1:A:221:TYR:H	1.39	0.86
1:B:185:GLN:HE21	1:B:185:GLN:N	1.75	0.84
1:B:220:ARG:HD3	1:B:221:TYR:H	1.41	0.84
1:A:185:GLN:HE21	1:A:185:GLN:N	1.77	0.83
2:A:400:EPE:H82	1:B:263:VAL:HG11	1.63	0.81
1:B:96:ARG:HH12	2:B:400:EPE:H101	1.46	0.80
1:A:220:ARG:HG2	1:A:220:ARG:HH11	1.46	0.80
1:A:263:VAL:HG11	2:B:400:EPE:H82	1.62	0.79
1:B:220:ARG:HG2	1:B:220:ARG:HH11	1.47	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ARG:HH12	2:A:400:EPE:H101	1.51	0.75
1:B:319:ARG:HB3	1:B:329:LEU:HD13	1.70	0.73
1:A:185:GLN:H	1:A:185:GLN:NE2	1.85	0.73
1:A:285:ASN:HB3	1:A:286:PRO:HD3	1.72	0.71
1:B:284:MET:O	1:B:286:PRO:HD2	1.90	0.71
1:B:370:ASN:HD22	1:B:372:PRO:HD2	1.55	0.70
1:B:285:ASN:HB3	1:B:286:PRO:HD3	1.73	0.69
1:A:276:PRO:HG3	1:A:323:TYR:CZ	2.27	0.69
1:B:185:GLN:H	1:B:185:GLN:NE2	1.82	0.68
1:A:106:HIS:HD2	1:A:108:ASN:H	1.43	0.68
1:A:319:ARG:HB3	1:A:329:LEU:HD13	1.77	0.67
1:B:281:ILE:HA	1:B:284:MET:HE3	1.78	0.66
1:B:276:PRO:HG3	1:B:323:TYR:CZ	2.32	0.64
1:B:106:HIS:CD2	1:B:108:ASN:H	2.16	0.64
1:A:284:MET:O	1:A:286:PRO:HD2	1.96	0.64
1:A:106:HIS:CD2	1:A:108:ASN:H	2.17	0.63
1:B:196:LEU:C	1:B:196:LEU:HD23	2.23	0.63
1:B:285:ASN:O	1:B:286:PRO:C	2.41	0.63
1:B:106:HIS:HD2	1:B:108:ASN:H	1.46	0.63
1:A:281:ILE:HA	1:A:284:MET:HE3	1.82	0.62
1:B:162:MET:HE2	1:B:247:LEU:HB2	1.80	0.62
1:A:285:ASN:O	1:A:286:PRO:C	2.42	0.62
1:B:180:ARG:HH22	2:B:400:EPE:H102	1.65	0.61
1:A:220:ARG:HD2	1:A:221:TYR:H	1.63	0.60
1:B:285:ASN:HB3	1:B:286:PRO:CD	2.32	0.59
1:A:298:ALA:O	1:A:300:PRO:HD3	2.02	0.59
1:A:217:ILE:H	1:A:217:ILE:HD13	1.68	0.58
1:A:162:MET:HE2	1:A:247:LEU:HB2	1.86	0.58
1:A:370:ASN:HD22	1:A:372:PRO:HD2	1.69	0.58
1:A:220:ARG:CD	1:A:221:TYR:N	2.63	0.58
1:A:285:ASN:HB3	1:A:286:PRO:CD	2.33	0.57
1:B:110:VAL:HG11	1:B:199:CYS:SG	2.44	0.56
1:B:220:ARG:HG2	1:B:220:ARG:NH1	2.20	0.56
1:B:90:GLY:C	1:B:92:ALA:H	2.13	0.55
1:A:180:ARG:HH22	2:A:400:EPE:H102	1.70	0.55
1:A:300:PRO:HB2	3:A:2064:HOH:O	2.05	0.55
1:A:90:GLY:C	1:A:92:ALA:H	2.14	0.55
1:A:196:LEU:C	1:A:196:LEU:HD23	2.31	0.54
1:A:220:ARG:HG2	1:A:220:ARG:NH1	2.19	0.54
1:B:316:LEU:HD22	1:B:320:LEU:HD22	1.89	0.54
1:B:370:ASN:HD22	1:B:370:ASN:C	2.17	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:ARG:HD2	1:B:221:TYR:H	1.70	0.53
1:A:96:ARG:HH12	2:A:400:EPE:C10	2.19	0.53
1:A:121:GLU:C	1:A:123:LYS:H	2.17	0.53
1:A:302:THR:HB	3:A:2064:HOH:O	2.08	0.53
1:B:96:ARG:HH12	2:B:400:EPE:C10	2.19	0.53
1:A:286:PRO:C	1:A:288:TYR:H	2.16	0.53
1:B:217:ILE:H	1:B:217:ILE:HD13	1.74	0.53
1:B:370:ASN:ND2	1:B:372:PRO:HD2	2.22	0.53
1:B:62:ILE:HD13	1:B:72:GLN:HB2	1.91	0.53
1:B:298:ALA:O	1:B:300:PRO:HD3	2.10	0.52
1:B:286:PRO:C	1:B:288:TYR:H	2.16	0.52
1:A:183:LYS:NZ	3:A:2030:HOH:O	2.43	0.51
1:B:286:PRO:O	1:B:288:TYR:N	2.38	0.51
1:A:316:LEU:HD22	1:A:320:LEU:HD22	1.92	0.50
1:A:370:ASN:HD22	1:A:370:ASN:C	2.20	0.50
1:A:276:PRO:HG3	1:A:323:TYR:CE2	2.47	0.50
1:A:62:ILE:HD13	1:A:72:GLN:HB2	1.94	0.50
1:A:88:LEU:HD12	1:A:127:TYR:HE2	1.76	0.50
1:A:155:VAL:HG12	1:A:159:LYS:HE3	1.94	0.49
1:A:42:ALA:HB1	1:A:114:TYR:HB3	1.94	0.49
1:A:98:LEU:O	1:A:102:ARG:HG3	2.12	0.49
1:B:330:THR:OG1	1:B:333:GLU:HG3	2.13	0.49
1:B:121:GLU:C	1:B:123:LYS:H	2.20	0.49
1:B:129:ASN:ND2	3:B:2019:HOH:O	2.46	0.48
1:A:225:PRO:HD3	1:A:241:TRP:CE2	2.48	0.48
1:B:228:ILE:HG21	1:B:266:LEU:HD13	1.95	0.48
1:A:286:PRO:O	1:A:288:TYR:N	2.36	0.48
1:B:155:VAL:HG12	1:B:159:LYS:HE3	1.95	0.47
1:A:330:THR:OG1	1:A:333:GLU:HG3	2.15	0.47
1:A:371:PRO:HB2	1:A:372:PRO:HD3	1.97	0.47
1:A:103:LYS:O	1:A:103:LYS:HG2	2.14	0.47
2:A:400:EPE:H82	1:B:263:VAL:CG1	2.41	0.47
1:B:276:PRO:HG3	1:B:323:TYR:CE2	2.50	0.46
1:A:344:ARG:HG2	1:A:379:PRO:HG3	1.96	0.46
1:B:301:TRP:HB3	1:B:314:ILE:HG23	1.97	0.46
1:B:217:ILE:O	1:B:218:CYS:CB	2.62	0.46
1:B:288:TYR:C	1:B:290:GLU:N	2.72	0.46
1:B:193:THR:O	1:B:194:ALA:HB3	2.15	0.46
1:A:96:ARG:NH1	2:A:400:EPE:H101	2.27	0.45
1:A:220:ARG:HD2	1:A:221:TYR:N	2.27	0.45
1:B:88:LEU:HD12	1:B:127:TYR:HE2	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:THR:O	1:A:194:ALA:HB3	2.17	0.45
1:B:135:VAL:HB	1:B:188:LEU:HB3	1.99	0.45
1:B:220:ARG:CD	1:B:221:TYR:N	2.67	0.45
1:B:371:PRO:HB2	1:B:372:PRO:HD3	1.99	0.45
1:B:42:ALA:HB1	1:B:114:TYR:HB3	1.98	0.45
1:B:225:PRO:HD3	1:B:241:TRP:CE2	2.52	0.45
1:A:263:VAL:CG1	2:B:400:EPE:H82	2.38	0.45
1:A:86:LYS:HD2	3:A:2005:HOH:O	2.16	0.44
1:B:72:GLN:HE21	1:B:72:GLN:HB3	1.59	0.44
1:B:98:LEU:O	1:B:102:ARG:HG3	2.17	0.44
1:A:217:ILE:O	1:A:218:CYS:CB	2.65	0.44
1:B:351:PRO:HD2	3:B:2023:HOH:O	2.18	0.44
1:B:263:VAL:O	1:B:267:VAL:HG23	2.17	0.44
1:A:249:GLU:HG3	1:A:254:GLN:C	2.43	0.44
1:A:220:ARG:HD3	1:A:221:TYR:CG	2.53	0.44
1:A:297:LYS:NZ	1:B:123:LYS:NZ	2.65	0.44
1:B:220:ARG:HD2	1:B:221:TYR:N	2.33	0.44
1:A:100:ILE:HG23	1:A:177:ILE:HD13	1.98	0.43
1:A:217:ILE:O	1:A:218:CYS:HB3	2.18	0.43
1:B:166:PHE:HZ	1:B:320:LEU:HD21	1.83	0.43
1:B:101:MET:HA	1:B:101:MET:HE2	2.00	0.43
1:B:249:GLU:HG3	1:B:254:GLN:C	2.43	0.43
1:A:297:LYS:HZ2	1:B:123:LYS:HZ1	1.65	0.43
1:A:72:GLN:OE1	1:A:81:LEU:HD22	2.19	0.43
1:B:196:LEU:HD23	1:B:197:LYS:N	2.33	0.43
1:B:86:LYS:HG2	1:B:129:ASN:ND2	2.33	0.43
1:B:173:HIS:CE1	1:B:236:SER:HB3	2.54	0.43
1:A:153:LEU:HD12	1:A:154:PRO:HD2	2.00	0.43
1:A:175:PHE:O	1:A:206:GLN:NE2	2.52	0.43
1:A:305:PHE:CD2	1:A:314:ILE:HG12	2.54	0.43
1:B:103:LYS:O	1:B:103:LYS:HG2	2.19	0.43
1:B:96:ARG:NH1	2:B:400:EPE:H101	2.24	0.43
1:B:357:PRO:O	1:B:359:LEU:HG	2.18	0.43
1:A:301:TRP:HB3	1:A:314:ILE:HG23	2.01	0.43
1:B:266:LEU:HD12	1:B:266:LEU:HA	1.89	0.43
1:B:180:ARG:HG2	1:B:238:ILE:HD11	2.00	0.42
1:B:238:ILE:HG13	1:B:239:ASP:N	2.34	0.42
1:B:175:PHE:O	1:B:206:GLN:NE2	2.52	0.42
1:B:319:ARG:HB3	1:B:329:LEU:CD1	2.46	0.42
1:A:288:TYR:C	1:A:290:GLU:N	2.75	0.42
1:B:256:ILE:C	1:B:258:PRO:HD3	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:285:ASN:CB	1:B:286:PRO:CD	2.98	0.42
1:A:101:MET:HA	1:A:101:MET:HE2	2.01	0.42
1:B:383:ARG:CG	1:B:384:ILE:H	2.32	0.42
1:A:118:SER:O	1:A:127:TYR:HB2	2.20	0.42
1:A:217:ILE:H	1:A:217:ILE:CD1	2.32	0.42
1:A:111:ARG:HG2	1:A:133:ASP:OD2	2.20	0.42
1:A:136:PRO:O	1:A:141:ARG:NH2	2.53	0.42
1:B:211:GLU:HA	1:B:212:PRO:HD3	1.88	0.41
1:A:205:LYS:HD2	2:A:400:EPE:O3S	2.20	0.41
1:B:217:ILE:O	1:B:218:CYS:HB3	2.21	0.41
1:A:90:GLY:O	1:A:92:ALA:N	2.53	0.41
1:A:135:VAL:HB	1:A:188:LEU:HB3	2.03	0.41
1:A:299:HIS:O	1:A:299:HIS:CG	2.73	0.41
1:A:299:HIS:O	1:A:300:PRO:O	2.39	0.41
1:B:135:VAL:HA	1:B:136:PRO:HD3	1.81	0.41
1:B:220:ARG:NH1	1:B:220:ARG:CG	2.83	0.41
1:B:349:LYS:HE2	1:B:355:ASP:OD1	2.21	0.41
1:B:370:ASN:C	1:B:370:ASN:ND2	2.79	0.41
1:B:205:LYS:HD2	2:B:400:EPE:O3S	2.21	0.40
1:B:220:ARG:HD3	1:B:221:TYR:CG	2.56	0.40
1:B:286:PRO:C	1:B:288:TYR:N	2.80	0.40
1:A:285:ASN:CB	1:A:286:PRO:CD	2.98	0.40
1:A:163:TYR:CE2	1:A:359:LEU:HB3	2.56	0.40
1:B:74:LYS:HG3	1:B:79:GLY:O	2.20	0.40
1:B:166:PHE:CZ	1:B:320:LEU:HD21	2.56	0.40
1:B:301:TRP:HB3	1:B:314:ILE:CG2	2.52	0.40
1:B:305:PHE:CD2	1:B:314:ILE:HG12	2.57	0.40
1:A:291:PHE:CE2	1:A:293:PHE:HB2	2.57	0.40
1:B:299:HIS:O	1:B:299:HIS:CG	2.75	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	350/352 (99%)	317 (91%)	24 (7%)	9 (3%)	4	15
1	B	348/352 (99%)	316 (91%)	23 (7%)	9 (3%)	4	15
All	All	698/704 (99%)	633 (91%)	47 (7%)	18 (3%)	4	15

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	LYS
1	A	285	ASN
1	A	287	ASN
1	A	300	PRO
1	B	123	LYS
1	B	220	ARG
1	B	285	ASN
1	B	300	PRO
1	A	220	ARG
1	A	286	PRO
1	B	47	GLY
1	B	286	PRO
1	B	287	ASN
1	A	77	ASP
1	A	136	PRO
1	B	136	PRO
1	B	77	ASP
1	A	91	LYS

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	310/310 (100%)	296 (96%)	14 (4%)	24	58
1	B	309/310 (100%)	296 (96%)	13 (4%)	26	61
All	All	619/620 (100%)	592 (96%)	27 (4%)	25	59

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	72	GLN
1	A	101	MET
1	A	169	LEU
1	A	185	GLN
1	A	217	ILE
1	A	220	ARG
1	A	227	LEU
1	A	250	LEU
1	A	266	LEU
1	A	286	PRO
1	A	300	PRO
1	A	316	LEU
1	A	320	LEU
1	B	72	GLN
1	B	101	MET
1	B	169	LEU
1	B	185	GLN
1	B	217	ILE
1	B	220	ARG
1	B	227	LEU
1	B	250	LEU
1	B	266	LEU
1	B	286	PRO
1	B	300	PRO
1	B	316	LEU
1	B	320	LEU

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

Mol	Chain	Res	Type
1	A	52	GLN
1	A	106	HIS
1	A	108	ASN
1	A	185	GLN
1	A	365	GLN
1	A	370	ASN
1	B	52	GLN
1	B	106	HIS
1	B	108	ASN
1	B	185	GLN
1	B	365	GLN
1	B	370	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

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	EPE	B	400	-	15,15,15	1.41	1 (6%)	19,20,20	1.14	3 (15%)
2	EPE	A	400	-	15,15,15	1.12	1 (6%)	19,20,20	1.16	2 (10%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EPE	B	400	-	-	2/9/19/19	0/1/1/1
2	EPE	A	400	-	-	3/9/19/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	EPE	C10-S	4.18	1.83	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	400	EPE	C10-S	2.23	1.80	1.77

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	400	EPE	C10-C9-N1	-2.68	102.22	112.36
2	A	400	EPE	C6-N1-C2	2.54	114.31	108.84
2	B	400	EPE	C10-C9-N1	-2.31	103.62	112.36
2	B	400	EPE	C6-N1-C2	2.29	113.77	108.84
2	B	400	EPE	O2S-S-C10	-2.09	103.56	106.73

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	400	EPE	C10-C9-N1-C2
2	B	400	EPE	C10-C9-N1-C2
2	A	400	EPE	C10-C9-N1-C6
2	B	400	EPE	C10-C9-N1-C6
2	A	400	EPE	N4-C7-C8-O8

There are no ring outliers.

2 monomers are involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	400	EPE	7	0
2	A	400	EPE	7	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](#)

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.