Full wwPDB X-ray Structure Validation Report (i)

Dec 10, 2023 – 12:28 pm GMT

PDB ID	:	1GNG
Title	:	Glycogen synthase kinase-3 beta (GSK3) complex with FRATtide peptide
Authors	:	Bax, B.; Carter, P.S.; Lewis, C.; Guy, A.R.; Bridges, A.; Tanner, R.; Pettman, G.; Mannix, C.; Culbert, A.A.; Brown, M.J.B.; Smith, D.G.; Reith, A.D.
Deposited on	:	2001-10-04
Resolution	:	2.60 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:

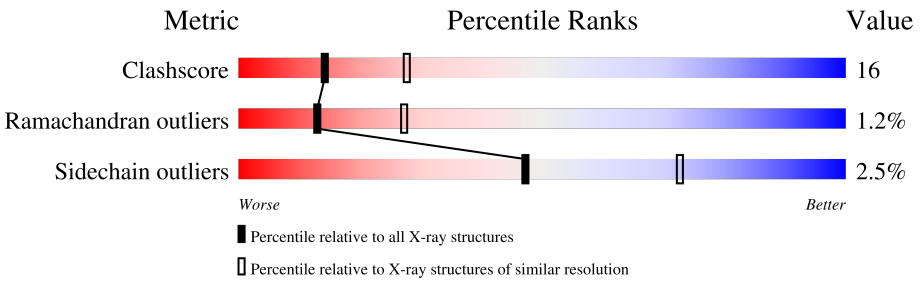
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.60 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	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	378	65% 27% • 7%
1	B	378	61% 32% • 6%
2	X	39	46% 15% 5% 33%
2	Y	39	44% 23% 33%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 6227 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
			Total	C	N	O	P	S			
1	A	350	2799	1798	480	509	1	11	0	0	1
1	B	357	2852	1826	492	522	1	11	0	0	1

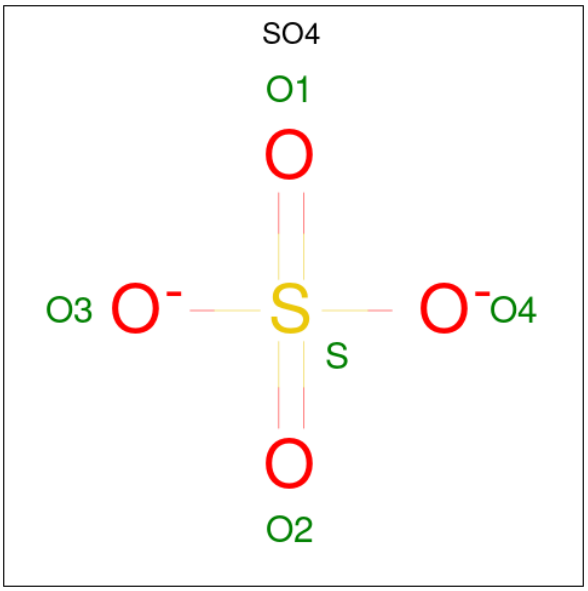
There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called FRATTIDE.

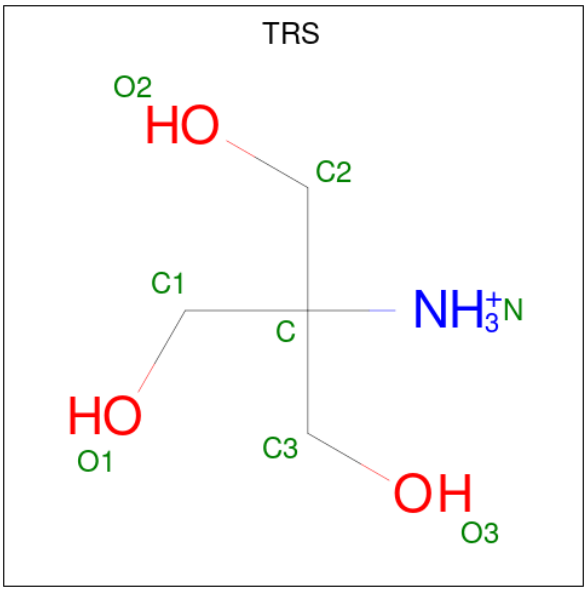
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	X	26	204	127	43	34	0	0	1
2	Y	26	204	127	43	34	0	0	1

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
4	B	1	8	4	1	3	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	76	76	76	0	0
			Total	O		
5	B	59	59	59	0	0
			Total	O		
5	X	3	3	3	0	0
			Total	O		
5	Y	2	2	2	0	0

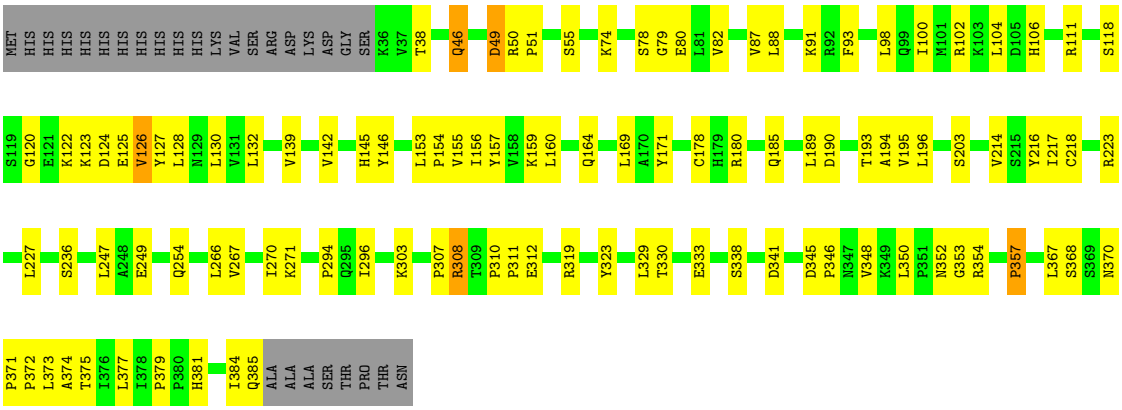
3 Residue-property plots (i)

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. 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.

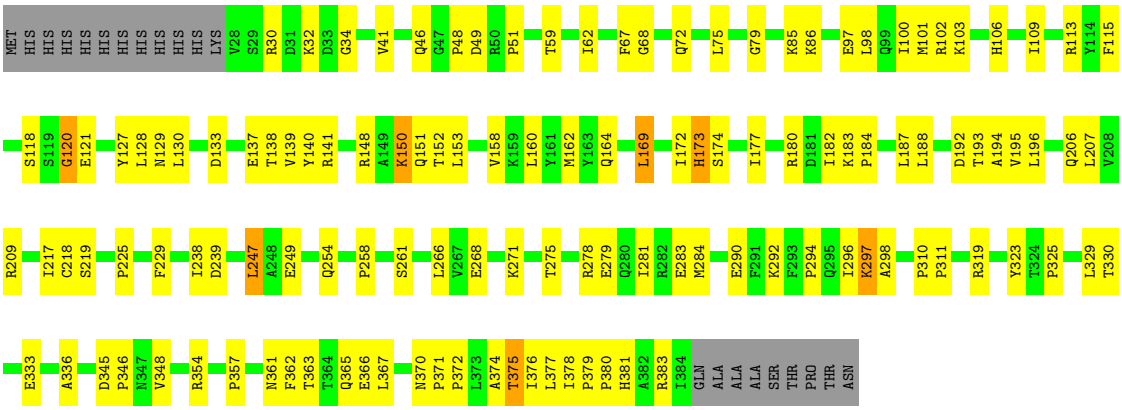
• Molecule 1: GLYCOGEN SYNTHASE KINASE-3 BETA

Chain A:



• Molecule 1: GLYCOGEN SYNTHASE KINASE-3 BETA

Chain B:

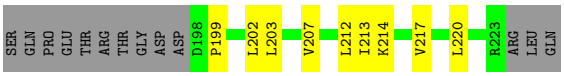


• Molecule 2: FRATTIDE

Chain X:

• Molecule 2: FRATTIDE

Chain Y:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α, β, γ	153.05Å 153.05Å 213.35Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	18.00 – 2.60	Depositor
% Data completeness (in resolution range)	99.9 (18.00-2.60)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.196 , 0.262	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6227	wwPDB-VP
Average B, all atoms (Å^2)	53.0	wwPDB-VP

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: PTR, TRS, SO4

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	0.41	0/2852	0.64	0/3880
1	B	0.42	0/2905	0.65	0/3948
2	X	0.48	0/206	0.71	0/277
2	Y	0.47	0/206	0.59	0/277
All	All	0.42	0/6169	0.64	0/8382

There are no bond length outliers.

There are no bond angle outliers.

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	2799	0	2815	83	0
1	B	2852	0	2864	104	1
2	X	204	0	217	13	0
2	Y	204	0	217	12	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
4	B	8	0	12	0	0
5	A	76	0	0	1	0
5	B	59	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	X	3	0	0	0	0
5	Y	2	0	0	0	0
All	All	6227	0	6125	190	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 16.

All (190) 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:297:LYS:HE3	1:B:298:ALA:H	0.95	1.07
1:B:297:LYS:HE3	1:B:298:ALA:N	1.73	1.04
1:A:296:ILE:HD11	2:X:217:VAL:HG13	1.52	0.90
1:B:380:PRO:HA	1:B:383:ARG:HH21	1.39	0.85
1:B:118:SER:HB2	1:B:127:TYR:HB2	1.63	0.79
1:B:346:PRO:HG3	1:B:381:HIS:CD2	2.17	0.79
1:A:130:LEU:HD12	1:A:130:LEU:H	1.48	0.78
1:A:330:THR:OG1	1:A:333:GLU:HG3	1.85	0.77
1:B:380:PRO:CA	1:B:383:ARG:HH21	1.96	0.76
1:A:346:PRO:HG3	1:A:381:HIS:CD2	2.23	0.73
1:B:151:GLN:HG2	1:B:152:THR:H	1.53	0.73
1:B:130:LEU:HD12	1:B:130:LEU:N	2.04	0.73
1:A:375:THR:HG21	1:B:372:PRO:CB	2.20	0.72
1:B:169:LEU:HD11	1:B:182:ILE:HD11	1.71	0.71
1:B:62:ILE:HD13	1:B:72:GLN:HB2	1.71	0.71
1:A:153:LEU:HD12	1:A:154:PRO:HD2	1.73	0.70
1:A:319:ARG:HB3	1:A:329:LEU:HD13	1.74	0.69
1:A:98:LEU:HB2	1:A:128:LEU:HD21	1.72	0.69
1:B:98:LEU:HD21	1:B:102:ARG:HD2	1.74	0.69
1:B:120:GLY:O	1:B:121:GLU:HG3	1.92	0.69
1:B:330:THR:OG1	1:B:333:GLU:HG3	1.93	0.68
1:A:185:GLN:N	1:A:185:GLN:OE1	2.26	0.67
1:A:130:LEU:HD12	1:A:130:LEU:N	2.09	0.66
1:B:140:TYR:HB2	1:B:184:PRO:HB2	1.78	0.66
1:B:323:TYR:O	1:B:325:PRO:HD3	1.97	0.65
1:A:350:LEU:HD12	1:A:354:ARG:HB2	1.78	0.65
1:B:380:PRO:HA	1:B:383:ARG:NH2	2.12	0.64
1:B:258:PRO:HD2	1:B:268:GLU:OE1	1.97	0.64
1:A:178:CYS:SG	1:A:236:SER:HA	2.38	0.64
1:B:138:THR:HG22	1:B:188:LEU:HD23	1.80	0.63
1:B:113:ARG:HD2	1:B:133:ASP:OD1	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:THR:HG22	1:B:376:ILE:HG12	1.82	0.62
1:A:180:ARG:HD3	1:A:203:SER:O	2.00	0.61
1:B:106:HIS:HB3	1:B:109:ILE:HG13	1.81	0.61
1:A:367:LEU:HD22	1:A:374:ALA:HB2	1.83	0.61
1:B:67:PHE:CE1	1:B:85:LYS:HE3	2.36	0.61
1:B:294:PRO:HG2	2:Y:217:VAL:HG11	1.81	0.60
1:B:141:ARG:HH11	1:B:141:ARG:HG3	1.66	0.60
1:B:279:GLU:O	1:B:283:GLU:HG2	2.02	0.60
1:A:91:LYS:HE2	1:A:126:VAL:HG13	1.84	0.59
1:A:120:GLY:HA3	1:A:125:GLU:O	2.02	0.59
2:Y:203:LEU:O	2:Y:207:VAL:HG23	2.02	0.59
1:A:384:ILE:HG12	1:A:385:GLN:N	2.18	0.59
1:B:98:LEU:HD23	1:B:102:ARG:HG3	1.82	0.59
1:B:100:ILE:HG23	1:B:177:ILE:HD13	1.85	0.58
1:A:341:ASP:OD1	1:B:319:ARG:NH2	2.37	0.58
1:B:271:LYS:HG3	2:Y:220:LEU:HD11	1.84	0.58
1:A:118:SER:HB2	1:A:127:TYR:HB2	1.86	0.57
1:B:290:GLU:OE1	2:Y:214:LYS:HB2	2.05	0.57
1:B:98:LEU:CD2	1:B:102:ARG:HD2	2.34	0.57
1:B:371:PRO:N	1:B:372:PRO:HD2	2.19	0.57
1:A:98:LEU:O	1:A:102:ARG:HG3	2.05	0.56
1:A:377:LEU:O	1:A:379:PRO:HD3	2.05	0.56
1:A:38:THR:O	1:A:55:SER:HA	2.05	0.56
1:A:82:VAL:HB	1:A:132:LEU:O	2.04	0.56
1:A:142:VAL:O	1:A:145:HIS:HB3	2.05	0.56
1:A:375:THR:HG21	1:B:372:PRO:HB2	1.87	0.56
1:B:363:THR:O	1:B:367:LEU:HD12	2.05	0.56
1:A:78:SER:C	1:A:80:GLU:H	2.08	0.56
1:B:162:MET:HE1	1:B:247:LEU:HB2	1.86	0.56
1:B:75:LEU:O	1:B:79:GLY:HA2	2.06	0.56
1:B:137:GLU:HA	1:B:137:GLU:OE1	2.05	0.56
1:B:172:ILE:HG13	1:B:173:HIS:N	2.21	0.56
1:A:345:ASP:O	1:A:348:VAL:HG12	2.07	0.55
1:A:294:PRO:CG	2:X:217:VAL:HG11	2.37	0.55
1:B:130:LEU:N	1:B:130:LEU:CD1	2.70	0.55
1:A:160:LEU:O	1:A:164:GLN:HG3	2.08	0.54
1:B:162:MET:CE	1:B:247:LEU:HB2	2.38	0.53
1:A:180:ARG:HH22	1:A:214:VAL:HG12	1.73	0.53
1:A:307:PRO:HD2	1:A:308:ARG:NH1	2.22	0.53
1:A:139:VAL:HA	1:A:189:LEU:HD11	1.89	0.53
1:B:153:LEU:HD23	1:B:158:VAL:HG22	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:PRO:HB2	1:B:284:MET:SD	2.49	0.53
1:B:217:ILE:O	1:B:218:CYS:HB2	2.09	0.53
1:B:362:PHE:CB	1:B:367:LEU:HD11	2.38	0.52
1:B:278:ARG:HG2	1:B:278:ARG:HH11	1.73	0.52
1:B:311:PRO:HD2	5:B:2048:HOH:O	2.10	0.52
1:B:183:LYS:HD3	1:B:219:SER:OG	2.10	0.52
1:B:67:PHE:CD1	1:B:68:GLY:N	2.77	0.52
1:B:292:LYS:O	2:Y:214:LYS:HE3	2.11	0.51
1:A:217:ILE:O	1:A:218:CYS:HB3	2.10	0.51
1:B:370:ASN:OD1	1:B:372:PRO:HG2	2.11	0.51
1:A:160:LEU:HD21	1:A:350:LEU:HD21	1.93	0.50
1:B:121:GLU:HB2	5:B:2010:HOH:O	2.10	0.50
1:A:352:ASN:ND2	1:A:354:ARG:HG3	2.27	0.50
1:B:98:LEU:HD23	1:B:98:LEU:O	2.11	0.50
1:B:195:VAL:HG22	1:B:357:PRO:HB3	1.94	0.50
1:B:169:LEU:HD11	1:B:182:ILE:CD1	2.39	0.50
1:B:249:GLU:HG3	1:B:254:GLN:C	2.32	0.50
1:A:74:LYS:HG3	1:A:79:GLY:O	2.11	0.50
1:B:362:PHE:HB3	1:B:367:LEU:HD11	1.93	0.50
1:A:352:ASN:HD21	1:A:354:ARG:HG3	1.77	0.49
1:A:368:SER:O	1:A:371:PRO:HD3	2.13	0.49
1:B:275:THR:HG23	1:B:296:ILE:HB	1.94	0.49
1:A:193:THR:O	1:A:194:ALA:HB3	2.14	0.48
1:B:103:LYS:NZ	1:B:206:GLN:OE1	2.46	0.48
1:A:217:ILE:O	1:A:218:CYS:CB	2.60	0.48
1:A:296:ILE:HD13	2:X:220:LEU:HD23	1.94	0.48
1:B:98:LEU:O	1:B:102:ARG:HG3	2.14	0.48
1:A:371:PRO:N	1:A:372:PRO:HD2	2.28	0.48
2:Y:199:PRO:HA	2:Y:202:LEU:HB3	1.95	0.48
1:A:375:THR:HG21	1:B:372:PRO:HB3	1.96	0.48
1:A:146:TYR:CE2	1:A:154:PRO:HD3	2.50	0.47
1:A:271:LYS:HG2	2:X:220:LEU:HD11	1.94	0.47
1:B:188:LEU:O	1:B:196:LEU:HA	2.14	0.47
1:A:155:VAL:O	1:A:159:LYS:HG3	2.15	0.47
1:B:160:LEU:O	1:B:164:GLN:HG3	2.14	0.47
1:B:367:LEU:HD22	1:B:374:ALA:HB2	1.97	0.47
1:A:93:PHE:CD1	1:A:93:PHE:N	2.82	0.47
2:X:203:LEU:O	2:X:207:VAL:HG23	2.14	0.47
1:A:267:VAL:O	1:A:271:LYS:HG3	2.15	0.47
1:A:294:PRO:HG2	2:X:217:VAL:HG11	1.95	0.47
1:A:372:PRO:HB2	1:B:375:THR:OG1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:PHE:CE2	2:Y:212:LEU:HD23	2.50	0.46
1:A:373:LEU:HD21	1:B:376:ILE:HD11	1.96	0.46
1:A:346:PRO:HG3	1:A:381:HIS:CG	2.50	0.46
1:A:196:LEU:C	1:A:196:LEU:HD23	2.36	0.46
1:B:370:ASN:C	1:B:372:PRO:HD2	2.35	0.46
1:A:130:LEU:H	1:A:130:LEU:CD1	2.24	0.46
1:A:153:LEU:HD12	1:A:154:PRO:CD	2.43	0.46
1:B:180:ARG:HG2	1:B:238:ILE:HD11	1.98	0.46
1:B:41:VAL:CG1	1:B:51:PRO:HB3	2.45	0.45
1:B:336:ALA:HB2	1:B:377:LEU:HD21	1.98	0.45
1:B:345:ASP:O	1:B:348:VAL:HG12	2.16	0.45
1:A:312:GLU:HB2	5:A:2061:HOH:O	2.16	0.45
1:A:195:VAL:HG22	1:A:357:PRO:HB3	1.98	0.45
1:A:156:ILE:HG23	1:A:157:TYR:N	2.31	0.45
1:B:106:HIS:HB3	1:B:109:ILE:CG1	2.45	0.45
2:X:202:LEU:O	2:X:206:LEU:HD22	2.17	0.45
1:B:173:HIS:HE1	1:B:239:ASP:OD2	2.00	0.44
1:B:193:THR:O	1:B:194:ALA:HB3	2.17	0.44
1:A:88:LEU:HD11	1:A:125:GLU:HB3	1.99	0.44
1:A:266:LEU:O	1:A:270:ILE:HG13	2.17	0.44
1:B:261:SER:HB2	2:Y:199:PRO:HB2	1.99	0.44
1:B:209:ARG:NH2	5:B:2026:HOH:O	2.46	0.44
1:A:249:GLU:HG3	1:A:254:GLN:C	2.37	0.44
1:B:148:ARG:C	1:B:150:LYS:H	2.21	0.44
1:A:294:PRO:HG2	2:X:217:VAL:HG21	2.00	0.44
2:Y:217:VAL:O	2:Y:220:LEU:HB3	2.18	0.44
1:B:98:LEU:HB2	1:B:128:LEU:HD21	2.00	0.44
1:A:50:ARG:HA	1:A:51:PRO:HD3	1.79	0.44
1:B:106:HIS:HE2	1:B:366:GLU:CD	2.19	0.44
2:Y:214:LYS:HB2	2:Y:214:LYS:HZ2	1.83	0.44
1:A:180:ARG:NH2	1:A:214:VAL:HG12	2.32	0.44
1:A:345:ASP:OD2	1:A:346:PRO:HD2	2.18	0.43
1:A:370:ASN:OD1	1:A:372:PRO:HG2	2.19	0.43
1:A:46:GLN:HE22	1:A:111:ARG:HG3	1.82	0.43
1:B:362:PHE:HB3	1:B:367:LEU:CD1	2.48	0.43
1:A:303:LYS:HA	1:A:303:LYS:HD3	1.80	0.43
1:B:139:VAL:HB	1:B:187:LEU:HB2	1.99	0.43
1:B:97:GLU:O	1:B:101:MET:HG2	2.18	0.43
1:B:192:ASP:HB3	1:B:354:ARG:NH1	2.34	0.43
1:B:115:PHE:HA	1:B:129:ASN:O	2.17	0.43
1:A:106:HIS:HB2	1:A:171:TYR:CE2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:106:HIS:NE2	1:B:366:GLU:OE1	2.43	0.43
1:B:266:LEU:HD12	1:B:266:LEU:O	2.19	0.43
1:B:278:ARG:HG2	1:B:278:ARG:NH1	2.34	0.43
1:A:223:ARG:HG3	1:A:227:LEU:HD12	2.00	0.43
1:A:345:ASP:HA	1:A:346:PRO:HD3	1.90	0.43
1:A:296:ILE:HD11	2:X:217:VAL:CG1	2.37	0.42
1:B:120:GLY:C	1:B:121:GLU:HG3	2.40	0.42
1:A:100:ILE:O	1:A:104:LEU:HG	2.20	0.42
1:B:32:LYS:HB3	1:B:32:LYS:HE2	1.80	0.42
2:X:214:LYS:HZ2	2:X:214:LYS:CB	2.33	0.42
1:A:296:ILE:CD1	2:X:220:LEU:HD23	2.50	0.42
1:B:98:LEU:HD23	1:B:98:LEU:C	2.41	0.41
1:B:141:ARG:HG3	1:B:141:ARG:NH1	2.34	0.41
1:A:46:GLN:HE21	1:A:46:GLN:HB2	1.68	0.41
1:B:128:LEU:HG	1:B:130:LEU:HD11	2.02	0.41
1:B:310:PRO:HA	1:B:311:PRO:HD3	1.87	0.41
1:A:310:PRO:HA	1:A:311:PRO:HD3	1.78	0.41
1:B:378:ILE:HA	1:B:379:PRO:HD3	1.86	0.41
1:B:362:PHE:HB2	1:B:367:LEU:HD11	2.01	0.41
1:B:271:LYS:HG3	2:Y:220:LEU:CD1	2.50	0.41
2:X:217:VAL:O	2:X:220:LEU:HB3	2.21	0.41
1:A:381:HIS:O	1:A:381:HIS:ND1	2.54	0.41
1:B:30:ARG:HB3	1:B:34:GLY:C	2.41	0.41
1:A:78:SER:C	1:A:80:GLU:N	2.74	0.41
1:A:122:LYS:O	1:A:124:ASP:N	2.54	0.41
1:B:86:LYS:HG3	1:B:129:ASN:ND2	2.36	0.41
1:A:87:VAL:O	1:A:127:TYR:HA	2.20	0.41
1:A:384:ILE:CG1	1:A:385:GLN:N	2.83	0.41
1:B:174:SER:OG	1:B:365:GLN:NE2	2.50	0.41
1:B:281:ILE:HD11	2:Y:213:ILE:CD1	2.51	0.41
1:B:377:LEU:O	1:B:379:PRO:HD3	2.20	0.41
1:B:361:ASN:OD1	1:B:361:ASN:N	2.46	0.41
2:X:208:LEU:HD23	2:X:208:LEU:HA	1.95	0.41
1:A:190:ASP:HB3	1:A:193:THR:OG1	2.21	0.40
1:A:373:LEU:HA	1:A:373:LEU:HD23	1.86	0.40
1:B:59:THR:HA	1:B:72:GLN:O	2.21	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:150:LYS:O	1:B:150:LYS:O[10_545]	2.03	0.17

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	347/378 (92%)	321 (92%)	22 (6%)	4 (1%)	13	27
1	B	354/378 (94%)	321 (91%)	28 (8%)	5 (1%)	11	22
2	X	24/39 (62%)	24 (100%)	0	0	100	100
2	Y	24/39 (62%)	23 (96%)	1 (4%)	0	100	100
All	All	749/834 (90%)	689 (92%)	51 (7%)	9 (1%)	13	27

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	ASP
1	A	123	LYS
1	B	49	ASP
1	B	120	GLY
1	B	150	LYS
1	A	357	PRO
1	B	46	GLN
1	A	353	GLY
1	B	48	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	309/335 (92%)	301 (97%)	8 (3%)	46	72
1	B	315/335 (94%)	308 (98%)	7 (2%)	52	76
2	X	23/36 (64%)	21 (91%)	2 (9%)	10	20
2	Y	23/36 (64%)	23 (100%)	0	100	100
All	All	670/742 (90%)	653 (98%)	17 (2%)	47	73

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	49	ASP
1	A	126	VAL
1	A	169	LEU
1	A	247	LEU
1	A	308	ARG
1	A	323	TYR
1	A	338	SER
1	B	169	LEU
1	B	173	HIS
1	B	207	LEU
1	B	247	LEU
1	B	297	LYS
1	B	329	LEU
1	B	375	THR
2	X	206	LEU
2	X	214	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	GLN
1	A	52	GLN
1	B	52	GLN
1	B	129	ASN
1	B	173	HIS
1	B	381	HIS
2	Y	200	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\#\|Z\| > 2$
1	PTR	B	216	1	15,16,17	0.82	0	19,22,24	0.41	0
1	PTR	A	216	1	15,16,17	1.10	1 (6%)	19,22,24	0.48	0

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
1	PTR	B	216	1	-	1/10/11/13	0/1/1/1
1	PTR	A	216	1	-	0/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	216	PTR	P-OH	-2.38	1.55	1.59

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	216	PTR	O-C-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

5 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	$\#\|Z\| > 2$
4	TRS	B	1386	-	7,7,7	0.74	0	9,9,9	0.43	0
3	SO4	B	1385	-	4,4,4	0.45	0	6,6,6	0.12	0
3	SO4	B	1384	-	4,4,4	0.29	0	6,6,6	0.30	0
3	SO4	A	1385	-	4,4,4	0.28	0	6,6,6	0.19	0
3	SO4	A	1386	-	4,4,4	0.33	0	6,6,6	0.13	0

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
4	TRS	B	1386	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1386	TRS	C1-C-C2-O2
4	B	1386	TRS	C3-C-C2-O2

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Mol	Chain	Res	Type	Atoms
4	B	1386	TRS	N-C-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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.