Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 04:57 PM GMT

PDB ID	:	4GST
Title	:	REACTION COORDINATE MOTION IN AN SNAR REACTION CATALYZED BY GLUTATHIONE TRANSFERASE
Authors	:	Ji, X.; Armstrong, R.N.; Gilliland, G.L.
Deposited on	:	1993-07-20
Resolution	:	1.90 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 (i) symbol.

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

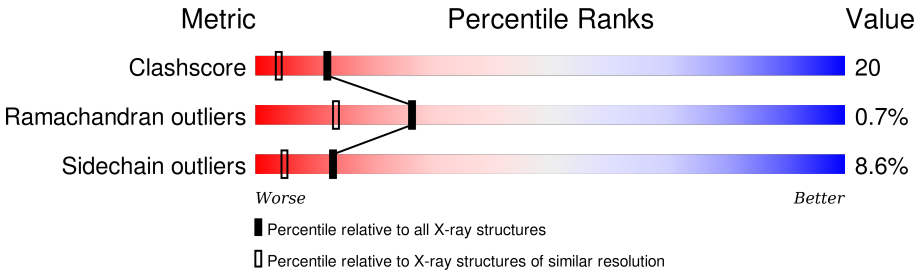
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 1.90 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	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)

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 <=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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	217	61% 31% 7%
1	B	217	53% 37% 8%

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	SO4	B	219	-	-	X	-

2 Entry composition

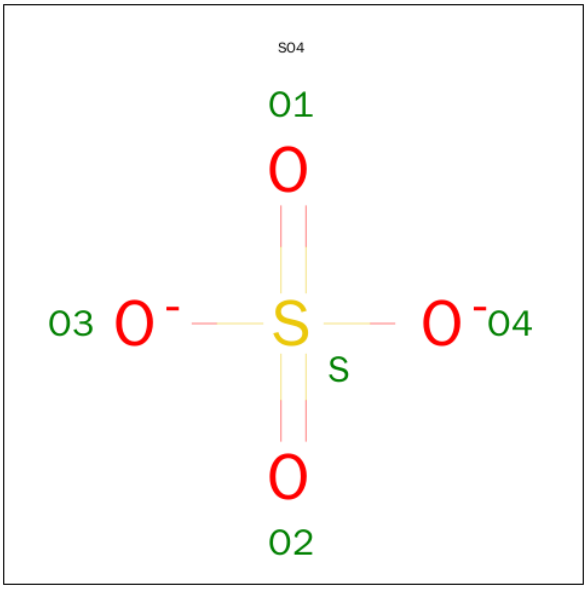
There are 4 unique types of molecules in this entry. The entry contains 4096 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 GLUTATHIONE S-TRANSFERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	217	Total	C	N	O	S	0	0	0
			1818	1177	303	327	11			
1	B	217	Total	C	N	O	S	0	0	0
			1818	1177	303	327	11			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

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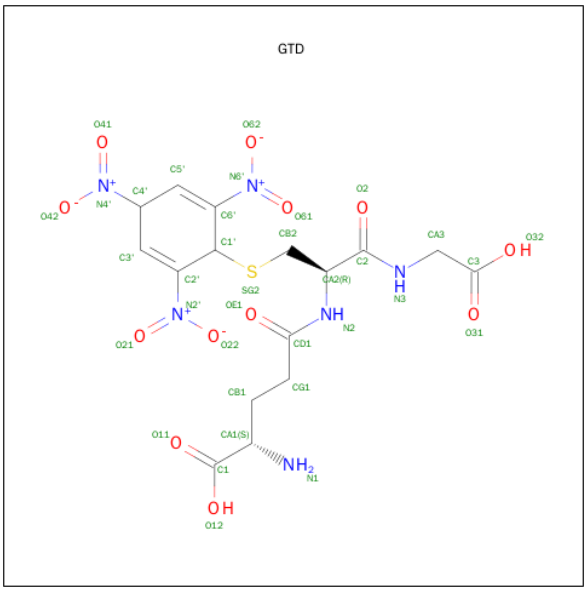
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is 1-(S-GLUTATHIONYL)-2,4,6-TRINITROCYCLOHEXA-2,5-DIENE (three-letter code: GTD) (formula: $C_{16}H_{20}N_6O_{12}S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C N O S 35 16 6 12 1	0	0
3	B	1	Total C N O S 35 16 6 12 1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	210	Total O 210 210	0	0
4	B	150	Total O 150 150	0	0

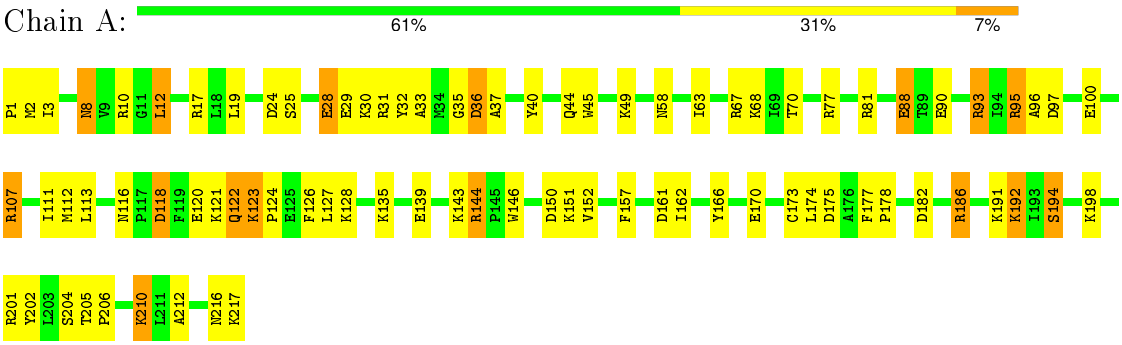
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

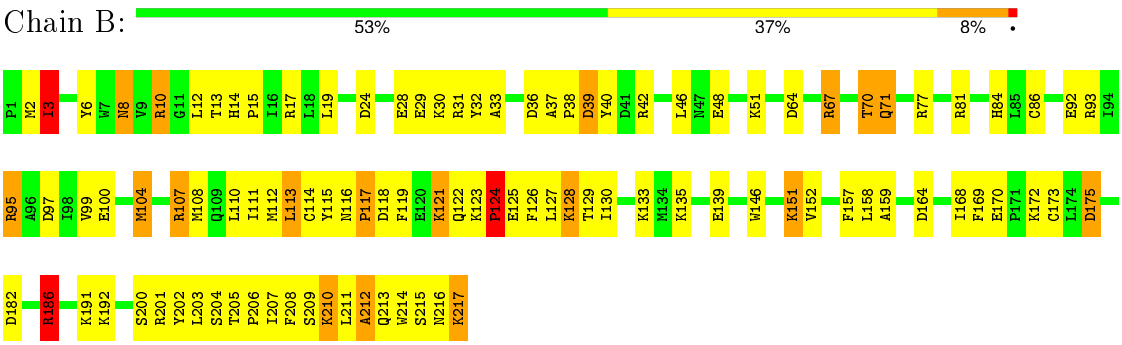
- Molecule 1: GLUTATHIONE S-TRANSFERASE

Chain A:



- Molecule 1: GLUTATHIONE S-TRANSFERASE

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	88.24Å 69.44Å 81.28Å 90.00° 106.01° 90.00°	Depositor
Resolution (Å)	(Not available) – 1.90	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-1.90)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	GPRLSA	Depositor
R, R_{free}	0.180 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4096	wwPDB-VP
Average B, all atoms (Å^2)	21.0	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: GTD, 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	0.97	0/1867	1.78	37/2515 (1.5%)
1	B	1.01	1/1867 (0.1%)	1.90	53/2515 (2.1%)
All	All	0.99	1/3734 (0.0%)	1.84	90/5030 (1.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3
1	B	0	1
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	29	GLU	CD-OE1	-5.31	1.19	1.25

All (90) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	67	ARG	NE-CZ-NH2	-15.05	112.78	120.30
1	B	67	ARG	NE-CZ-NH1	14.70	127.65	120.30
1	A	95	ARG	NE-CZ-NH1	12.59	126.60	120.30
1	B	17	ARG	NE-CZ-NH1	11.01	125.81	120.30
1	B	67	ARG	CD-NE-CZ	10.48	138.28	123.60
1	B	93	ARG	NE-CZ-NH1	10.07	125.33	120.30
1	B	42	ARG	NE-CZ-NH1	9.94	125.27	120.30
1	A	17	ARG	NE-CZ-NH1	9.45	125.03	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	81	ARG	NE-CZ-NH1	9.21	124.91	120.30
1	A	31	ARG	NE-CZ-NH2	-8.78	115.91	120.30
1	B	107	ARG	CG-CD-NE	8.74	130.16	111.80
1	B	6	TYR	CB-CG-CD2	8.58	126.15	121.00
1	A	67	ARG	NE-CZ-NH2	-8.41	116.10	120.30
1	B	97	ASP	CB-CG-OD1	8.28	125.75	118.30
1	B	93	ARG	NE-CZ-NH2	-8.27	116.17	120.30
1	A	194	SER	N-CA-CB	8.16	122.74	110.50
1	A	202	TYR	CB-CG-CD2	-8.12	116.13	121.00
1	B	64	ASP	CB-CG-OD1	7.88	125.39	118.30
1	A	186	ARG	NE-CZ-NH1	7.78	124.19	120.30
1	B	201	ARG	CD-NE-CZ	7.51	134.12	123.60
1	B	157	PHE	CB-CG-CD1	7.51	126.06	120.80
1	B	175	ASP	CB-CG-OD1	7.42	124.98	118.30
1	A	29	GLU	CG-CD-OE2	-7.40	103.50	118.30
1	A	161	ASP	CB-CG-OD2	7.37	124.93	118.30
1	B	77	ARG	NE-CZ-NH2	-7.32	116.64	120.30
1	A	202	TYR	CB-CG-CD1	7.30	125.38	121.00
1	B	10	ARG	NE-CZ-NH2	-7.22	116.69	120.30
1	A	70	THR	N-CA-CB	7.13	123.86	110.30
1	B	157	PHE	CB-CG-CD2	-7.09	115.84	120.80
1	B	186	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	95	ARG	O-C-N	7.03	133.95	122.70
1	A	81	ARG	CD-NE-CZ	6.99	133.39	123.60
1	A	107	ARG	NE-CZ-NH2	6.94	123.77	120.30
1	B	77	ARG	NE-CZ-NH1	6.90	123.75	120.30
1	B	186	ARG	NE-CZ-NH2	-6.85	116.88	120.30
1	B	92	GLU	CG-CD-OE1	6.77	131.84	118.30
1	B	42	ARG	CG-CD-NE	6.73	125.93	111.80
1	A	201	ARG	NE-CZ-NH2	6.66	123.63	120.30
1	B	31	ARG	NE-CZ-NH1	-6.65	116.97	120.30
1	A	161	ASP	OD1-CG-OD2	-6.63	110.71	123.30
1	A	175	ASP	CB-CG-OD1	6.44	124.10	118.30
1	B	95	ARG	CD-NE-CZ	6.37	132.52	123.60
1	B	46	LEU	CB-CA-C	6.36	122.29	110.20
1	B	200	SER	O-C-N	6.36	132.87	122.70
1	A	161	ASP	CB-CG-OD1	6.32	123.99	118.30
1	B	81	ARG	NH1-CZ-NH2	-6.29	112.48	119.40
1	B	201	ARG	NE-CZ-NH1	6.23	123.41	120.30
1	A	118	ASP	CB-CG-OD1	6.21	123.89	118.30
1	B	100	GLU	CB-CA-C	6.04	122.49	110.40
1	A	157	PHE	CB-CG-CD1	6.00	125.00	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	110	LEU	CB-CA-C	5.99	121.59	110.20
1	B	84	HIS	CA-CB-CG	-5.99	103.42	113.60
1	B	32	TYR	CB-CG-CD2	-5.97	117.42	121.00
1	B	164	ASP	CB-CG-OD2	-5.93	112.96	118.30
1	A	97	ASP	CB-CG-OD2	-5.89	113.00	118.30
1	B	164	ASP	CB-CG-OD1	5.86	123.57	118.30
1	A	182	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	B	175	ASP	CB-CA-C	5.78	121.96	110.40
1	A	17	ARG	NH1-CZ-NH2	-5.78	113.04	119.40
1	A	107	ARG	CD-NE-CZ	5.64	131.50	123.60
1	A	186	ARG	CA-CB-CG	5.61	125.73	113.40
1	B	33	ALA	CB-CA-C	-5.60	101.70	110.10
1	A	173	CYS	CB-CA-C	5.57	121.53	110.40
1	B	200	SER	N-CA-CB	5.54	118.80	110.50
1	B	70	THR	N-CA-CB	5.53	120.81	110.30
1	B	104	MET	CB-CA-C	5.53	121.45	110.40
1	B	182	ASP	CB-CG-OD2	-5.52	113.33	118.30
1	B	3	ILE	N-CA-CB	5.52	123.49	110.80
1	A	175	ASP	CB-CG-OD2	-5.51	113.34	118.30
1	A	175	ASP	CB-CA-C	5.49	121.39	110.40
1	A	29	GLU	CG-CD-OE1	5.48	129.26	118.30
1	B	200	SER	CA-C-O	-5.40	108.77	120.10
1	B	28	GLU	CA-CB-CG	5.38	125.24	113.40
1	A	95	ARG	CD-NE-CZ	5.37	131.12	123.60
1	B	6	TYR	CB-CG-CD1	-5.30	117.82	121.00
1	B	71	GLN	CB-CG-CD	5.27	125.31	111.60
1	A	166	TYR	O-C-N	5.23	131.06	122.70
1	A	162	ILE	O-C-N	5.21	131.04	122.70
1	A	96	ALA	O-C-N	-5.18	114.41	122.70
1	B	71	GLN	OE1-CD-NE2	-5.16	110.04	121.90
1	B	70	THR	O-C-N	5.14	130.93	122.70
1	A	36	ASP	CB-CG-OD1	-5.11	113.70	118.30
1	A	186	ARG	CD-NE-CZ	5.10	130.74	123.60
1	A	166	TYR	CB-CG-CD2	5.10	124.06	121.00
1	B	30	LYS	CD-CE-NZ	-5.08	100.02	111.70
1	A	58	ASN	CB-CG-OD1	5.04	131.69	121.60
1	B	48	GLU	OE1-CD-OE2	5.04	129.35	123.30
1	B	159	ALA	O-C-N	5.04	130.76	122.70
1	B	32	TYR	CB-CG-CD1	5.03	124.02	121.00
1	B	158	LEU	CB-CG-CD2	-5.00	102.50	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	144	ARG	Sidechain
1	A	186	ARG	Sidechain
1	A	93	ARG	Sidechain
1	B	186	ARG	Sidechain

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	1818	0	1805	53	4
1	B	1818	0	1805	93	4
2	A	20	0	0	0	0
2	B	10	0	0	3	0
3	A	35	0	18	1	0
3	B	35	0	17	2	0
4	A	210	0	0	4	0
4	B	150	0	0	0	0
All	All	4096	0	3645	146	4

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 20.

All (146) 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:123:LYS:O	1:B:127:LEU:HG	1.55	1.06
1:B:127:LEU:HA	1:B:130:ILE:HD12	1.48	0.95
1:B:125:GLU:OE1	1:B:128:LYS:HE2	1.68	0.93
1:A:107:ARG:O	1:A:111:ILE:HD12	1.69	0.90
1:B:168:ILE:HG22	1:B:214:TRP:HZ2	1.40	0.86
1:B:111:ILE:HD11	3:B:220:GTD:O42	1.77	0.85
1:B:119:PHE:CE2	1:B:214:TRP:HB2	2.16	0.80
1:A:191:LYS:HE3	1:A:192:LYS:HZ2	1.48	0.79
1:B:122:GLN:C	1:B:124:PRO:HD2	2.04	0.79
1:B:111:ILE:HG23	1:B:115:TYR:CD1	2.19	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:PHE:HB2	1:B:213:GLN:HG3	1.67	0.77
1:A:8:ASN:H	1:A:8:ASN:HD22	1.37	0.73
1:B:186:ARG:HG3	2:B:219:SO4:O1	1.90	0.72
1:A:191:LYS:HE3	1:A:192:LYS:NZ	2.05	0.71
1:B:123:LYS:HG3	1:B:169:PHE:CZ	2.26	0.71
1:A:122:GLN:NE2	1:A:122:GLN:HA	2.06	0.71
1:B:24:ASP:HB2	1:B:192:LYS:NZ	2.08	0.69
1:B:113:LEU:HD21	1:B:169:PHE:CZ	2.29	0.67
1:B:209:SER:C	1:B:211:LEU:H	1.97	0.66
1:A:8:ASN:HD22	1:A:8:ASN:N	1.93	0.66
1:A:191:LYS:CE	1:A:192:LYS:HZ2	2.09	0.66
1:A:77:ARG:NH2	1:A:100:GLU:OE1	2.28	0.66
1:B:111:ILE:HG13	1:B:208:PHE:HE1	1.61	0.66
1:B:111:ILE:HG13	1:B:208:PHE:CE1	2.31	0.65
1:B:209:SER:O	1:B:211:LEU:N	2.29	0.65
1:B:207:ILE:HG13	1:B:215:SER:OG	1.97	0.65
1:A:113:LEU:HD22	1:A:126:PHE:CG	2.33	0.64
1:A:191:LYS:CE	1:A:192:LYS:NZ	2.61	0.64
1:B:209:SER:C	1:B:211:LEU:N	2.51	0.64
1:A:90:GLU:OE1	1:A:93:ARG:NH2	2.22	0.64
1:B:108:MET:O	1:B:112:MET:HG3	1.96	0.63
1:B:135:LYS:O	1:B:139:GLU:HG3	1.98	0.63
1:B:119:PHE:HB2	1:B:213:GLN:CG	2.29	0.61
1:A:45:TRP:CZ2	1:A:49:LYS:HG3	2.36	0.61
1:A:135:LYS:NZ	1:A:139:GLU:OE2	2.30	0.61
1:B:8:ASN:N	1:B:8:ASN:HD22	1.99	0.61
1:A:1:PRO:HG2	1:A:28:GLU:HG2	1.83	0.60
1:B:107:ARG:O	1:B:111:ILE:HD12	2.02	0.60
1:B:24:ASP:CB	1:B:192:LYS:NZ	2.64	0.59
1:B:172:LYS:HD2	1:B:175:ASP:OD2	2.02	0.59
1:A:123:LYS:HD3	1:A:127:LEU:HD11	1.85	0.59
1:A:35:GLY:O	1:A:40:TYR:HA	2.03	0.58
1:B:123:LYS:N	1:B:124:PRO:CD	2.66	0.58
1:B:118:ASP:O	1:B:121:LYS:HB2	2.03	0.58
1:B:2:MET:C	1:B:3:ILE:HD12	2.22	0.58
1:B:123:LYS:N	1:B:124:PRO:HD2	2.19	0.58
1:A:191:LYS:NZ	1:A:192:LYS:NZ	2.52	0.57
1:B:118:ASP:HB3	1:B:121:LYS:HB2	1.85	0.57
1:B:208:PHE:HE2	1:B:214:TRP:CZ3	2.22	0.57
1:B:113:LEU:HD22	1:B:126:PHE:CD2	2.39	0.56
1:B:3:ILE:N	1:B:3:ILE:HD12	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:PRO:CG	1:A:28:GLU:HG2	2.35	0.56
1:A:30:LYS:NZ	4:A:312:HOH:O	2.34	0.56
1:A:121:LYS:NZ	4:A:388:HOH:O	2.39	0.56
1:B:70:THR:O	1:B:71:GLN:HB2	2.07	0.55
1:B:119:PHE:HZ	1:B:169:PHE:HE2	1.55	0.55
1:A:194:SER:O	1:A:198:LYS:HD2	2.06	0.55
1:A:36:ASP:HB3	4:A:407:HOH:O	2.07	0.55
1:B:125:GLU:HA	1:B:128:LYS:HB2	1.89	0.55
1:B:168:ILE:HG22	1:B:214:TRP:CZ2	2.31	0.55
1:B:129:THR:OG1	1:B:133:LYS:HE2	2.06	0.54
1:B:8:ASN:H	1:B:8:ASN:HD22	1.54	0.54
1:B:186:ARG:CD	2:B:219:SO4:O1	2.55	0.54
1:B:118:ASP:HB3	1:B:121:LYS:HD3	1.90	0.54
1:B:168:ILE:CG2	1:B:214:TRP:HZ2	2.17	0.54
1:B:119:PHE:CZ	1:B:169:PHE:HE2	2.26	0.54
1:B:10:ARG:HB3	1:B:207:ILE:HA	1.90	0.53
1:A:77:ARG:CZ	1:A:100:GLU:OE1	2.57	0.53
1:B:111:ILE:HD11	3:B:220:GTD:N4'	2.24	0.52
1:A:8:ASN:ND2	1:A:8:ASN:H	2.06	0.52
1:B:122:GLN:C	1:B:124:PRO:CD	2.76	0.50
1:B:123:LYS:CG	1:B:169:PHE:CZ	2.93	0.50
1:A:88:GLU:OE1	1:A:151:LYS:NZ	2.45	0.50
1:B:202:TYR:CE2	1:B:204:SER:HB3	2.46	0.50
1:B:127:LEU:CD2	1:B:169:PHE:CE1	2.95	0.49
1:B:14:HIS:N	1:B:15:PRO:CD	2.75	0.49
1:B:24:ASP:HB2	1:B:192:LYS:HZ1	1.75	0.49
1:B:208:PHE:HE2	1:B:214:TRP:HZ3	1.61	0.49
1:A:124:PRO:O	1:A:128:LYS:HD2	2.12	0.49
1:A:37:ALA:HB2	1:A:40:TYR:CZ	2.48	0.49
1:B:146:TRP:CE2	1:B:152:VAL:HG22	2.47	0.49
1:B:125:GLU:HA	1:B:128:LYS:HD3	1.94	0.48
1:B:186:ARG:CG	2:B:219:SO4:O1	2.59	0.48
1:A:2:MET:CE	1:A:25:SER:HB3	2.43	0.48
1:B:86:CYS:O	1:B:151:LYS:HE2	2.13	0.48
1:A:122:GLN:NE2	1:A:122:GLN:CA	2.76	0.48
1:B:37:ALA:HB1	1:B:38:PRO:HA	1.95	0.48
1:B:107:ARG:O	1:B:111:ILE:CD1	2.62	0.48
1:A:146:TRP:CE2	1:A:152:VAL:HG22	2.49	0.47
1:B:127:LEU:HD23	1:B:169:PHE:HE1	1.80	0.47
1:B:215:SER:O	1:B:215:SER:OG	2.33	0.47
1:A:212:ALA:HB3	1:A:216:ASN:HB3	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:LYS:HG3	1:B:210:LYS:H	1.51	0.47
1:A:118:ASP:O	1:A:122:GLN:HB2	2.14	0.47
1:B:118:ASP:CB	1:B:121:LYS:HD3	2.45	0.46
1:B:119:PHE:CD2	1:B:213:GLN:HB2	2.50	0.46
1:B:202:TYR:CZ	1:B:204:SER:HB3	2.50	0.46
1:B:130:ILE:HG21	1:B:173:CYS:HB2	1.97	0.46
1:A:111:ILE:HD11	3:A:222:GTD:O42	2.16	0.46
1:B:168:ILE:HD13	1:B:207:ILE:HD11	1.97	0.46
1:A:191:LYS:NZ	1:A:192:LYS:HZ2	2.11	0.46
1:B:119:PHE:CD2	1:B:213:GLN:O	2.69	0.46
1:B:212:ALA:C	1:B:213:GLN:NE2	2.69	0.46
1:A:107:ARG:HG2	1:A:111:ILE:CD1	2.46	0.46
1:B:205:THR:HB	1:B:206:PRO:HA	1.97	0.46
1:A:24:ASP:OD2	1:A:192:LYS:HE2	2.16	0.46
1:B:116:ASN:OD1	1:B:117:PRO:HD2	2.16	0.45
1:A:8:ASN:ND2	1:A:8:ASN:N	2.63	0.45
1:A:123:LYS:O	1:A:127:LEU:HG	2.16	0.45
1:B:127:LEU:HD21	1:B:169:PHE:CE1	2.52	0.45
1:A:3:ILE:HD12	1:A:3:ILE:N	2.32	0.45
1:A:95:ARG:NH2	1:A:144:ARG:NE	2.64	0.45
1:B:3:ILE:N	1:B:3:ILE:CD1	2.79	0.45
1:A:146:TRP:CE2	1:A:152:VAL:CG2	3.00	0.45
1:B:127:LEU:CD2	1:B:169:PHE:HE1	2.29	0.44
1:B:111:ILE:O	1:B:111:ILE:HG22	2.16	0.44
1:B:118:ASP:CG	1:B:121:LYS:HD3	2.37	0.44
1:A:210:LYS:HD2	4:A:386:HOH:O	2.17	0.44
1:B:114:CYS:HA	1:B:119:PHE:CD1	2.53	0.44
1:A:116:ASN:OD1	1:A:118:ASP:N	2.37	0.44
1:B:119:PHE:HE2	1:B:214:TRP:HB2	1.78	0.44
1:A:123:LYS:N	1:A:124:PRO:CD	2.80	0.44
1:A:63:ILE:HD12	1:A:68:LYS:HG2	1.99	0.43
1:B:126:PHE:C	1:B:128:LYS:N	2.70	0.43
1:B:130:ILE:CG2	1:B:173:CYS:HB2	2.48	0.43
1:B:95:ARG:O	1:B:99:VAL:HG23	2.19	0.43
1:B:39:ASP:O	1:B:40:TYR:HB2	2.18	0.43
1:A:30:LYS:HD3	1:A:32:TYR:CZ	2.54	0.43
1:B:12:LEU:HD12	1:B:12:LEU:C	2.39	0.43
1:B:127:LEU:HD23	1:B:169:PHE:CE1	2.53	0.42
1:A:10:ARG:HD2	1:A:204:SER:O	2.20	0.42
1:A:32:TYR:HD2	1:A:44:GLN:HG2	1.84	0.42
1:B:125:GLU:O	1:B:128:LYS:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:33:ALA:H	1:A:44:GLN:NE2	2.19	0.41
1:A:1:PRO:HG2	1:A:28:GLU:CG	2.50	0.41
1:A:205:THR:HA	1:A:206:PRO:C	2.41	0.41
1:B:127:LEU:HA	1:B:130:ILE:CD1	2.34	0.41
1:B:114:CYS:HA	1:B:119:PHE:CE1	2.55	0.41
1:B:113:LEU:HD22	1:B:126:PHE:CE2	2.55	0.41
1:A:12:LEU:HB3	1:A:107:ARG:HD3	2.03	0.41
1:B:146:TRP:CD2	1:B:152:VAL:HG22	2.56	0.41
1:B:119:PHE:CG	1:B:213:GLN:HB2	2.56	0.40
1:B:24:ASP:CG	1:B:192:LYS:NZ	2.75	0.40
1:A:177:PHE:HA	1:A:178:PRO:HD2	1.84	0.40
1:B:13:THR:HG22	1:B:13:THR:O	2.21	0.40
1:B:104:MET:O	1:B:108:MET:HG2	2.22	0.40

All (4) 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:A:191:LYS:NZ	1:B:117:PRO:C[3_455]	1.87	0.33
1:A:88:GLU:OE2	1:B:217:LYS:NZ[3_455]	2.11	0.09
1:A:191:LYS:NZ	1:B:118:ASP:N[3_455]	2.14	0.06
1:A:191:LYS:NZ	1:B:117:PRO:O[3_455]	2.18	0.02

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	215/217 (99%)	209 (97%)	6 (3%)	0	100 100
1	B	215/217 (99%)	202 (94%)	10 (5%)	3 (1%)	14 4
All	All	430/434 (99%)	411 (96%)	16 (4%)	3 (1%)	26 14

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	210	LYS
1	B	124	PRO
1	B	212	ALA

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	197/197 (100%)	181 (92%)	16 (8%)	15 5
1	B	197/197 (100%)	179 (91%)	18 (9%)	12 4
All	All	394/394 (100%)	360 (91%)	34 (9%)	13 5

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	12	LEU
1	A	19	LEU
1	A	28	GLU
1	A	88	GLU
1	A	112	MET
1	A	120	GLU
1	A	122	GLN
1	A	123	LYS
1	A	143	LYS
1	A	150	ASP
1	A	170	GLU
1	A	174	LEU
1	A	192	LYS
1	A	210	LYS
1	A	217	LYS
1	B	3	ILE
1	B	8	ASN
1	B	19	LEU
1	B	36	ASP

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Mol	Chain	Res	Type
1	B	39	ASP
1	B	51	LYS
1	B	67	ARG
1	B	113	LEU
1	B	117	PRO
1	B	121	LYS
1	B	124	PRO
1	B	128	LYS
1	B	151	LYS
1	B	170	GLU
1	B	191	LYS
1	B	203	LEU
1	B	216	ASN
1	B	217	LYS

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

Mol	Chain	Res	Type
1	A	8	ASN
1	A	44	GLN
1	A	122	GLN
1	B	8	ASN
1	B	122	GLN
1	B	213	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

8 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	SO4	A	218	-	4,4,4	1.36	0	6,6,6	0.28	0
2	SO4	A	219	-	4,4,4	1.31	0	6,6,6	0.30	0
2	SO4	A	220	-	4,4,4	1.43	0	6,6,6	0.75	0
2	SO4	A	221	-	4,4,4	1.44	0	6,6,6	0.56	0
3	GTD	A	222	-	19,35,35	1.60	2 (10%)	17,48,48	2.43	7 (41%)
2	SO4	B	218	-	4,4,4	1.33	0	6,6,6	0.95	0
2	SO4	B	219	-	4,4,4	1.50	0	6,6,6	0.58	0
3	GTD	B	220	-	19,35,35	1.38	4 (21%)	17,48,48	1.95	3 (17%)

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	SO4	A	218	-	-	0/0/0/0	0/0/0/0
2	SO4	A	219	-	-	0/0/0/0	0/0/0/0
2	SO4	A	220	-	-	0/0/0/0	0/0/0/0
2	SO4	A	221	-	-	0/0/0/0	0/0/0/0
3	GTD	A	222	-	-	0/27/55/55	0/1/1/1
2	SO4	B	218	-	-	0/0/0/0	0/0/0/0
2	SO4	B	219	-	-	0/0/0/0	0/0/0/0
3	GTD	B	220	-	-	0/27/55/55	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	222	GTD	C1'-SG2	-4.68	1.74	1.84
3	B	220	GTD	C1'-SG2	-3.08	1.78	1.84
3	B	220	GTD	C4'-C3'	-2.50	1.39	1.49
3	B	220	GTD	C4'-C5'	-2.47	1.39	1.49

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	222	GTD	C4'-C5'	-2.31	1.40	1.49
3	B	220	GTD	OE1-CD1	2.37	1.28	1.23

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	220	GTD	C3'-C2'-N2'	-4.52	113.10	118.42
3	A	222	GTD	CA3-N3-C2	-4.10	116.70	122.34
3	A	222	GTD	C3'-C2'-N2'	-3.34	114.48	118.42
3	B	220	GTD	CA3-N3-C2	-2.48	118.94	122.34
3	A	222	GTD	OE1-CD1-N2	-2.12	119.42	123.01
3	A	222	GTD	C3-CA3-N3	2.19	117.38	111.74
3	A	222	GTD	O2-C2-N3	2.87	128.84	123.08
3	A	222	GTD	CG1-CD1-N2	2.98	120.69	115.83
3	B	220	GTD	C5'-C6'-N6'	5.50	124.88	118.42
3	A	222	GTD	C5'-C6'-N6'	5.87	125.32	118.42

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	222	GTD	1	0
2	B	219	SO4	3	0
3	B	220	GTD	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

EDS was not executed - this section will therefore be empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.