Full wwPDB X-ray Structure Validation Report (i)

Jul 27, 2021 – 11:04 am BST

PDB ID	:	6SY1
Title	:	Crystal structure of the human 2-oxoadipate dehydrogenase DHTKD1 (E1)
Authors	:	Bezerra, G.A.; Foster, W.; Shrestha, L.; Pena, I.A.; Coker, J.; Kolker, S.; Nicola, B.B.; von Delft, F.; Edwards, A.; Arrowsmith, C.; Bountra, C.; Yue, W.W.; Structural Genomics Consortium (SGC)
Deposited on	:	2019-09-26
Resolution	:	1.87 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 following versions of software and data (see references (i)) were used in the production of this report:

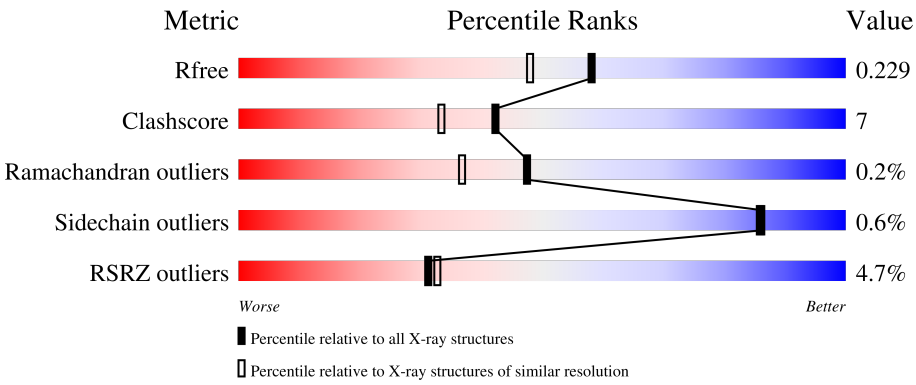
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.22
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.22

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 1.87 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	898	5% 86% 10% ·
1	B	898	4% 84% 12% ·

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 14484 atoms, of which 32 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 Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	859	6663	4249	1150	1226	38	0	0	0
1	B	861	6668	4245	1154	1231	38	0	0	0

There are 46 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	22	MET	-	initiating methionine	UNP Q96HY7
A	23	HIS	-	expression tag	UNP Q96HY7
A	24	HIS	-	expression tag	UNP Q96HY7
A	25	HIS	-	expression tag	UNP Q96HY7
A	26	HIS	-	expression tag	UNP Q96HY7
A	27	HIS	-	expression tag	UNP Q96HY7
A	28	HIS	-	expression tag	UNP Q96HY7
A	29	SER	-	expression tag	UNP Q96HY7
A	30	SER	-	expression tag	UNP Q96HY7
A	31	GLY	-	expression tag	UNP Q96HY7
A	32	VAL	-	expression tag	UNP Q96HY7
A	33	ASP	-	expression tag	UNP Q96HY7
A	34	LEU	-	expression tag	UNP Q96HY7
A	35	GLY	-	expression tag	UNP Q96HY7
A	36	THR	-	expression tag	UNP Q96HY7
A	37	GLU	-	expression tag	UNP Q96HY7
A	38	ASN	-	expression tag	UNP Q96HY7
A	39	LEU	-	expression tag	UNP Q96HY7
A	40	TYR	-	expression tag	UNP Q96HY7
A	41	PHE	-	expression tag	UNP Q96HY7
A	42	GLN	-	expression tag	UNP Q96HY7
A	43	SER	-	expression tag	UNP Q96HY7
A	44	MET	-	expression tag	UNP Q96HY7
B	22	MET	-	initiating methionine	UNP Q96HY7

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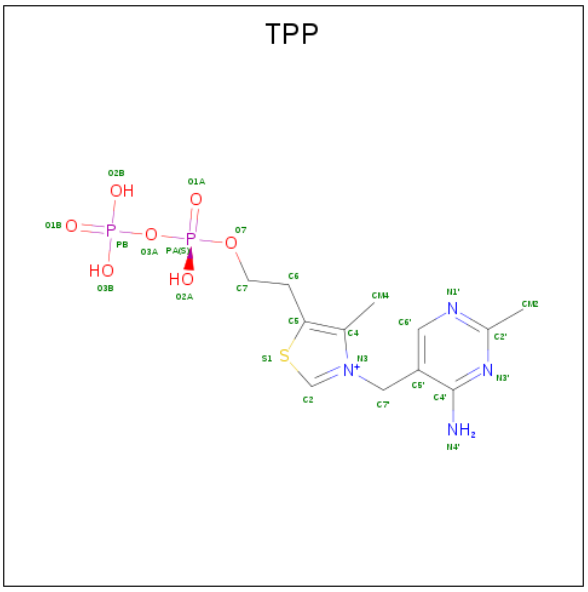
Chain	Residue	Modelled	Actual	Comment	Reference
B	23	HIS	-	expression tag	UNP Q96HY7
B	24	HIS	-	expression tag	UNP Q96HY7
B	25	HIS	-	expression tag	UNP Q96HY7
B	26	HIS	-	expression tag	UNP Q96HY7
B	27	HIS	-	expression tag	UNP Q96HY7
B	28	HIS	-	expression tag	UNP Q96HY7
B	29	SER	-	expression tag	UNP Q96HY7
B	30	SER	-	expression tag	UNP Q96HY7
B	31	GLY	-	expression tag	UNP Q96HY7
B	32	VAL	-	expression tag	UNP Q96HY7
B	33	ASP	-	expression tag	UNP Q96HY7
B	34	LEU	-	expression tag	UNP Q96HY7
B	35	GLY	-	expression tag	UNP Q96HY7
B	36	THR	-	expression tag	UNP Q96HY7
B	37	GLU	-	expression tag	UNP Q96HY7
B	38	ASN	-	expression tag	UNP Q96HY7
B	39	LEU	-	expression tag	UNP Q96HY7
B	40	TYR	-	expression tag	UNP Q96HY7
B	41	PHE	-	expression tag	UNP Q96HY7
B	42	GLN	-	expression tag	UNP Q96HY7
B	43	SER	-	expression tag	UNP Q96HY7
B	44	MET	-	expression tag	UNP Q96HY7

- Molecule 2 is THIAMINE DIPHOSPHATE (three-letter code: TPP) (formula: $C_{12}H_{19}N_4O_7P_2S$).



Mol	Chain	Residues	Atoms							ZeroOcc	AltConf
			Total	C	H	N	O	P	S		
2	A	1	42	12	16	4	7	2	1	0	0
2	B	1	42	12	16	4	7	2	1	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
3	A	2	2	2	0	0
3	B	1	1	1	0	0

- Molecule 4 is water.

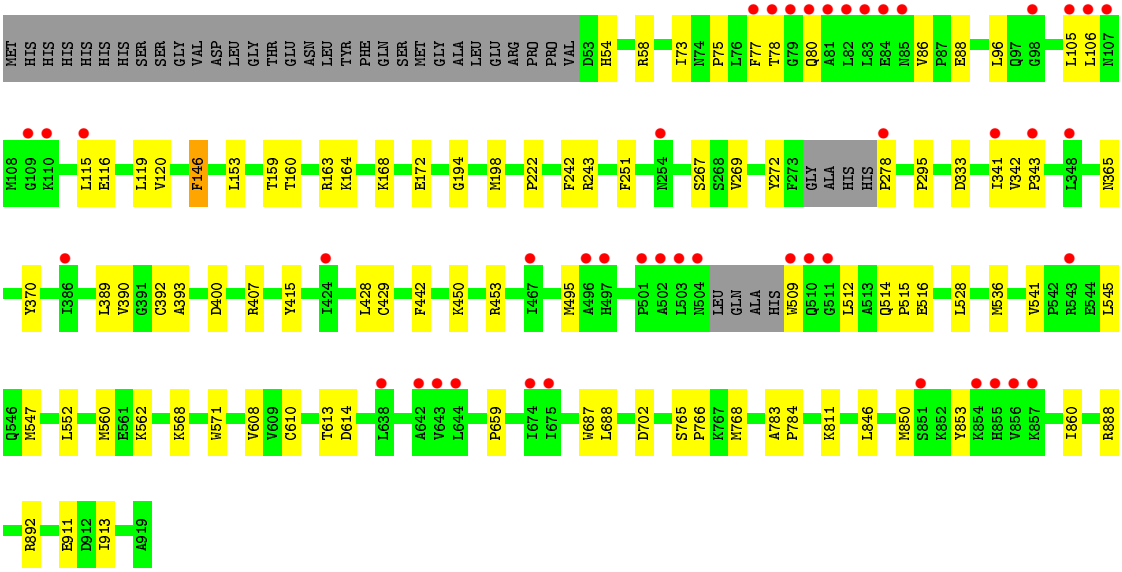
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
4	A	524	524	524	0	0
4	B	542	542	542	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

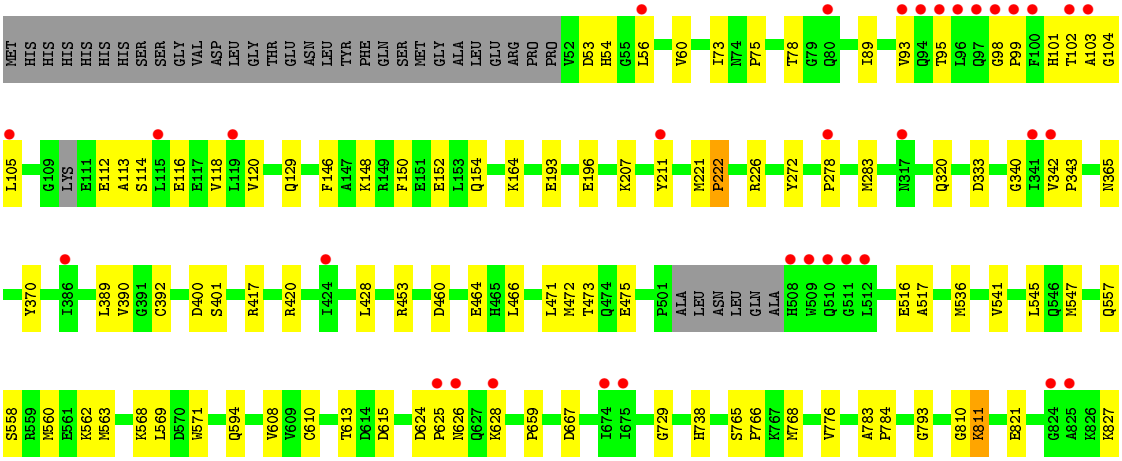
• Molecule 1: Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial

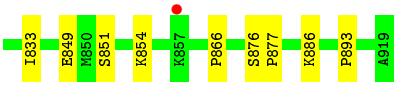
Chain A:



• Molecule 1: Probable 2-oxoglutarate dehydrogenase E1 component DHKTD1, mitochondrial

Chain B:




I833
E849
M850
S851
K854
K857
P866
S876
P877
K886
P893
A919

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	78.55Å 81.22Å 86.90Å 63.43° 76.96° 72.06°	Depositor
Resolution (Å)	46.01 – 1.87 46.01 – 1.87	Depositor EDS
% Data completeness (in resolution range)	96.5 (46.01-1.87) 96.5 (46.01-1.87)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.30 (at 1.87Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.190 , 0.230 0.189 , 0.229	Depositor DCC
R_{free} test set	7091 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å^2)	21.7	Xtriage
Anisotropy	0.679	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 42.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	14484	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.40% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: TPP, MG

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	0.39	1/6827 (0.0%)	0.54	0/9261
1	B	0.41	1/6829 (0.0%)	0.55	0/9264
All	All	0.40	2/13656 (0.0%)	0.55	0/18525

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	392	CYS	CB-SG	-5.73	1.72	1.81
1	A	392	CYS	CB-SG	-5.31	1.73	1.81

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	6663	0	6492	82	0
1	B	6668	0	6496	101	0
2	A	26	16	16	1	0
2	B	26	16	16	0	0
3	A	2	0	0	0	0
3	B	1	0	0	0	0
4	A	524	0	0	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	542	0	0	5	0
All	All	14452	32	13020	182	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 7.

All (182) 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:53:ASP:HB3	1:B:102:THR:OG1	1.58	1.03
1:A:811:LYS:HE2	4:A:1148:HOH:O	1.61	0.96
1:A:547:MET:HE1	1:A:552:LEU:HD23	1.49	0.93
1:B:516:GLU:OE1	4:B:1101:HOH:O	1.87	0.92
1:A:389:LEU:HD12	1:A:390:VAL:HG13	1.50	0.90
1:A:536:MET:HE1	1:A:560:MET:HG2	1.52	0.90
1:B:613:THR:HG23	1:B:615:ASP:H	1.37	0.88
1:B:628:LYS:HE3	1:B:628:LYS:HA	1.56	0.88
1:B:886:LYS:NZ	4:B:1102:HOH:O	1.99	0.88
1:B:610:CYS:SG	1:B:613:THR:HG22	2.14	0.87
1:A:243:ARG:HG3	1:A:495:MET:HE3	1.59	0.85
1:B:562:LYS:HB3	1:B:569:LEU:HD22	1.59	0.84
1:A:541:VAL:HG11	1:A:545:LEU:HD22	1.62	0.81
1:B:536:MET:HE3	1:B:563:MET:HB2	1.62	0.81
1:B:101:HIS:CB	1:B:112:GLU:HA	2.11	0.81
1:A:547:MET:HG3	1:A:608:VAL:HG11	1.62	0.80
1:A:547:MET:HE1	1:A:552:LEU:CD2	2.13	0.78
1:B:272:TYR:CE2	1:B:278:PRO:HG3	2.21	0.76
1:B:417:ARG:O	1:B:420:ARG:NH1	2.19	0.76
1:A:545:LEU:HG	1:A:610:CYS:HB2	1.68	0.75
1:A:528:LEU:HD21	1:A:783:ALA:HB2	1.68	0.74
1:B:562:LYS:HB3	1:B:569:LEU:CD2	2.18	0.73
1:B:473:THR:HG21	4:B:1526:HOH:O	1.88	0.72
1:B:628:LYS:HA	1:B:628:LYS:CE	2.19	0.72
1:B:102:THR:HG22	1:B:104:GLY:H	1.56	0.71
1:B:536:MET:HE3	1:B:563:MET:CB	2.19	0.71
1:B:626:ASN:O	1:B:628:LYS:HD2	1.90	0.70
1:B:536:MET:CE	1:B:563:MET:HB2	2.22	0.69
1:A:272:TYR:CE2	1:A:278:PRO:HB3	2.28	0.68
1:B:116:GLU:O	1:B:120:VAL:HG23	1.93	0.68
1:A:116:GLU:O	1:A:120:VAL:HG23	1.93	0.67
1:B:101:HIS:CB	1:B:113:ALA:H	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:272:TYR:HE2	1:B:278:PRO:HG3	1.61	0.66
1:B:473:THR:HG22	1:B:475:GLU:N	2.10	0.66
1:A:198:MET:SD	4:A:1370:HOH:O	2.54	0.66
1:B:221:MET:CE	1:B:283:MET:HE1	2.25	0.66
1:B:221:MET:HE2	1:B:283:MET:CE	2.27	0.65
1:B:114:SER:O	1:B:118:VAL:HG23	1.96	0.65
1:B:150:PHE:O	1:B:154:GLN:HG3	1.97	0.64
1:B:148:LYS:HE2	1:B:152:GLU:OE2	1.98	0.64
1:B:221:MET:HG3	1:B:222:PRO:HD2	1.79	0.63
1:B:53:ASP:O	1:B:105:LEU:HD11	1.99	0.63
1:B:536:MET:CE	1:B:560:MET:HG2	2.28	0.63
1:B:821:GLU:OE1	1:B:827:LYS:HE2	1.99	0.62
1:B:221:MET:CE	1:B:283:MET:CE	2.78	0.62
1:B:221:MET:HE3	1:B:226:ARG:HG3	1.82	0.62
1:A:768:MET:SD	1:A:811:LYS:HE3	2.40	0.62
1:B:536:MET:CE	1:B:560:MET:HA	2.30	0.62
1:B:833:ILE:HD12	1:B:849:GLU:CG	2.29	0.62
1:A:77:PHE:HB3	1:A:80:GLN:HG3	1.82	0.61
1:A:516:GLU:HB2	4:A:1509:HOH:O	1.99	0.61
1:B:536:MET:SD	1:B:560:MET:HG2	2.40	0.61
1:B:207:LYS:HE2	1:B:211:TYR:OH	2.00	0.61
1:B:571:TRP:CE2	1:B:766:PRO:HG3	2.35	0.61
1:A:514:GLN:OE1	1:A:515:PRO:HD2	2.00	0.61
1:A:389:LEU:CD1	1:A:390:VAL:HG13	2.28	0.60
1:A:242:PHE:HB2	1:A:495:MET:SD	2.42	0.60
1:A:768:MET:HE2	1:A:811:LYS:HG3	1.84	0.60
1:A:547:MET:HG3	1:A:608:VAL:CG1	2.31	0.59
1:B:460:ASP:O	1:B:464:GLU:HG3	2.01	0.59
1:B:78:THR:HG22	4:B:1459:HOH:O	2.02	0.59
1:B:221:MET:HE1	1:B:283:MET:HE1	1.83	0.59
1:A:571:TRP:CE2	1:A:766:PRO:HG3	2.39	0.58
1:B:768:MET:HE2	1:B:811:LYS:HD3	1.86	0.58
1:B:102:THR:HG21	1:B:105:LEU:HG	1.86	0.57
1:B:53:ASP:CB	1:B:102:THR:OG1	2.45	0.57
1:B:536:MET:HE1	1:B:560:MET:HA	1.87	0.57
1:B:833:ILE:HD12	1:B:849:GLU:HG2	1.87	0.57
1:A:115:LEU:HD21	1:A:119:LEU:HD11	1.87	0.57
1:A:160:THR:O	1:A:164:LYS:HG3	2.05	0.56
1:B:793:GLY:HA2	1:B:833:ILE:HD13	1.86	0.56
1:A:846:LEU:O	1:A:850:MET:HG3	2.05	0.56
1:A:243:ARG:HG3	1:A:495:MET:CE	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:ARG:CG	1:A:495:MET:HE3	2.35	0.55
1:B:389:LEU:HD12	1:B:390:VAL:HG13	1.88	0.55
1:B:547:MET:HG3	1:B:608:VAL:HG11	1.89	0.55
1:A:75:PRO:HB3	1:A:400:ASP:HB2	1.89	0.54
1:B:56:LEU:O	1:B:60:VAL:HG23	2.06	0.54
1:B:866:PRO:HB3	1:B:893:PRO:O	2.07	0.53
1:A:267:SER:OG	1:A:269:VAL:HG13	2.08	0.53
1:A:77:PHE:O	1:A:80:GLN:HG3	2.08	0.53
1:A:272:TYR:CZ	1:A:278:PRO:HB3	2.43	0.53
1:A:509:TRP:CE3	1:A:512:LEU:HD12	2.44	0.53
1:B:417:ARG:HA	1:B:420:ARG:NH1	2.24	0.53
1:A:295:PRO:HG3	1:A:341:ILE:HD11	1.89	0.53
1:B:473:THR:HG22	1:B:475:GLU:H	1.74	0.53
1:B:129:GLN:HG2	1:B:401:SER:OG	2.08	0.53
1:B:417:ARG:HA	1:B:420:ARG:HH11	1.74	0.53
1:B:320:GLN:HG3	4:B:1305:HOH:O	2.08	0.53
1:B:342:VAL:HB	1:B:343:PRO:HD3	1.90	0.53
1:A:911:GLU:OE2	4:A:1101:HOH:O	2.19	0.52
1:B:768:MET:CE	1:B:811:LYS:HD3	2.39	0.52
1:A:243:ARG:NE	4:A:1110:HOH:O	2.42	0.52
1:A:768:MET:HE2	1:A:811:LYS:CG	2.39	0.51
1:A:251:PHE:CZ	1:A:688:LEU:HD13	2.45	0.51
1:B:164:LYS:HE3	1:B:471:LEU:O	2.09	0.51
1:B:783:ALA:HB1	1:B:784:PRO:HD2	1.92	0.51
1:B:628:LYS:HE3	1:B:628:LYS:CA	2.28	0.51
1:B:75:PRO:HB3	1:B:400:ASP:HB2	1.91	0.50
1:B:221:MET:CE	1:B:226:ARG:HG3	2.42	0.50
1:B:610:CYS:CB	1:B:613:THR:HG22	2.42	0.50
1:A:442:PHE:HE1	1:A:450:LYS:HG2	1.77	0.49
1:A:768:MET:CE	1:A:811:LYS:CG	2.91	0.49
1:A:77:PHE:O	1:A:80:GLN:CG	2.60	0.49
1:A:702:ASP:OD1	1:A:811:LYS:NZ	2.34	0.49
1:B:541:VAL:CG2	1:B:547:MET:HE2	2.42	0.49
1:A:73:ILE:HG13	1:A:428:LEU:HD22	1.96	0.48
1:B:102:THR:HG22	1:B:103:ALA:N	2.27	0.48
1:A:159:THR:O	1:A:163:ARG:HG3	2.14	0.48
1:A:547:MET:HE2	1:A:552:LEU:HG	1.96	0.48
1:A:242:PHE:CB	1:A:495:MET:SD	3.02	0.47
1:A:765:SER:HB2	1:A:766:PRO:HD2	1.96	0.47
1:B:102:THR:CG2	1:B:105:LEU:HG	2.44	0.47
1:A:547:MET:CE	1:A:552:LEU:HG	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:THR:HG23	4:A:1407:HOH:O	2.14	0.47
1:A:562:LYS:HD2	1:A:568:LYS:O	2.14	0.46
1:B:89:ILE:O	1:B:93:VAL:HG23	2.15	0.46
1:B:221:MET:HE2	1:B:283:MET:HE2	1.95	0.46
1:B:610:CYS:HB3	1:B:613:THR:CG2	2.45	0.46
1:A:146:PHE:CE2	1:A:415:TYR:CD1	3.04	0.46
1:B:536:MET:HE2	1:B:560:MET:HA	1.97	0.46
1:B:95:THR:HG22	1:B:95:THR:O	2.15	0.46
1:A:105:LEU:O	1:A:106:LEU:HG	2.16	0.46
1:B:466:LEU:HD12	1:B:472:MET:HE1	1.97	0.46
1:B:466:LEU:HD12	1:B:472:MET:CE	2.46	0.46
1:B:610:CYS:HB3	1:B:613:THR:HG22	1.98	0.46
1:A:96:LEU:HD23	1:B:54:HIS:NE2	2.31	0.46
1:A:77:PHE:HB3	1:A:80:GLN:CG	2.47	0.45
1:B:102:THR:HG22	1:B:104:GLY:N	2.28	0.45
1:B:389:LEU:CD1	1:B:390:VAL:HG13	2.45	0.45
1:A:768:MET:CE	1:A:811:LYS:HG2	2.47	0.45
1:A:343:PRO:HB3	1:A:389:LEU:HD21	1.99	0.45
1:B:765:SER:HB2	1:B:766:PRO:HD2	1.98	0.45
2:A:1001:TPP:H6'	1:B:594:GLN:OE1	2.16	0.45
1:B:73:ILE:HG13	1:B:428:LEU:HD22	1.98	0.45
1:B:833:ILE:HD12	1:B:849:GLU:HG3	1.96	0.45
1:B:876:SER:HB3	1:B:877:PRO:HD3	1.99	0.45
1:A:541:VAL:CG1	1:A:545:LEU:HD22	2.40	0.45
1:A:783:ALA:HB1	1:A:784:PRO:HD2	1.98	0.45
1:B:541:VAL:HG21	1:B:547:MET:HE2	1.99	0.45
1:B:568:LYS:HA	1:B:776:VAL:HB	1.99	0.45
1:B:624:ASP:OD2	1:B:625:PRO:O	2.35	0.45
1:A:168:LYS:O	1:A:172:GLU:HG3	2.16	0.44
1:A:194:GLY:O	1:A:429:CYS:HB2	2.17	0.44
1:A:536:MET:CA	1:A:536:MET:HE3	2.47	0.44
1:A:562:LYS:HA	1:A:562:LYS:HD3	1.74	0.44
1:B:558:SER:OG	1:B:562:LYS:HE2	2.18	0.44
1:B:876:SER:HB3	1:B:877:PRO:CD	2.48	0.43
1:B:98:GLY:HA2	1:B:99:PRO:HD3	1.87	0.43
1:A:115:LEU:HD21	1:A:119:LEU:CD1	2.49	0.43
1:A:768:MET:CE	1:A:811:LYS:HG3	2.47	0.43
1:B:164:LYS:HE2	1:B:472:MET:HG2	2.01	0.43
1:A:146:PHE:HE2	1:A:415:TYR:CD1	2.37	0.43
1:A:251:PHE:CZ	1:A:688:LEU:CD1	3.02	0.43
1:A:453:ARG:HA	1:A:453:ARG:HD3	1.92	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PHE:CB	1:A:80:GLN:HG3	2.48	0.42
1:A:86:VAL:CG1	1:A:88:GLU:OE1	2.67	0.42
1:A:768:MET:HE1	1:A:811:LYS:HG2	2.01	0.42
1:B:453:ARG:HA	1:B:453:ARG:HD3	1.85	0.42
1:B:517:ALA:O	1:B:729:GLY:HA3	2.20	0.42
1:A:860:ILE:HD11	1:A:888:ARG:NH2	2.35	0.42
1:B:545:LEU:C	1:B:545:LEU:HD23	2.40	0.42
1:B:738:HIS:CE1	1:B:810:GLY:HA3	2.55	0.42
1:A:783:ALA:HB1	1:A:784:PRO:CD	2.50	0.41
1:A:892:ARG:HG3	1:A:913:ILE:HD11	2.00	0.41
1:A:153:LEU:O	1:A:407:ARG:HD3	2.20	0.41
1:A:536:MET:HE3	1:A:536:MET:HA	2.01	0.41
1:B:851:SER:HA	1:B:854:LYS:HE2	2.02	0.41
1:A:547:MET:HE1	1:A:552:LEU:CG	2.50	0.41
1:B:340:GLY:C	1:B:343:PRO:HD2	2.40	0.41
1:A:687:TRP:O	1:A:688:LEU:HB2	2.20	0.41
1:A:333:ASP:HB3	1:A:365:ASN:HA	2.02	0.41
1:A:613:THR:O	1:A:614:ASP:HB2	2.21	0.41
1:B:221:MET:CG	1:B:222:PRO:HD2	2.50	0.41
1:A:54:HIS:O	1:A:58:ARG:HG3	2.21	0.41
1:A:77:PHE:HB3	1:A:80:GLN:OE1	2.21	0.41
1:B:193:GLU:HA	1:B:196:GLU:OE2	2.20	0.41
1:A:342:VAL:HB	1:A:343:PRO:CD	2.50	0.40
1:B:765:SER:HB2	1:B:766:PRO:CD	2.51	0.40
1:B:102:THR:CG2	1:B:103:ALA:N	2.85	0.40
1:A:146:PHE:CZ	1:A:393:ALA:HB1	2.56	0.40
1:B:333:ASP:HB3	1:B:365:ASN:HA	2.03	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	853/898 (95%)	827 (97%)	24 (3%)	2 (0%)	47	37
1	B	855/898 (95%)	828 (97%)	25 (3%)	2 (0%)	47	37
All	All	1708/1796 (95%)	1655 (97%)	49 (3%)	4 (0%)	47	37

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	222	PRO
1	B	222	PRO
1	A	659	PRO
1	B	659	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	711/776 (92%)	708 (100%)	3 (0%)	91	90
1	B	712/776 (92%)	707 (99%)	5 (1%)	84	83
All	All	1423/1552 (92%)	1415 (99%)	8 (1%)	86	86

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	146	PHE
1	A	370	TYR
1	A	853	TYR
1	B	146	PHE
1	B	370	TYR
1	B	557	GLN
1	B	667	ASP
1	B	811	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	317	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

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	TPP	B	1001	3	22,27,27	0.67	0	29,40,40	0.97	2 (6%)
2	TPP	A	1001	3	22,27,27	0.69	0	29,40,40	0.97	1 (3%)

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	TPP	B	1001	3	-	3/16/17/17	0/2/2/2
2	TPP	A	1001	3	-	3/16/17/17	0/2/2/2

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1001	TPP	C6-C5-C4	2.69	129.59	127.43
2	B	1001	TPP	O3B-PB-O3A	2.26	112.20	104.64
2	B	1001	TPP	C6-C5-C4	2.12	129.14	127.43

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1001	TPP	C4-C5-C6-C7
2	A	1001	TPP	C4-C5-C6-C7
2	B	1001	TPP	PA-O3A-PB-O1B
2	A	1001	TPP	PA-O3A-PB-O1B
2	B	1001	TPP	C4'-C5'-C7'-N3
2	A	1001	TPP	PA-O3A-PB-O3B

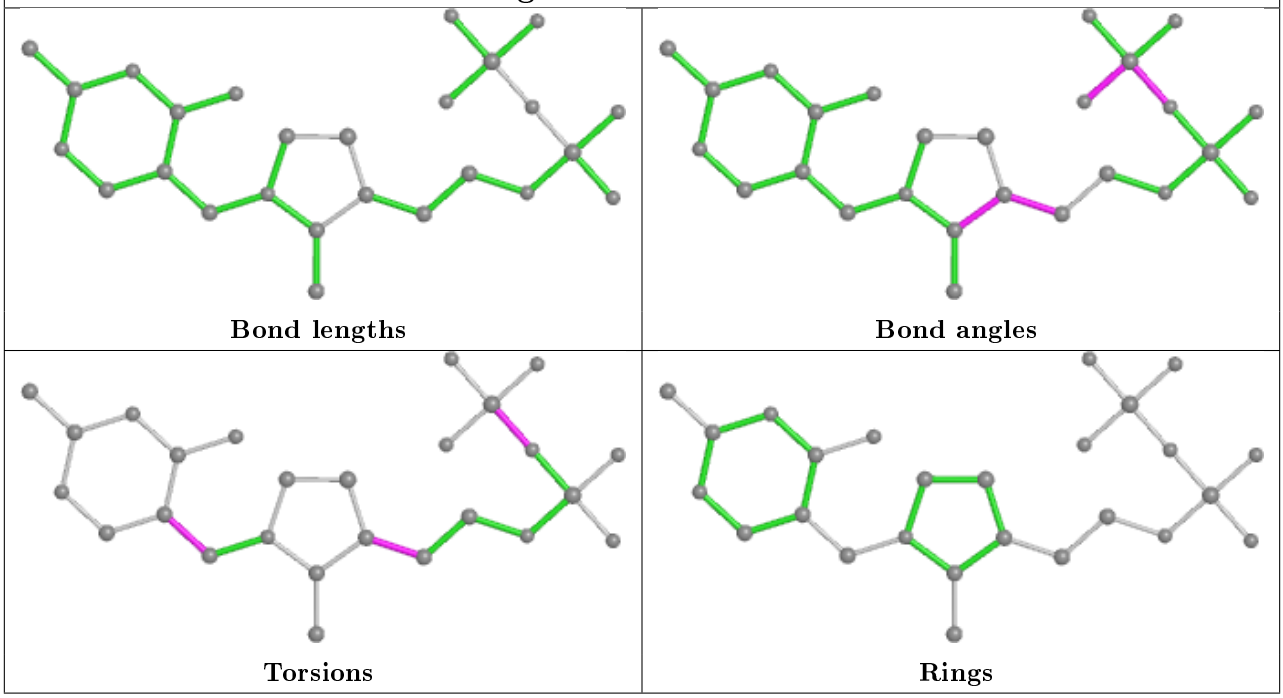
There are no ring outliers.

1 monomer is involved in 1 short contact:

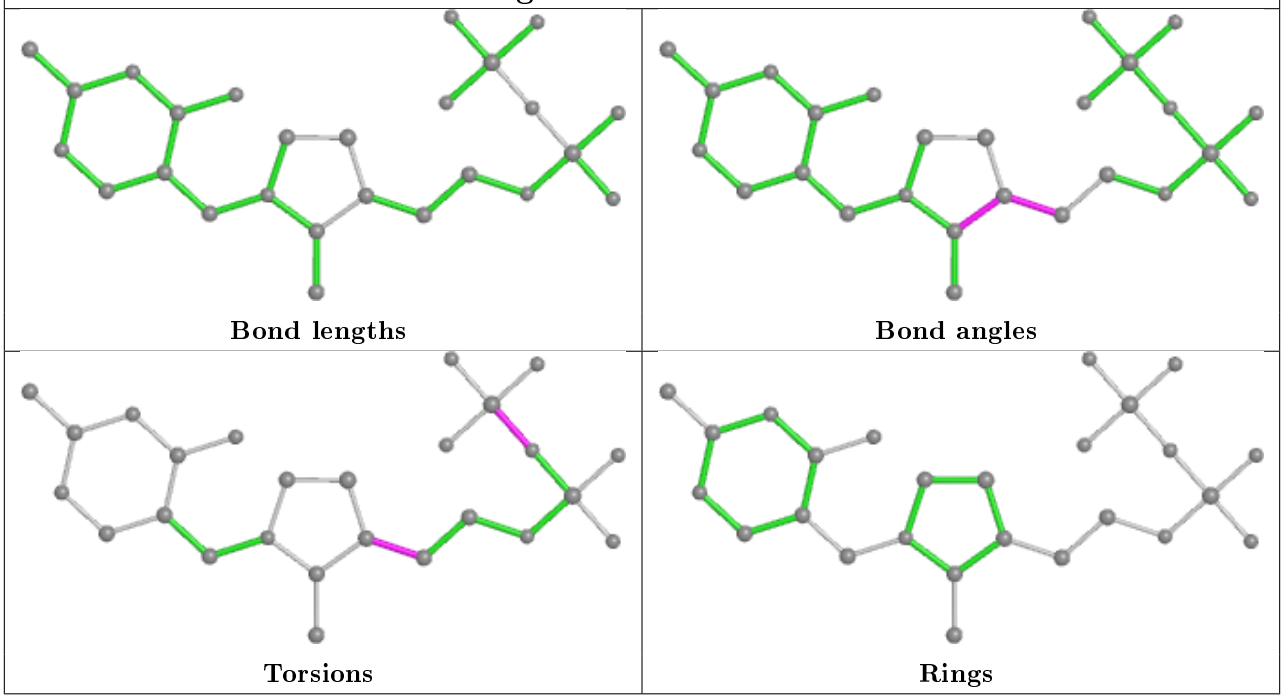
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	TPP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand TPP B 1001



Ligand TPP A 1001



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	859/898 (95%)	0.16	45 (5%)	27	28	14, 23, 46, 72	0
1	B	861/898 (95%)	0.08	35 (4%)	37	39	14, 24, 46, 87	0
All	All	1720/1796 (95%)	0.12	80 (4%)	31	33	14, 24, 46, 87	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	103	ALA	9.0
1	A	510	GLN	6.9
1	B	508	HIS	6.6
1	B	99	PRO	5.9
1	A	83	LEU	5.8
1	B	97	GLN	5.6
1	A	84	GLU	5.3
1	B	98	GLY	5.2
1	A	115	LEU	5.1
1	A	98	GLY	4.7
1	B	511	GLY	4.5
1	B	93	VAL	4.5
1	A	502	ALA	4.2
1	A	503	LEU	4.2
1	A	109	GLY	4.1
1	A	82	LEU	4.0
1	A	79	GLY	3.9
1	B	100	PHE	3.8
1	A	81	ALA	3.8
1	A	107	ASN	3.5
1	B	825	ALA	3.5
1	A	854	LYS	3.5
1	B	211	TYR	3.4
1	B	105	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	501	PRO	3.2
1	B	625	PRO	3.2
1	B	510	GLN	3.2
1	A	497	HIS	3.2
1	B	509	TRP	3.1
1	A	106	LEU	3.1
1	B	824	GLY	3.1
1	A	77	PHE	3.0
1	B	626	ASN	3.0
1	A	496	ALA	3.0
1	B	341	ILE	2.9
1	A	341	ILE	2.9
1	B	512	LEU	2.8
1	B	674	ILE	2.8
1	A	504	ASN	2.7
1	B	115	LEU	2.7
1	A	467	ILE	2.7
1	B	80	GLN	2.7
1	A	278	PRO	2.6
1	A	78	THR	2.6
1	A	85	ASN	2.6
1	B	56	LEU	2.6
1	A	857	LYS	2.5
1	A	855	HIS	2.5
1	A	674	ILE	2.5
1	A	675	ILE	2.5
1	A	851	SER	2.5
1	B	96	LEU	2.5
1	A	80	GLN	2.4
1	B	119	LEU	2.4
1	B	386	ILE	2.4
1	A	638	LEU	2.4
1	A	509	TRP	2.4
1	B	102	THR	2.4
1	B	857	LYS	2.3
1	B	278	PRO	2.3
1	A	110	LYS	2.3
1	A	543	ARG	2.2
1	A	343	PRO	2.2
1	B	95	THR	2.2
1	A	642	ALA	2.2
1	A	511	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	856	VAL	2.2
1	A	386	ILE	2.2
1	B	94	GLN	2.2
1	B	424	ILE	2.1
1	B	675	ILE	2.1
1	A	105	LEU	2.1
1	A	643	VAL	2.1
1	B	628	LYS	2.1
1	A	424	ILE	2.1
1	A	348	LEU	2.1
1	A	254	ASN	2.0
1	B	317	ASN	2.0
1	B	342	VAL	2.0
1	A	644	LEU	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 monosaccharides in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	TPP	A	1001	26/26	0.98	0.10	15,19,23,24	0
2	TPP	B	1001	26/26	0.98	0.10	17,20,23,25	0
3	MG	A	1003	1/1	0.98	0.18	22,22,22,22	0
3	MG	A	1002	1/1	0.99	0.08	18,18,18,18	0
3	MG	B	1002	1/1	0.99	0.10	18,18,18,18	0

6.5 Other polymers (i)

There are no such residues in this entry.