



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 10:29 am BST

PDB ID : 3NAL  
Title : SR Ca(2+)-ATPase in the HnE2 state complexed with the Thapsigargin derivative DTB  
Authors : Winther, A.M.L.; Sonntag, Y.; Olesen, C.; Moller, J.V.; Nissen, P.  
Deposited on : 2010-06-02  
Resolution : 2.65 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](mailto: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 following versions of software and data (see [references ⓘ](#)) 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 : 2.11  
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) : 2.11

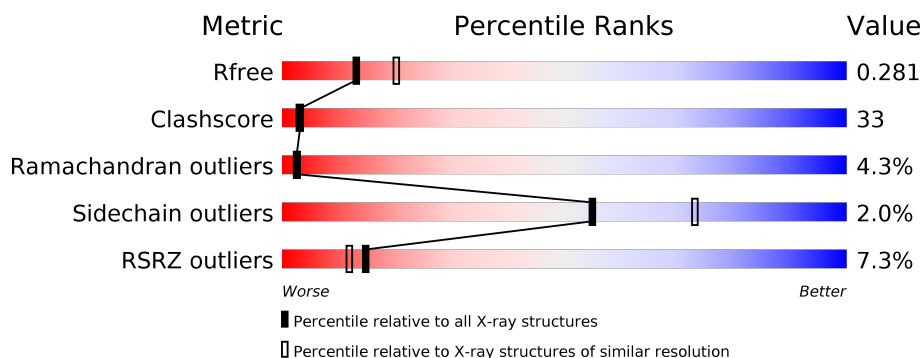
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.65 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	1332 (2.68-2.64)
Clashscore	141614	1374 (2.68-2.64)
Ramachandran outliers	138981	1349 (2.68-2.64)
Sidechain outliers	138945	1349 (2.68-2.64)
RSRZ outliers	127900	1318 (2.68-2.64)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	994	

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
3	MG	A	996	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7787 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 SERCA1a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	994	Total	C	N	O	S	0	0	0
			7671	4876	1287	1451	57			

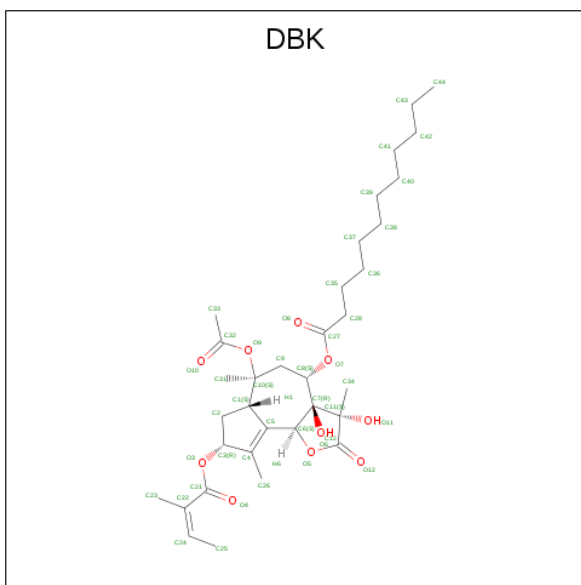
- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	K	0	0
			1	1		

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

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

- Molecule 4 is (3S,3aR,4S,6S,6aS,8R,9bS)-6-(acetyloxy)-3,3a-dihydroxy-3,6,9-trimethyl-8-[[[(2Z)-2-methylbut-2-enoyl]oxy]-2-oxo-2,3,3a,4,5,6,6a,7,8,9b-decahydroazuleno[4,5-b]furan-4-yl dodecanoate (three-letter code: DBK) (formula: C<sub>34</sub>H<sub>52</sub>O<sub>10</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			44	34	10		

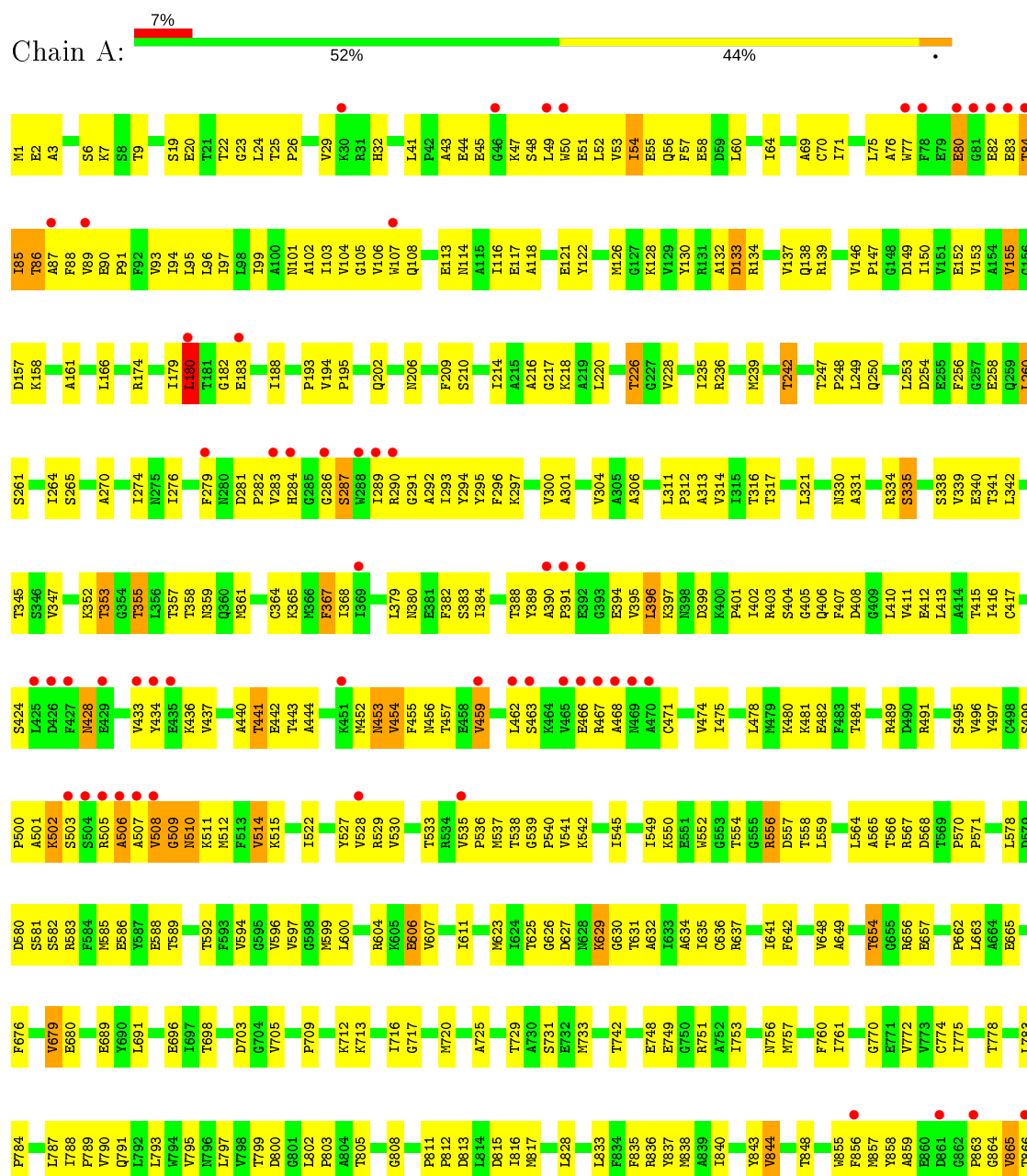
- Molecule 5 is water.

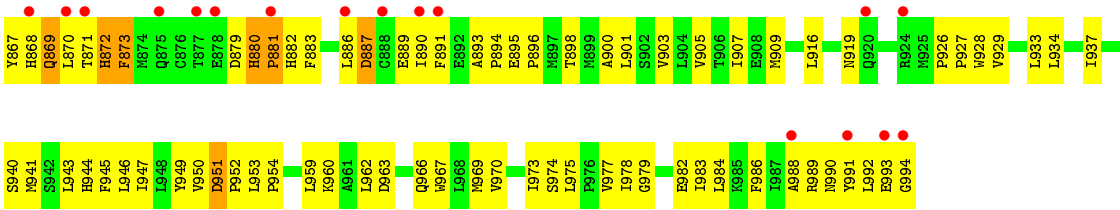
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	70	Total O 70 70	0	0

### 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 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: SERCA1a





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.33Å 71.33Å 591.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.65 49.72 – 2.65	Depositor EDS
% Data completeness (in resolution range)	97.5 (50.00-2.65) 97.5 (49.72-2.65)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.02 (at 2.65Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.255 , 0.283 0.248 , 0.281	Depositor DCC
$R_{free}$ test set	1322 reflections (2.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.3	Xtriage
Anisotropy	0.298	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 63.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	7787	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.31% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.50	0/7812	0.69	0/10592

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

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	7671	0	7766	514	0
2	A	1	0	0	0	0
3	A	1	0	0	0	0
4	A	44	0	52	15	0
5	A	70	0	0	5	0
All	All	7787	0	7818	518	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 33.

All (518) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:527:TYR:HB2	1:A:592:THR:HG22	1.26	1.10
1:A:679:VAL:HG12	1:A:680:GLU:H	1.05	1.09
1:A:342:LEU:O	1:A:345:THR:HG23	1.53	1.06
1:A:866:THR:HG23	1:A:867:TYR:H	1.10	1.06
1:A:856:PHE:O	1:A:864:GLY:HA2	1.63	0.99
1:A:654:THR:HG22	1:A:657:GLU:HG3	1.48	0.96
1:A:866:THR:HG23	1:A:867:TYR:N	1.79	0.95
1:A:459:VAL:HG23	1:A:462:LEU:HD12	1.48	0.95
1:A:751:ARG:HD2	1:A:817:MET:HE2	1.48	0.94
1:A:408:ASP:O	1:A:411:VAL:HG22	1.70	0.91
1:A:248:PRO:HG2	1:A:340:GLU:OE2	1.71	0.90
1:A:679:VAL:HG12	1:A:680:GLU:N	1.84	0.90
1:A:133:ASP:O	1:A:134:ARG:HG3	1.72	0.89
1:A:334:ARG:O	1:A:335:SER:HB3	1.71	0.89
1:A:679:VAL:CG1	1:A:680:GLU:H	1.87	0.87
1:A:283:VAL:HG13	1:A:284:HIS:ND1	1.89	0.87
1:A:751:ARG:HD2	1:A:817:MET:CE	2.05	0.86
1:A:950:VAL:O	1:A:954:PRO:HD3	1.73	0.86
1:A:500:PRO:HG2	1:A:509:GLY:HA2	1.58	0.85
1:A:50:TRP:O	1:A:54:ILE:HG12	1.75	0.85
1:A:153:VAL:HB	1:A:214:ILE:CD1	2.08	0.83
1:A:927:PRO:HB2	1:A:934:LEU:HD21	1.60	0.83
1:A:19:SER:OG	1:A:22:THR:HB	1.78	0.83
1:A:857:MET:SD	1:A:866:THR:O	2.37	0.83
1:A:909:MET:HE3	1:A:937:ILE:HG12	1.60	0.82
1:A:453:ASN:HB3	1:A:471:CYS:SG	2.20	0.81
1:A:153:VAL:HB	1:A:214:ILE:HD11	1.61	0.81
1:A:77:TRP:HB2	1:A:88:PHE:CE1	2.15	0.81
1:A:55:GLU:HA	1:A:58:GLU:HG2	1.63	0.81
1:A:951:ASP:O	1:A:954:PRO:HD2	1.80	0.81
1:A:748:GLU:HG3	1:A:817:MET:HE3	1.62	0.80
1:A:865:VAL:O	1:A:865:VAL:HG12	1.80	0.80
1:A:654:THR:HG22	1:A:657:GLU:H	1.46	0.80
1:A:80:GLU:CB	1:A:83:GLU:HB2	2.12	0.80
1:A:77:TRP:HB2	1:A:88:PHE:CZ	2.17	0.79
1:A:869:GLN:HG3	1:A:872:HIS:ND1	1.98	0.78
1:A:500:PRO:CG	1:A:509:GLY:HA2	2.13	0.78
1:A:898:THR:HG21	1:A:960:LYS:H	1.48	0.78
1:A:361:MET:HB3	1:A:599:MET:HE3	1.66	0.78
1:A:388:THR:HG22	1:A:390:ALA:H	1.47	0.78
1:A:894:PRO:O	1:A:898:THR:HG23	1.83	0.78
1:A:247:THR:HB	1:A:250:GLN:HG3	1.66	0.77

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:869:GLN:HG3	1:A:872:HIS:CE1	2.20	0.77
1:A:907:ILE:HG23	1:A:977:VAL:HG21	1.66	0.77
1:A:9:THR:HG23	1:A:166:LEU:HD23	1.67	0.76
1:A:879:ASP:OD1	1:A:882:HIS:HB3	1.85	0.76
1:A:969:MET:O	1:A:973:ILE:HG13	1.84	0.76
1:A:527:TYR:HB2	1:A:592:THR:CG2	2.12	0.75
1:A:880:HIS:N	1:A:881:PRO:HD3	2.02	0.75
1:A:974:SER:O	1:A:977:VAL:HG23	1.87	0.75
1:A:99:ILE:O	1:A:103:ILE:HG12	1.87	0.74
1:A:286:GLY:O	1:A:287:SER:HB2	1.88	0.74
1:A:361:MET:HE3	1:A:599:MET:HG3	1.68	0.74
1:A:86:THR:O	1:A:89:VAL:HG22	1.87	0.74
1:A:408:ASP:HA	1:A:411:VAL:HG13	1.68	0.73
1:A:689:GLU:HG3	1:A:713:LYS:CE	2.19	0.73
1:A:361:MET:HB3	1:A:599:MET:CE	2.19	0.73
1:A:411:VAL:HA	1:A:454:VAL:HG11	1.71	0.73
1:A:870:LEU:HD11	1:A:891:PHE:HE1	1.54	0.73
1:A:441:THR:HA	1:A:599:MET:HE2	1.71	0.72
1:A:527:TYR:CB	1:A:592:THR:HG22	2.13	0.72
1:A:654:THR:CG2	1:A:657:GLU:HG3	2.19	0.72
1:A:749:GLU:O	1:A:753:ILE:HG12	1.88	0.72
1:A:397:LYS:CB	1:A:402:ILE:HD11	2.19	0.72
1:A:397:LYS:HB3	1:A:402:ILE:HD11	1.71	0.72
1:A:941:MET:O	1:A:944:HIS:HB3	1.89	0.72
1:A:253:LEU:HD12	4:A:997:DBK:H43	1.73	0.71
1:A:9:THR:HG23	1:A:166:LEU:CD2	2.21	0.70
1:A:558:THR:HG22	1:A:634:ALA:HB1	1.74	0.70
1:A:253:LEU:O	1:A:253:LEU:HD23	1.90	0.70
1:A:791:GLN:HB3	1:A:901:LEU:HD12	1.74	0.70
1:A:281:ASP:HB3	1:A:282:PRO:CD	2.22	0.69
1:A:44:GLU:HG3	1:A:117:GLU:OE2	1.92	0.69
1:A:226:THR:HG21	5:A:1053:HOH:O	1.91	0.69
1:A:289:ILE:O	1:A:293:ILE:HG12	1.92	0.69
1:A:580:ASP:OD2	1:A:583:ARG:HD3	1.93	0.69
1:A:106:VAL:HG13	1:A:107:TRP:H	1.58	0.69
1:A:866:THR:CG2	1:A:867:TYR:N	2.53	0.69
1:A:654:THR:HG23	1:A:656:ARG:H	1.57	0.68
1:A:114:ASN:HB3	1:A:117:GLU:HG2	1.73	0.68
1:A:869:GLN:CG	1:A:872:HIS:ND1	2.56	0.68
1:A:407:PHE:O	1:A:411:VAL:HG13	1.94	0.68
1:A:6:SER:HA	1:A:194:VAL:O	1.94	0.68

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:CYS:O	1:A:474:VAL:HG22	1.94	0.68
1:A:453:ASN:CB	1:A:471:CYS:SG	2.81	0.67
1:A:249:LEU:HG	4:A:997:DBK:H42	1.75	0.67
1:A:32:HIS:CB	1:A:146:VAL:HG11	2.25	0.67
1:A:951:ASP:HB2	1:A:952:PRO:HD3	1.76	0.67
1:A:436:LYS:HG3	1:A:443:THR:HG21	1.76	0.67
1:A:802:LEU:HB2	1:A:803:PRO:HD3	1.76	0.67
1:A:253:LEU:HD12	4:A:997:DBK:C43	2.23	0.67
1:A:44:GLU:HG3	1:A:117:GLU:CD	2.14	0.67
1:A:549:ILE:HD11	1:A:596:VAL:HG11	1.75	0.67
1:A:879:ASP:CG	1:A:882:HIS:HB3	2.15	0.67
1:A:909:MET:CE	1:A:937:ILE:HA	2.25	0.66
1:A:689:GLU:HG3	1:A:713:LYS:HE2	1.78	0.66
1:A:926:PRO:HD2	1:A:929:VAL:HG23	1.78	0.66
1:A:95:LEU:O	1:A:99:ILE:HG12	1.96	0.65
1:A:313:ALA:O	1:A:317:THR:HG23	1.97	0.65
1:A:394:GLU:CD	1:A:396:LEU:HD21	2.17	0.65
1:A:47:LYS:HA	1:A:51:GLU:OE1	1.97	0.65
1:A:865:VAL:HG12	1:A:868:HIS:HB2	1.78	0.65
1:A:416:ILE:HD11	1:A:566:THR:HG22	1.78	0.65
1:A:368:ILE:HD13	1:A:410:LEU:CD2	2.27	0.65
1:A:80:GLU:CG	1:A:83:GLU:HB2	2.27	0.64
1:A:909:MET:HE3	1:A:937:ILE:HG23	1.80	0.64
1:A:530:VAL:HG23	1:A:533:THR:OG1	1.97	0.64
1:A:32:HIS:HB3	1:A:146:VAL:CG1	2.28	0.64
1:A:607:VAL:O	1:A:611:ILE:HG12	1.97	0.64
1:A:415:THR:HA	1:A:475:ILE:HD13	1.79	0.64
1:A:254:ASP:O	1:A:258:GLU:HG2	1.98	0.63
1:A:85:ILE:C	1:A:87:ALA:H	2.01	0.63
1:A:775:ILE:O	1:A:778:THR:HG22	1.99	0.63
1:A:813:ASP:O	1:A:816:ILE:HG13	1.98	0.63
1:A:886:LEU:HD12	1:A:887:ASP:O	1.98	0.63
1:A:155:VAL:HG22	1:A:216:ALA:HA	1.81	0.63
1:A:416:ILE:HD12	1:A:594:VAL:HG11	1.80	0.63
1:A:606:GLU:CD	1:A:606:GLU:H	2.01	0.62
1:A:748:GLU:HA	1:A:817:MET:HE1	1.81	0.62
1:A:943:LEU:O	1:A:946:LEU:HB3	1.98	0.62
1:A:436:LYS:CG	1:A:443:THR:HG21	2.29	0.62
1:A:179:ILE:HG12	5:A:1062:HOH:O	2.00	0.62
1:A:507:ALA:C	1:A:509:GLY:H	2.02	0.62
1:A:249:LEU:HD11	4:A:997:DBK:H40	1.81	0.62

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:757:MET:HA	1:A:760:PHE:CE2	2.34	0.62
1:A:48:SER:O	1:A:52:LEU:N	2.23	0.62
1:A:835:PHE:O	1:A:838:MET:HB3	1.98	0.62
1:A:331:ALA:HB1	1:A:733:MET:HE1	1.81	0.62
1:A:146:VAL:HG13	1:A:147:PRO:HD2	1.80	0.62
1:A:23:GLY:HA3	1:A:130:TYR:O	2.00	0.62
1:A:411:VAL:CB	1:A:454:VAL:HG11	2.30	0.62
1:A:394:GLU:HG3	1:A:396:LEU:HD21	1.81	0.61
1:A:950:VAL:O	1:A:954:PRO:CD	2.46	0.61
1:A:988:ALA:HA	1:A:992:LEU:HD23	1.81	0.61
1:A:535:VAL:HG13	1:A:536:PRO:HD2	1.82	0.61
1:A:368:ILE:HD13	1:A:410:LEU:HD23	1.83	0.61
1:A:557:ASP:HB3	1:A:559:LEU:HG	1.83	0.61
1:A:979:GLY:O	1:A:983:ILE:HG13	2.01	0.61
1:A:122:TYR:HA	1:A:158:LYS:NZ	2.16	0.61
1:A:843:TYR:CE2	1:A:977:VAL:HG22	2.36	0.61
1:A:950:VAL:HB	1:A:953:LEU:HD12	1.82	0.61
1:A:855:TRP:HA	1:A:859:ALA:HB2	1.82	0.61
1:A:155:VAL:CG2	1:A:217:GLY:H	2.13	0.60
1:A:408:ASP:HA	1:A:411:VAL:CG1	2.30	0.60
1:A:82:GLU:OE2	1:A:85:ILE:HB	2.00	0.60
4:A:997:DBK:H31	4:A:997:DBK:O10	1.98	0.60
1:A:556:ARG:HH11	1:A:556:ARG:HG2	1.66	0.60
1:A:837:TYR:HB2	4:A:997:DBK:H33	1.82	0.60
1:A:32:HIS:HB3	1:A:146:VAL:HG11	1.83	0.60
1:A:317:THR:O	1:A:321:LEU:HG	2.01	0.60
1:A:725:ALA:O	1:A:729:THR:HG23	2.01	0.60
1:A:848:THR:HA	1:A:903:VAL:HG11	1.83	0.60
1:A:882:HIS:O	1:A:883:PHE:HB2	2.01	0.60
1:A:537:MET:HE3	1:A:542:LYS:HD2	1.83	0.60
1:A:394:GLU:CG	1:A:396:LEU:HD21	2.32	0.60
1:A:416:ILE:HD11	1:A:566:THR:CG2	2.31	0.60
1:A:474:VAL:HG23	1:A:475:ILE:N	2.16	0.60
1:A:312:PRO:O	1:A:316:THR:HG23	2.01	0.59
1:A:260:LEU:O	1:A:260:LEU:HD12	2.03	0.59
1:A:869:GLN:O	1:A:869:GLN:HG2	2.03	0.59
1:A:402:ILE:HG22	1:A:403:ARG:N	2.17	0.59
1:A:174:ARG:HD3	1:A:188:ILE:HG12	1.84	0.59
1:A:580:ASP:O	1:A:582:SER:N	2.36	0.59
1:A:871:THR:C	1:A:873:PHE:H	2.06	0.59
1:A:629:LYS:O	1:A:632:ALA:N	2.35	0.59

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:VAL:O	1:A:93:VAL:HG23	2.02	0.59
1:A:879:ASP:C	1:A:881:PRO:CD	2.71	0.58
1:A:512:MET:HE3	1:A:571:PRO:HD2	1.85	0.58
1:A:60:LEU:HD21	1:A:261:SER:HB2	1.84	0.58
1:A:412:GLU:OE1	1:A:529:ARG:HD2	2.02	0.58
1:A:870:LEU:HD11	1:A:891:PHE:CE1	2.38	0.58
1:A:106:VAL:HG13	1:A:107:TRP:N	2.17	0.58
1:A:788:ILE:HG22	1:A:790:VAL:H	1.68	0.58
1:A:848:THR:HG22	1:A:903:VAL:HG13	1.85	0.58
1:A:101:ASN:C	1:A:101:ASN:OD1	2.41	0.58
1:A:247:THR:HG22	1:A:340:GLU:OE1	2.03	0.58
1:A:334:ARG:O	1:A:335:SER:CB	2.48	0.58
1:A:411:VAL:HG12	1:A:454:VAL:HG13	1.86	0.57
1:A:76:ALA:HB1	1:A:87:ALA:O	2.03	0.57
1:A:545:ILE:O	1:A:549:ILE:HG12	2.04	0.57
1:A:270:ALA:O	1:A:274:ILE:HG12	2.05	0.57
1:A:134:ARG:NH1	1:A:138:GLN:HG2	2.19	0.57
1:A:247:THR:CG2	1:A:340:GLU:OE1	2.53	0.57
1:A:500:PRO:CD	1:A:509:GLY:HA2	2.35	0.57
1:A:866:THR:CG2	1:A:867:TYR:H	1.92	0.57
1:A:264:ILE:HG22	1:A:265:SER:N	2.18	0.57
1:A:507:ALA:O	1:A:509:GLY:N	2.38	0.57
1:A:953:LEU:HB2	1:A:954:PRO:HD3	1.87	0.57
1:A:962:LEU:HD13	1:A:966:GLN:HB2	1.87	0.57
1:A:411:VAL:HA	1:A:454:VAL:HG21	1.87	0.57
1:A:415:THR:HA	1:A:475:ILE:HG21	1.87	0.57
1:A:24:LEU:HD12	1:A:149:ASP:HB3	1.86	0.57
1:A:32:HIS:HB2	1:A:146:VAL:HG11	1.86	0.57
1:A:283:VAL:HG13	1:A:284:HIS:CE1	2.40	0.56
1:A:367:PHE:CD2	1:A:596:VAL:HG22	2.39	0.56
1:A:440:ALA:HA	1:A:443:THR:HG22	1.87	0.56
1:A:97:ILE:HD11	1:A:797:LEU:HD11	1.87	0.56
1:A:101:ASN:OD1	1:A:102:ALA:N	2.38	0.56
1:A:901:LEU:CD2	1:A:944:HIS:HE1	2.18	0.56
1:A:444:ALA:HB3	1:A:599:MET:HE1	1.88	0.56
1:A:565:ALA:HA	1:A:594:VAL:HG12	1.88	0.56
1:A:161:ALA:HA	1:A:210:SER:HB2	1.87	0.56
1:A:397:LYS:HB2	1:A:402:ILE:HD11	1.88	0.56
1:A:179:ILE:O	1:A:705:VAL:HG12	2.05	0.56
1:A:80:GLU:HB2	1:A:83:GLU:HB2	1.88	0.56
1:A:478:LEU:HD21	1:A:505:ARG:NH1	2.20	0.55

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:412:GLU:OE2	1:A:566:THR:HG21	2.06	0.55
1:A:865:VAL:CG1	1:A:865:VAL:O	2.50	0.55
1:A:179:ILE:HG13	1:A:180:LEU:N	2.20	0.55
1:A:870:LEU:CD1	1:A:891:PHE:HE1	2.17	0.55
1:A:480:LYS:HB3	1:A:499:SER:O	2.06	0.55
1:A:880:HIS:N	1:A:881:PRO:CD	2.70	0.55
4:A:997:DBK:C27	4:A:997:DBK:O11	2.54	0.55
1:A:774:CYS:SG	1:A:787:LEU:HD12	2.47	0.55
1:A:455:PHE:HB2	1:A:457:THR:HG23	1.88	0.55
1:A:748:GLU:HG3	1:A:817:MET:CE	2.33	0.55
1:A:383:SER:C	1:A:384:ILE:HD12	2.27	0.55
1:A:411:VAL:HG12	1:A:454:VAL:CG1	2.37	0.55
1:A:463:SER:O	1:A:467:ARG:HB2	2.07	0.55
1:A:462:LEU:HD22	1:A:466:GLU:OE1	2.07	0.55
1:A:411:VAL:CA	1:A:454:VAL:HG11	2.36	0.54
1:A:83:GLU:O	1:A:84:THR:HG23	2.08	0.54
1:A:411:VAL:HA	1:A:454:VAL:CG1	2.37	0.54
1:A:411:VAL:HB	1:A:454:VAL:HG11	1.88	0.54
1:A:895:GLU:N	1:A:896:PRO:HD2	2.23	0.54
1:A:331:ALA:HB1	1:A:733:MET:CE	2.36	0.54
1:A:1:MET:HG2	1:A:1:MET:O	2.08	0.54
1:A:580:ASP:C	1:A:582:SER:H	2.09	0.54
1:A:756:ASN:ND2	1:A:808:GLY:O	2.33	0.54
1:A:903:VAL:O	1:A:907:ILE:HG13	2.07	0.54
1:A:247:THR:CG2	1:A:248:PRO:HD2	2.38	0.54
1:A:126:MET:HG3	1:A:139:ARG:NH1	2.23	0.54
1:A:157:ASP:HB2	1:A:214:ILE:HD12	1.88	0.54
1:A:412:GLU:OE2	1:A:529:ARG:NH1	2.41	0.54
1:A:585:MET:O	1:A:589:THR:HG23	2.08	0.54
1:A:559:LEU:HD23	1:A:600:LEU:HB2	1.88	0.54
1:A:900:ALA:O	1:A:903:VAL:HG12	2.08	0.54
1:A:226:THR:HG22	5:A:1006:HOH:O	2.08	0.53
1:A:901:LEU:C	1:A:901:LEU:HD23	2.28	0.53
1:A:909:MET:HE3	1:A:937:ILE:CG1	2.36	0.53
1:A:508:VAL:HG23	1:A:511:LYS:HE2	1.89	0.53
1:A:474:VAL:CG2	1:A:475:ILE:N	2.70	0.53
1:A:951:ASP:O	1:A:952:PRO:C	2.46	0.53
1:A:648:VAL:O	1:A:648:VAL:HG12	2.08	0.53
1:A:879:ASP:C	1:A:881:PRO:HD3	2.28	0.53
1:A:311:LEU:HB3	1:A:312:PRO:HD3	1.91	0.53
1:A:397:LYS:HB2	1:A:402:ILE:CD1	2.38	0.53

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:442:GLU:HG2	1:A:515:LYS:NZ	2.23	0.53
1:A:567:ARG:HD3	1:A:570:PRO:HA	1.91	0.53
1:A:864:GLY:C	1:A:866:THR:H	2.12	0.53
1:A:367:PHE:C	1:A:367:PHE:CD1	2.82	0.53
1:A:636:CYS:HB3	1:A:641:ILE:HB	1.90	0.53
1:A:865:VAL:HG21	1:A:870:LEU:HD13	1.91	0.53
1:A:536:PRO:O	1:A:538:THR:HG23	2.08	0.53
1:A:791:GLN:HB3	1:A:901:LEU:CD1	2.38	0.53
1:A:452:MET:O	1:A:454:VAL:N	2.42	0.52
1:A:54:ILE:O	1:A:57:PHE:N	2.36	0.52
1:A:153:VAL:HB	1:A:214:ILE:HD13	1.91	0.52
1:A:334:ARG:NH1	1:A:729:THR:HA	2.24	0.52
1:A:80:GLU:HB2	1:A:83:GLU:CB	2.39	0.52
1:A:301:ALA:HA	1:A:789:PRO:HG3	1.91	0.52
1:A:963:ASP:OD1	1:A:966:GLN:HG3	2.10	0.52
1:A:249:LEU:CD1	4:A:997:DBK:H40	2.40	0.52
1:A:772:VAL:HG21	4:A:997:DBK:H23	1.91	0.52
1:A:495:SER:HB3	1:A:514:VAL:HG12	1.92	0.52
1:A:654:THR:HG23	1:A:656:ARG:N	2.25	0.52
1:A:717:GLY:O	1:A:731:SER:HB2	2.09	0.52
1:A:146:VAL:HG13	1:A:147:PRO:CD	2.39	0.52
1:A:424:SER:O	1:A:437:VAL:HB	2.09	0.51
1:A:871:THR:O	1:A:873:PHE:N	2.42	0.51
1:A:811:PRO:HG3	1:A:929:VAL:CG1	2.41	0.51
4:A:997:DBK:H9	4:A:997:DBK:O10	2.10	0.51
1:A:966:GLN:O	1:A:969:MET:HB3	2.10	0.51
1:A:25:THR:HB	1:A:26:PRO:CD	2.41	0.51
1:A:113:GLU:HG3	1:A:334:ARG:HH22	1.76	0.51
1:A:388:THR:HG22	1:A:390:ALA:N	2.20	0.51
1:A:879:ASP:OD2	1:A:882:HIS:HB3	2.10	0.51
1:A:22:THR:HG22	1:A:23:GLY:O	2.10	0.51
1:A:416:ILE:CD1	1:A:594:VAL:HG11	2.40	0.51
1:A:857:MET:HB3	1:A:866:THR:O	2.11	0.51
1:A:330:ASN:O	1:A:742:THR:HG21	2.11	0.51
1:A:926:PRO:HB2	1:A:928:TRP:CE2	2.46	0.51
1:A:281:ASP:HB3	1:A:282:PRO:HD2	1.93	0.51
1:A:412:GLU:OE1	1:A:529:ARG:CD	2.58	0.51
1:A:235:ILE:HG23	1:A:709:PRO:HG3	1.93	0.51
1:A:886:LEU:C	1:A:886:LEU:HD12	2.32	0.51
1:A:417:CYS:SG	1:A:564:LEU:HD11	2.51	0.50
1:A:527:TYR:CD2	1:A:592:THR:HG22	2.45	0.50

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:256:PHE:CD1	4:A:997:DBK:H35	2.45	0.50
1:A:291:GLY:O	1:A:294:TYR:HB3	2.12	0.50
1:A:292:ALA:HB1	1:A:296:PHE:HE2	1.75	0.50
1:A:202:GLN:CD	1:A:489:ARG:HH11	2.14	0.50
1:A:260:LEU:HD11	1:A:306:ALA:HB1	1.93	0.50
1:A:388:THR:HG22	1:A:389:TYR:N	2.26	0.50
1:A:788:ILE:HG23	1:A:789:PRO:HD2	1.93	0.50
1:A:986:PHE:CZ	1:A:990:ASN:ND2	2.79	0.50
1:A:380:ASN:O	1:A:382:PHE:CD2	2.65	0.50
1:A:836:ARG:O	1:A:840:ILE:HG12	2.12	0.50
1:A:898:THR:HG22	1:A:959:LEU:CD2	2.41	0.50
1:A:7:LYS:O	1:A:193:PRO:HB3	2.12	0.50
1:A:541:VAL:O	1:A:545:ILE:HG13	2.12	0.50
1:A:193:PRO:HA	1:A:206:ASN:ND2	2.26	0.50
1:A:116:ILE:HG23	1:A:236:ARG:HG3	1.94	0.50
1:A:556:ARG:HG2	1:A:556:ARG:NH1	2.27	0.50
1:A:679:VAL:CG1	1:A:680:GLU:N	2.57	0.50
1:A:863:PRO:CG	1:A:890:ILE:HG21	2.42	0.50
1:A:114:ASN:HB3	1:A:117:GLU:CG	2.41	0.49
1:A:247:THR:HG23	1:A:248:PRO:HD2	1.94	0.49
1:A:396:LEU:HD23	1:A:401:PRO:HA	1.94	0.49
1:A:879:ASP:OD1	1:A:882:HIS:CB	2.58	0.49
1:A:304:VAL:HG13	1:A:793:LEU:CD2	2.41	0.49
1:A:962:LEU:HD12	1:A:967:TRP:CD1	2.47	0.49
1:A:384:ILE:HD12	1:A:384:ILE:N	2.27	0.49
1:A:433:VAL:HG12	1:A:434:TYR:N	2.27	0.49
1:A:550:LYS:O	1:A:554:THR:HB	2.12	0.49
1:A:813:ASP:HB3	1:A:815:ASP:OD1	2.13	0.49
1:A:161:ALA:CA	1:A:210:SER:HB2	2.42	0.49
1:A:342:LEU:O	1:A:345:THR:CG2	2.44	0.49
1:A:637:ARG:HG2	1:A:642:PHE:HB2	1.94	0.49
1:A:748:GLU:HA	1:A:817:MET:CE	2.43	0.49
4:A:997:DBK:C31	4:A:997:DBK:O10	2.60	0.49
1:A:253:LEU:HD12	4:A:997:DBK:H43A	1.94	0.49
1:A:441:THR:HA	1:A:599:MET:CE	2.41	0.49
1:A:459:VAL:HG22	1:A:467:ARG:HD2	1.95	0.49
1:A:843:TYR:CD2	1:A:977:VAL:HG22	2.48	0.49
1:A:380:ASN:O	1:A:382:PHE:CE2	2.65	0.49
1:A:501:ALA:O	1:A:502:LYS:HG2	2.13	0.49
1:A:944:HIS:O	1:A:947:ILE:HG12	2.12	0.49
1:A:988:ALA:HA	1:A:992:LEU:CD2	2.43	0.49

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:LEU:HB2	4:A:997:DBK:H41A	1.95	0.49
1:A:481:LYS:HD3	1:A:484:THR:CG2	2.43	0.48
1:A:118:ALA:O	1:A:121:GLU:HG2	2.13	0.48
1:A:130:TYR:CE1	1:A:137:VAL:HB	2.48	0.48
1:A:358:THR:O	1:A:359:ASN:HB3	2.12	0.48
1:A:909:MET:HE2	1:A:940:SER:HB2	1.95	0.48
1:A:836:ARG:HG2	1:A:984:LEU:HD13	1.95	0.48
1:A:919:ASN:O	1:A:989:ARG:HD3	2.13	0.48
1:A:436:LYS:HG3	1:A:443:THR:CG2	2.44	0.48
1:A:770:GLY:HA3	1:A:844:VAL:CG2	2.43	0.48
1:A:94:ILE:O	1:A:97:ILE:HB	2.13	0.48
1:A:528:VAL:HG23	1:A:528:VAL:O	2.12	0.48
1:A:174:ARG:CD	1:A:188:ILE:HG12	2.43	0.48
1:A:926:PRO:HD2	1:A:929:VAL:CG2	2.44	0.48
1:A:174:ARG:HB2	1:A:216:ALA:HB3	1.95	0.48
1:A:364:CYS:O	1:A:383:SER:HA	2.14	0.48
1:A:402:ILE:CG2	1:A:403:ARG:N	2.76	0.48
1:A:604:ARG:HB2	1:A:607:VAL:HG23	1.94	0.48
1:A:395:VAL:O	1:A:396:LEU:HD23	2.14	0.48
1:A:962:LEU:CD1	1:A:967:TRP:CD1	2.96	0.48
1:A:629:LYS:O	1:A:631:THR:N	2.47	0.48
1:A:478:LEU:HD21	1:A:505:ARG:HH12	1.79	0.47
1:A:564:LEU:O	1:A:594:VAL:HG12	2.14	0.47
1:A:453:ASN:HB2	1:A:471:CYS:SG	2.54	0.47
1:A:365:LYS:HB3	1:A:552:TRP:CH2	2.49	0.47
1:A:580:ASP:C	1:A:582:SER:N	2.67	0.47
1:A:202:GLN:NE2	1:A:489:ARG:HD2	2.28	0.47
1:A:428:ASN:H	1:A:428:ASN:HD22	1.63	0.47
1:A:415:THR:HG22	1:A:475:ILE:HG23	1.95	0.47
1:A:962:LEU:HB2	1:A:966:GLN:OE1	2.15	0.47
1:A:967:TRP:O	1:A:970:VAL:HB	2.15	0.47
1:A:992:LEU:O	1:A:994:GLY:N	2.44	0.47
1:A:102:ALA:O	1:A:106:VAL:HG12	2.14	0.47
1:A:345:THR:HG22	1:A:716:ILE:HD13	1.97	0.47
1:A:2:GLU:CD	1:A:2:GLU:H	2.17	0.47
1:A:945:PHE:HD1	1:A:949:TYR:HE2	1.62	0.47
1:A:25:THR:O	1:A:29:VAL:HG23	2.14	0.47
1:A:85:ILE:C	1:A:87:ALA:N	2.67	0.47
1:A:69:ALA:HB2	1:A:94:ILE:HG21	1.97	0.47
1:A:249:LEU:HB2	1:A:340:GLU:OE1	2.14	0.47
1:A:783:LEU:HB2	1:A:784:PRO:CD	2.45	0.47

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:909:MET:CE	1:A:937:ILE:HG23	2.44	0.47
1:A:146:VAL:CG1	1:A:147:PRO:HD2	2.45	0.46
1:A:48:SER:H	1:A:51:GLU:HB2	1.80	0.46
1:A:85:ILE:O	1:A:87:ALA:N	2.48	0.46
1:A:500:PRO:HG2	1:A:509:GLY:CA	2.39	0.46
1:A:80:GLU:CB	1:A:83:GLU:CB	2.90	0.46
1:A:122:TYR:HA	1:A:158:LYS:HZ3	1.79	0.46
1:A:442:GLU:HG2	1:A:515:LYS:HZ2	1.79	0.46
1:A:45:GLU:HG3	1:A:45:GLU:O	2.16	0.46
1:A:898:THR:HG22	1:A:959:LEU:HA	1.98	0.46
1:A:412:GLU:HA	1:A:415:THR:OG1	2.16	0.46
1:A:751:ARG:HD2	1:A:817:MET:HE1	1.91	0.46
1:A:783:LEU:C	1:A:783:LEU:HD12	2.36	0.46
1:A:146:VAL:CG1	1:A:147:PRO:CD	2.94	0.46
1:A:871:THR:C	1:A:873:PHE:N	2.69	0.46
1:A:253:LEU:C	1:A:253:LEU:HD23	2.35	0.46
1:A:503:SER:HA	1:A:506:ALA:HB2	1.98	0.46
1:A:900:ALA:HA	1:A:903:VAL:HG12	1.97	0.46
1:A:811:PRO:HG3	1:A:929:VAL:HG11	1.98	0.46
1:A:478:LEU:HD11	1:A:505:ARG:NH1	2.30	0.45
1:A:905:VAL:O	1:A:909:MET:HG2	2.16	0.45
1:A:522:ILE:HG22	1:A:542:LYS:HE3	1.98	0.45
1:A:413:LEU:HG	1:A:564:LEU:HD12	1.98	0.45
1:A:898:THR:HG21	1:A:960:LYS:N	2.24	0.45
1:A:56:GLN:NE2	1:A:105:GLY:HA3	2.32	0.45
1:A:355:THR:HG21	1:A:720:MET:CE	2.46	0.45
1:A:55:GLU:HA	1:A:58:GLU:CG	2.40	0.45
1:A:19:SER:HG	1:A:22:THR:HB	1.80	0.45
1:A:507:ALA:C	1:A:509:GLY:N	2.70	0.45
1:A:352:LYS:HE3	1:A:625:THR:OG1	2.16	0.45
1:A:70:CYS:O	1:A:71:ILE:C	2.53	0.45
1:A:505:ARG:O	1:A:507:ALA:N	2.50	0.45
1:A:482:GLU:HB2	1:A:497:TYR:O	2.15	0.45
1:A:182:GLY:O	1:A:183:GLU:C	2.54	0.45
1:A:152:GLU:OE2	1:A:218:LYS:HE3	2.17	0.45
1:A:455:PHE:O	1:A:456:ASN:HB2	2.17	0.45
1:A:530:VAL:O	1:A:530:VAL:HG23	2.17	0.45
1:A:539:GLY:N	1:A:540:PRO:HD2	2.31	0.45
1:A:60:LEU:HD21	1:A:261:SER:CB	2.47	0.45
1:A:855:TRP:CA	1:A:859:ALA:HB2	2.47	0.45
1:A:462:LEU:HB3	1:A:466:GLU:HG3	1.99	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:811:PRO:HA	1:A:812:PRO:HD3	1.82	0.45
1:A:48:SER:O	1:A:49:LEU:C	2.56	0.44
1:A:856:PHE:HB3	1:A:870:LEU:CD2	2.47	0.44
1:A:300:VAL:HG23	1:A:301:ALA:N	2.31	0.44
1:A:689:GLU:CD	1:A:713:LYS:HZ1	2.21	0.44
1:A:865:VAL:O	1:A:866:THR:HG22	2.17	0.44
1:A:391:PRO:HD3	1:A:434:TYR:CD2	2.52	0.44
1:A:757:MET:O	1:A:761:ILE:HG13	2.18	0.44
1:A:783:LEU:HB3	1:A:871:THR:HG22	2.00	0.44
1:A:405:GLY:C	1:A:407:PHE:H	2.21	0.44
1:A:404:SER:OG	1:A:452:MET:HB2	2.18	0.44
1:A:478:LEU:HG	1:A:505:ARG:HH11	1.83	0.44
1:A:662:PRO:HD2	1:A:665:GLU:OE1	2.18	0.44
1:A:527:TYR:HD2	1:A:592:THR:HG22	1.82	0.43
1:A:96:LEU:HA	1:A:96:LEU:HD23	1.86	0.43
1:A:239:MET:O	1:A:242:THR:HG22	2.18	0.43
1:A:478:LEU:CG	1:A:505:ARG:NH1	2.81	0.43
1:A:691:LEU:O	1:A:696:GLU:HB2	2.17	0.43
1:A:799:THR:HG22	5:A:1066:HOH:O	2.17	0.43
1:A:662:PRO:O	1:A:663:LEU:C	2.57	0.43
1:A:294:TYR:HD2	1:A:295:TYR:CD1	2.37	0.43
1:A:453:ASN:O	1:A:453:ASN:CG	2.56	0.43
1:A:789:PRO:O	1:A:793:LEU:HG	2.18	0.43
1:A:80:GLU:HB3	1:A:83:GLU:HB2	1.98	0.43
1:A:909:MET:CE	1:A:940:SER:HB2	2.48	0.43
1:A:314:VAL:HG22	1:A:805:THR:HG23	2.01	0.43
1:A:411:VAL:HA	1:A:454:VAL:CG2	2.49	0.43
1:A:459:VAL:CG2	1:A:467:ARG:HD2	2.49	0.43
1:A:909:MET:HE1	1:A:937:ILE:HA	1.99	0.43
1:A:133:ASP:O	1:A:134:ARG:CG	2.56	0.43
1:A:799:THR:HG21	5:A:1040:HOH:O	2.18	0.43
1:A:41:LEU:HB3	1:A:236:ARG:HD2	2.00	0.43
1:A:898:THR:CG2	1:A:959:LEU:HA	2.49	0.43
1:A:180:LEU:HD12	1:A:705:VAL:CG1	2.49	0.42
1:A:484:THR:HG22	1:A:496:VAL:HG12	2.01	0.42
1:A:77:TRP:HB2	1:A:88:PHE:HE1	1.75	0.42
1:A:865:VAL:CG2	1:A:870:LEU:HD13	2.49	0.42
1:A:978:ILE:O	1:A:982:GLU:HG2	2.19	0.42
1:A:412:GLU:O	1:A:416:ILE:HG13	2.20	0.42
1:A:530:VAL:CG2	1:A:533:THR:OG1	2.65	0.42
1:A:416:ILE:CD1	1:A:566:THR:HG22	2.47	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:VAL:O	1:A:56:GLN:HB2	2.19	0.42
1:A:20:GLU:HG3	1:A:166:LEU:HD13	2.00	0.42
1:A:844:VAL:HG12	1:A:907:ILE:HG21	2.01	0.42
1:A:90:GLU:HB3	1:A:91:PRO:CD	2.50	0.42
1:A:453:ASN:O	1:A:453:ASN:OD1	2.37	0.42
1:A:69:ALA:HB2	1:A:94:ILE:CG2	2.49	0.42
1:A:828:LEU:HB2	4:A:997:DBK:H28	2.01	0.42
1:A:85:ILE:HG23	1:A:86:THR:N	2.33	0.42
1:A:901:LEU:CD2	1:A:944:HIS:CE1	2.99	0.42
1:A:491:ARG:HE	1:A:588:GLU:CD	2.22	0.42
1:A:748:GLU:CG	1:A:817:MET:HE3	2.42	0.42
1:A:104:VAL:O	1:A:108:GLN:HB2	2.20	0.42
1:A:623:MET:HE1	1:A:635:ILE:CG2	2.50	0.42
1:A:95:LEU:HD23	1:A:95:LEU:HA	1.85	0.42
1:A:174:ARG:NE	1:A:188:ILE:CG1	2.82	0.42
1:A:276:ILE:HD12	1:A:279:PHE:CD2	2.55	0.42
1:A:529:ARG:NH2	1:A:568:ASP:OD1	2.52	0.42
1:A:180:LEU:HA	1:A:180:LEU:HD12	1.87	0.41
1:A:242:THR:HG21	1:A:712:LYS:HG2	2.02	0.41
1:A:462:LEU:HB3	1:A:466:GLU:CD	2.40	0.41
1:A:54:ILE:O	1:A:55:GLU:C	2.58	0.41
1:A:114:ASN:CB	1:A:117:GLU:HG2	2.47	0.41
1:A:347:VAL:HG21	1:A:696:GLU:OE1	2.20	0.41
1:A:900:ALA:O	1:A:903:VAL:CG1	2.68	0.41
1:A:56:GLN:CD	1:A:105:GLY:HA3	2.40	0.41
1:A:228:VAL:CG1	1:A:228:VAL:O	2.67	0.41
1:A:390:ALA:HA	1:A:391:PRO:HD3	1.85	0.41
1:A:689:GLU:CD	1:A:713:LYS:NZ	2.74	0.41
1:A:75:LEU:HD13	1:A:297:LYS:HG3	2.03	0.41
1:A:909:MET:HE3	1:A:937:ILE:CG2	2.49	0.41
1:A:947:ILE:HA	1:A:953:LEU:HD13	2.03	0.41
1:A:975:LEU:HD23	1:A:975:LEU:HA	1.83	0.41
1:A:128:LYS:HE3	1:A:152:GLU:O	2.20	0.41
1:A:155:VAL:HG23	1:A:217:GLY:H	1.84	0.41
1:A:56:GLN:OE1	1:A:105:GLY:HA3	2.20	0.41
1:A:509:GLY:O	1:A:510:ASN:C	2.58	0.41
1:A:863:PRO:HG2	1:A:890:ILE:HG21	2.02	0.41
1:A:132:ALA:C	1:A:134:ARG:H	2.23	0.41
1:A:338:SER:O	1:A:339:VAL:C	2.58	0.41
1:A:856:PHE:CG	1:A:870:LEU:HD21	2.55	0.41
1:A:180:LEU:CD2	1:A:209:PHE:HB3	2.50	0.41

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:462:LEU:HB3	1:A:466:GLU:CG	2.51	0.41
1:A:795:VAL:O	1:A:800:ASP:HB2	2.21	0.41
1:A:24:LEU:HG	1:A:149:ASP:HA	2.03	0.41
1:A:648:VAL:O	1:A:649:ALA:C	2.59	0.41
1:A:833:LEU:HD11	1:A:837:TYR:CE2	2.56	0.41
1:A:150:ILE:CG2	1:A:220:LEU:HD11	2.51	0.41
1:A:281:ASP:HB3	1:A:282:PRO:HD3	2.00	0.41
1:A:353:THR:O	1:A:357:THR:OG1	2.32	0.41
1:A:60:LEU:O	1:A:64:ILE:HG13	2.21	0.41
1:A:77:TRP:CG	1:A:77:TRP:O	2.73	0.41
1:A:882:HIS:O	1:A:883:PHE:CB	2.66	0.41
1:A:113:GLU:CG	1:A:334:ARG:HH22	2.34	0.41
1:A:379:LEU:CD1	1:A:379:LEU:N	2.84	0.41
1:A:583:ARG:O	1:A:586:GLU:HB3	2.21	0.41
1:A:893:ALA:HA	1:A:894:PRO:HD3	1.80	0.41
1:A:788:ILE:HA	1:A:788:ILE:HD13	1.80	0.40
1:A:869:GLN:HG2	1:A:872:HIS:ND1	2.35	0.40
1:A:676:PHE:HB3	1:A:679:VAL:CG2	2.51	0.40
1:A:379:LEU:HD12	1:A:379:LEU:N	2.37	0.40
1:A:444:ALA:CB	1:A:599:MET:HE1	2.50	0.40
1:A:626:GLY:O	1:A:627:ASP:C	2.58	0.40
1:A:916:LEU:HD11	1:A:933:LEU:HD23	2.03	0.40
1:A:950:VAL:HG12	1:A:952:PRO:HD2	2.02	0.40
1:A:155:VAL:HG22	1:A:217:GLY:H	1.84	0.40
1:A:290:ARG:HB3	1:A:290:ARG:NH1	2.37	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	992/994 (100%)	853 (86%)	96 (10%)	43 (4%)	2 3

All (43) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	ALA
1	A	80	GLU
1	A	86	THR
1	A	287	SER
1	A	453	ASN
1	A	506	ALA
1	A	508	VAL
1	A	629	LYS
1	A	887	ASP
1	A	133	ASP
1	A	180	LEU
1	A	335	SER
1	A	502	LYS
1	A	510	ASN
1	A	581	SER
1	A	630	GLY
1	A	865	VAL
1	A	869	GLN
1	A	872	HIS
1	A	880	HIS
1	A	84	THR
1	A	353	THR
1	A	509	GLY
1	A	881	PRO
1	A	993	GLU
1	A	3	ALA
1	A	85	ILE
1	A	399	ASP
1	A	991	TYR
1	A	406	GLN
1	A	454	VAL
1	A	468	ALA
1	A	556	ARG
1	A	578	LEU
1	A	703	ASP
1	A	858	TYR
1	A	873	PHE
1	A	951	ASP
1	A	679	VAL
1	A	54	ILE
1	A	155	VAL
1	A	459	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	195	PRO

### 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	840/840 (100%)	823 (98%)	17 (2%)	55 73

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

Mol	Chain	Res	Type
1	A	180	LEU
1	A	226	THR
1	A	242	THR
1	A	260	LEU
1	A	341	THR
1	A	355	THR
1	A	367	PHE
1	A	396	LEU
1	A	428	ASN
1	A	441	THR
1	A	514	VAL
1	A	597	VAL
1	A	606	GLU
1	A	654	THR
1	A	698	THR
1	A	844	VAL
1	A	889	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	202	GLN
1	A	796	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 carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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$
4	DBK	A	997	-	41,46,46	1.31	2 (4%)	39,68,68	2.35	13 (33%)

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	DBK	A	997	-	-	0/30/92/92	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	997	DBK	C4-C5	5.80	1.39	1.34
4	A	997	DBK	O9-C10	-3.02	1.43	1.48

All (13) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	997	DBK	C3-O3-C21	-6.87	109.57	116.22
4	A	997	DBK	C8-O7-C27	-5.58	107.41	117.92
4	A	997	DBK	O7-C27-C28	4.58	121.37	111.50
4	A	997	DBK	O9-C32-C33	4.14	118.21	110.68
4	A	997	DBK	O3-C21-C22	3.91	121.33	111.52
4	A	997	DBK	O7-C8-C9	3.25	112.44	106.63
4	A	997	DBK	C10-O9-C32	-3.19	113.97	121.53
4	A	997	DBK	O12-C12-C11	-3.14	125.13	128.28
4	A	997	DBK	C11-C7-C6	-2.94	97.36	103.03
4	A	997	DBK	C26-C4-C5	-2.35	123.95	129.82
4	A	997	DBK	O7-C27-O8	-2.30	118.13	123.70
4	A	997	DBK	O3-C21-O4	-2.25	119.03	123.32
4	A	997	DBK	C26-C4-C3	2.09	125.01	120.95

There are no chirality outliers.

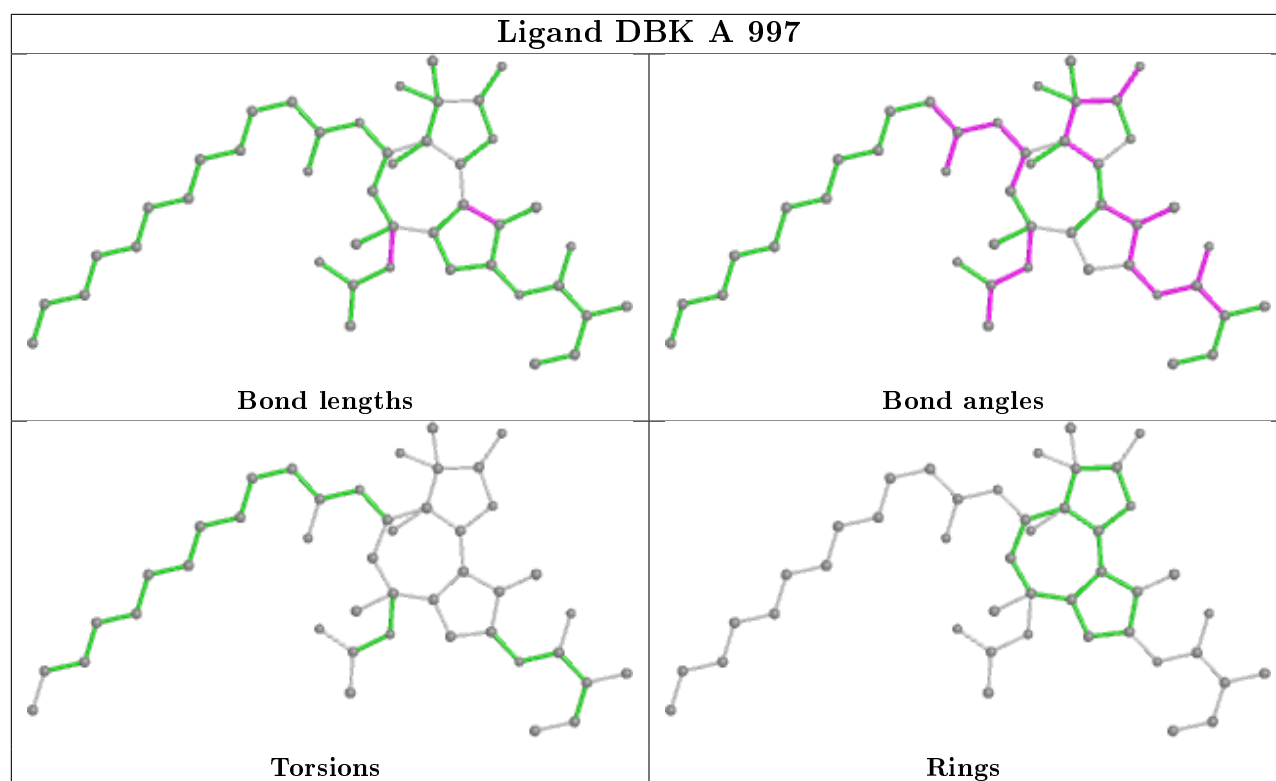
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	997	DBK	15	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 than 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.



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	994/994 (100%)	0.45	73 (7%)	15 12	41, 74, 126, 151	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	81	GLY	9.1
1	A	878	GLU	7.3
1	A	80	GLU	6.6
1	A	82	GLU	6.4
1	A	288	TRP	6.4
1	A	283	VAL	6.0
1	A	506	ALA	5.9
1	A	507	ALA	5.7
1	A	877	THR	5.4
1	A	434	TYR	5.2
1	A	84	THR	4.9
1	A	468	ALA	4.7
1	A	425	LEU	4.7
1	A	508	VAL	4.7
1	A	504	SER	4.6
1	A	50	TRP	4.5
1	A	994	GLY	4.4
1	A	503	SER	4.4
1	A	505	ARG	4.1
1	A	861	ASP	3.9
1	A	290	ARG	3.9
1	A	886	LEU	3.8
1	A	462	LEU	3.8
1	A	279	PHE	3.8
1	A	467	ARG	3.7
1	A	463	SER	3.6
1	A	87	ALA	3.6

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	890	ILE	3.5
1	A	284	HIS	3.4
1	A	856	PHE	3.2
1	A	866	THR	3.2
1	A	863	PRO	3.1
1	A	924	ARG	3.1
1	A	888	CYS	3.0
1	A	433	VAL	3.0
1	A	286	GLY	3.0
1	A	289	ILE	3.0
1	A	868	HIS	2.9
1	A	991	TYR	2.9
1	A	46	GLY	2.9
1	A	993	GLU	2.9
1	A	459	VAL	2.8
1	A	435	GLU	2.8
1	A	107	TRP	2.7
1	A	465	VAL	2.7
1	A	469	ASN	2.6
1	A	881	PRO	2.6
1	A	920	GLN	2.6
1	A	391	PRO	2.5
1	A	891	PHE	2.5
1	A	988	ALA	2.5
1	A	83	GLU	2.4
1	A	466	GLU	2.4
1	A	875	GLN	2.3
1	A	426	ASP	2.3
1	A	535	VAL	2.3
1	A	180	LEU	2.3
1	A	451	LYS	2.3
1	A	30	LYS	2.2
1	A	77	TRP	2.2
1	A	871	THR	2.2
1	A	528	VAL	2.2
1	A	89	VAL	2.2
1	A	392	GLU	2.1
1	A	49	LEU	2.1
1	A	470	ALA	2.1
1	A	183	GLU	2.1
1	A	78	PHE	2.1
1	A	427	PHE	2.1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	870	LEU	2.0
1	A	429	GLU	2.0
1	A	369	ILE	2.0
1	A	390	ALA	2.0

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

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

## 6.3 Carbohydrates [i](#)

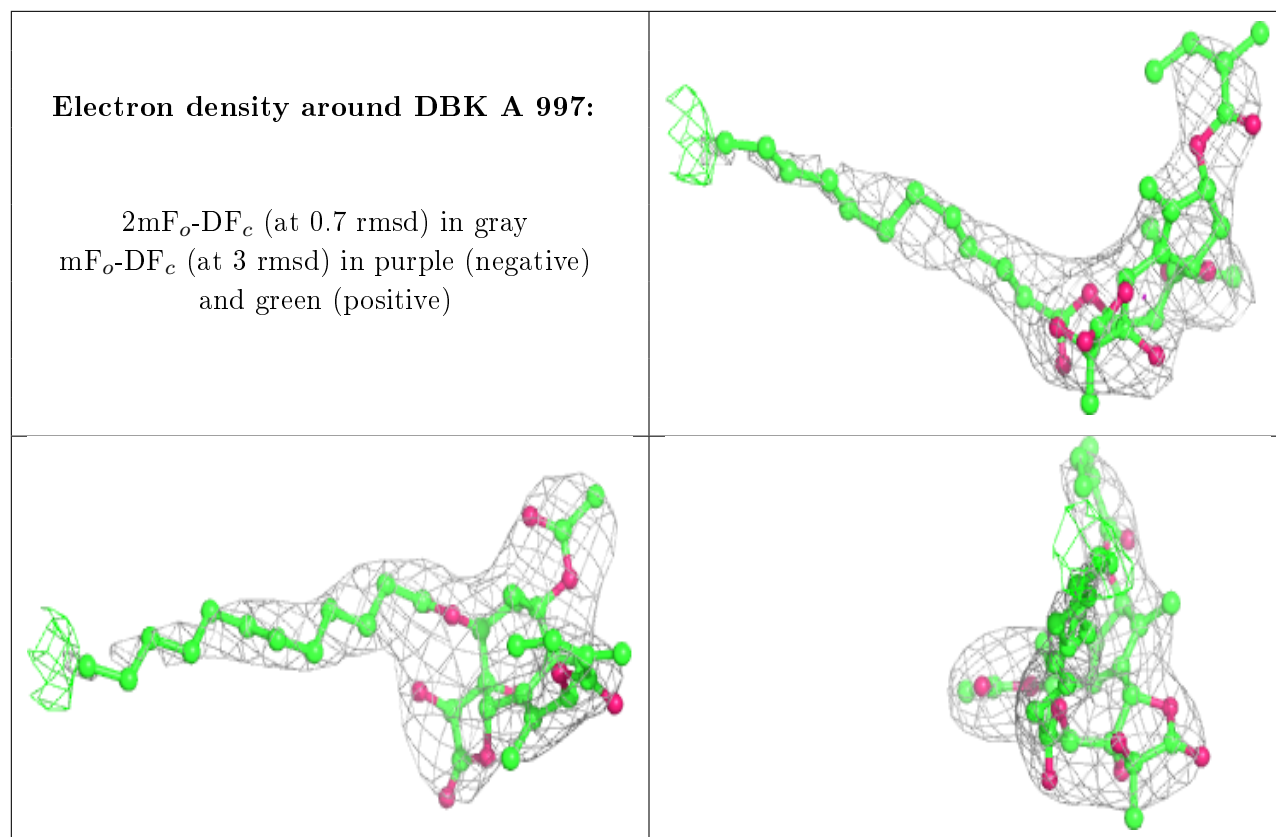
There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
3	MG	A	996	1/1	0.65	0.54	81,81,81,81	0
4	DBK	A	997	44/44	0.91	0.28	74,83,89,91	0
2	K	A	995	1/1	0.99	0.13	67,67,67,67	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.