

Full wwPDB X-ray Structure Validation Report (i)

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PDD ID	÷	21 W H
Title	:	Structure of yeast Elongation Factor 3 in complex with ADPNP
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Deposited on	:	2006-06-30
Resolution	:	3.00 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 (1)) 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 (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 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	А	986	4% 64%	34%	
1	В	986	% 	27%	••

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	SO4	А	2976	-	-	Х	-



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2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 15348 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 ELONGATION FACTOR 3A.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	А	973	Total 7579	C 4790	N 1297	O 1455	${ m S} 37$	0	0	1
1	В	981	Total 7647	C 4829	N 1316	O 1465	${ m S} 37$	0	0	1

• Molecule 2 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: $C_{10}H_{17}N_6O_{12}P_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf		
0		1	Total	С	Ν	Ο	Р	0	0	
	T	31	10	6	12	3	0	0		
0	2 B	D	1	Total	С	Ν	Ο	Р	0	0
			31	10	6	12	3	U	U	

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{c cc} Total & O & S \\ \hline 5 & 4 & 1 \end{array}$	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: ELONGATION FACTOR 3A

• Molecule 1: ELONGATION FACTOR 3A









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	98.73Å 107.55Å 207.24Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
$\mathbf{Bosolution} \left(\overset{\wedge}{\mathbf{A}} \right)$	58.12 - 3.00	Depositor
Resolution (A)	58.12 - 3.00	EDS
% Data completeness	99.1 (58.12-3.00)	Depositor
(in resolution range)	99.2 (58.12-3.00)	EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$2.71 (at 3.01 \text{\AA})$	Xtriage
Refinement program	CNS 1.1	Depositor
B B.	0.240 , 0.276	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.232 , (Not available)	DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor $(Å^2)$	45.6	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent $k_{sol}(e/A^3), B_{sol}(A^2)$	0.36 , 42.2	EDS
L-test for $twinning^2$	$ \langle L \rangle = 0.47, \langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	15348	wwPDB-VP
Average B, all atoms $(Å^2)$	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.66% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: ANP, $\mathrm{SO4}$

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	Bo	nd lengths	Bond angles		
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.52	2/7717~(0.0%)	0.68	4/10456~(0.0%)	
1	В	0.55	6/7790~(0.1%)	0.70	4/10555~(0.0%)	
All	All	0.54	8/15507~(0.1%)	0.69	8/21011~(0.0%)	

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	А	0	1
1	В	0	1
All	All	0	2

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(Å)
1	В	726	THR	C-N	-10.39	1.10	1.34
1	В	973	SER	CB-OG	-7.25	1.32	1.42
1	В	726	THR	C-O	-6.03	1.11	1.23
1	А	773	ARG	C-N	-5.84	1.20	1.34
1	В	654	TYR	CD2-CE2	-5.67	1.30	1.39
1	А	773	ARG	C-O	-5.61	1.12	1.23
1	В	975	HIS	C-O	5.28	1.33	1.23
1	В	726	THR	N-CA	-5.09	1.36	1.46

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
1	В	726	THR	O-C-N	-9.09	108.16	122.70



Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	773	ARG	C-N-CA	8.21	142.22	121.70
1	А	419	ASN	C-N-CA	6.33	137.52	121.70
1	А	759	PHE	N-CA-C	6.28	127.96	111.00
1	В	881	LEU	CA-CB-CG	-5.80	101.96	115.30
1	В	231	ALA	C-N-CA	5.63	135.79	121.70
1	А	434	GLU	N-CA-C	-5.36	96.53	111.00
1	В	434	GLU	N-CA-C	-5.13	97.15	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	А	654	TYR	Sidechain
1	В	726	THR	Mainchain

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	А	7579	0	7625	286	0
1	В	7647	0	7674	282	0
2	А	31	0	13	4	0
2	В	31	0	13	2	0
3	А	25	0	0	6	0
3	В	35	0	0	5	0
All	All	15348	0	15325	554	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 18.

All (554) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	${f Interatomic} \ {f distance} \ ({ m \AA})$	Clash overlap (Å)
1:B:227:HIS:CE1	1:B:264:LYS:HE3	1.79	1.17
1:B:532:THR:H	1:B:535:MET:HE3	1.03	1.07



	lous puge	Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlan (Å)
1:A:76:GLN:HB2	1:A:774:GLN:HE21	1 20	1.05
1:A:67:MET:HE2	1:A:109:ALA:HA	1.40	1.04
1:A:76:GLN:HB2	1:A:774:GLN:NE2	1.74	1.01
1:B:731:ARG:H	1:B:915:HIS:HD2	1.03	0.98
1:B:67:MET:HE2	1:B:109:ALA:HA	1.49	0.94
1:A:231:ALA:HB2	1:B:778:ASN:OD1	1.67	0.94
1:A:372:ILE:HD11	1:A:410:ALA:HB1	1.49	0.93
1:B:797:ALA:HB2	1:B:816:LEU:HG	1.51	0.92
1:A:731:ARG:HH12	1:A:865:GLN:HE21	1.16	0.92
1:B:731:ARG:H	1:B:915:HIS:CD2	1.86	0.91
1:B:532:THR:N	1:B:535:MET:HE3	1.87	0.89
1:A:871:ARG:O	1:A:875:GLU:HG3	1.73	0.89
1:A:227:HIS:CE1	1:A:264:LYS:HZ2	1.92	0.87
1:A:227:HIS:CE1	1:A:264:LYS:NZ	2.43	0.86
1:A:731:ARG:H	1:A:915:HIS:HD2	1.19	0.86
1:A:67:MET:CE	1:A:109:ALA:HA	2.04	0.86
1:A:867:ARG:NH1	1:B:528:GLU:HG3	1.88	0.86
1:A:538:MET:CE	1:A:542:ALA:HB3	2.07	0.85
1:B:532:THR:H	1:B:535:MET:CE	1.89	0.84
1:B:419:ASN:ND2	1:B:618:ARG:HD3	1.92	0.84
1:B:825:SER:O	1:B:827:ARG:HG2	1.78	0.83
1:A:779:ASP:HB3	1:A:782:ALA:HB3	1.59	0.82
1:B:372:ILE:HD11	1:B:410:ALA:HB1	1.59	0.82
1:B:798:GLY:HA2	1:B:851:MET:CE	2.08	0.82
1:A:227:HIS:ND1	1:A:264:LYS:NZ	2.27	0.82
1:B:816:LEU:HD23	1:B:830:PRO:HA	1.59	0.82
1:B:231:ALA:O	1:B:233:THR:N	2.11	0.82
1:B:710:ILE:HD13	1:B:948:ILE:HD13	1.60	0.80
1:B:67:MET:CE	1:B:109:ALA:HA	2.11	0.80
1:B:729:ASN:HB3	1:B:865:GLN:NE2	1.97	0.80
1:B:175:SER:HA	1:B:178:MET:CE	2.12	0.79
1:B:175:SER:HA	1:B:178:MET:HE2	1.63	0.79
1:A:867:ARG:HH11	1:B:528:GLU:HG3	1.48	0.78
1:B:709:LEU:HD21	1:B:970:MET:CE	2.14	0.78
1:B:486:GLN:HB3	1:B:490:ARG:NH1	1.98	0.78
1:B:535:MET:O	1:B:538:MET:HG2	1.85	0.77
1:B:180:ASP:O	1:B:186:LYS:HE3	1.84	0.77
1:B:798:GLY:HA2	1:B:851:MET:HE1	1.65	0.77
1:A:67:MET:CE	1:A:94:ILE:HG23	2.13	0.77
1:A:774:GLN:O	1:A:776:ASN:N	2.17	0.77
1:A:731:ARG:H	1:A:915:HIS:CD2	2.02	0.76



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:634:ALA:HA	1:B:637:TYR:CE1	2.20	0.76
1:A:200:VAL:HG21	1:A:245:ILE:HD12	1.67	0.76
1:A:757:TRP:CH2	1:A:765:ARG:HD2	2.21	0.76
1:A:635:LYS:HA	1:A:642:ASN:OD1	1.86	0.76
1:B:227:HIS:HE1	1:B:264:LYS:HE3	1.46	0.76
1:B:794:ARG:HD3	1:B:831:MET:CE	2.16	0.76
1:A:422:ASP:OD2	1:A:619:LYS:NZ	2.19	0.75
1:B:794:ARG:HD3	1:B:831:MET:HE1	1.68	0.75
1:B:419:ASN:OD1	1:B:420:PHE:N	2.18	0.75
1:A:276:VAL:HB	1:A:319:VAL:HG11	1.69	0.75
1:B:538:MET:CE	1:B:542:ALA:HB3	2.16	0.75
1:B:45:VAL:HG11	1:B:86:TYR:CE2	2.21	0.75
1:A:262:LYS:HD2	1:A:300:ILE:HD11	1.67	0.75
1:A:528:GLU:HG3	1:B:867:ARG:HH12	1.52	0.74
1:A:656:GLU:HG3	3:A:2978:SO4:O3	1.87	0.74
1:A:706:LYS:O	1:A:710:ILE:HG12	1.87	0.74
1:A:597:HIS:HD2	1:A:638:GLU:O	1.71	0.74
1:A:641:SER:HA	1:A:887:ILE:HD11	1.70	0.74
1:B:219:PRO:HB3	1:B:252:ARG:NH1	2.03	0.74
1:A:538:MET:HE2	1:A:542:ALA:HB3	1.70	0.73
1:B:67:MET:CE	1:B:94:ILE:HG23	2.19	0.73
1:A:528:GLU:HG3	1:B:867:ARG:NH1	2.04	0.73
1:A:752:SER:O	1:A:756:GLN:HG3	1.88	0.72
1:B:639:GLU:OE2	1:B:645:LEU:HD21	1.89	0.72
1:B:709:LEU:HD21	1:B:970:MET:HE1	1.71	0.72
1:B:779:ASP:CG	1:B:782:ALA:HB3	2.11	0.72
1:A:61:LYS:HG3	1:A:62:THR:HG23	1.70	0.72
1:B:671:MET:SD	1:B:712:VAL:HG11	2.29	0.71
1:A:640:LEU:HD11	1:A:884:ASP:OD2	1.90	0.71
1:A:390:MET:HE3	1:A:403:LEU:HD13	1.73	0.71
1:B:731:ARG:N	1:B:915:HIS:HD2	1.84	0.71
1:A:76:GLN:CB	1:A:774:GLN:NE2	2.51	0.70
1:B:532:THR:HG22	1:B:535:MET:HG3	1.73	0.70
1:A:731:ARG:HH12	1:A:865:GLN:NE2	1.90	0.70
1:A:223:PRO:HB3	1:A:261:ILE:HD13	1.74	0.69
1:A:340:THR:HG21	1:A:369:ALA:HA	1.73	0.69
1:A:200:VAL:CG2	1:A:245:ILE:HD12	2.22	0.69
1:A:499:ASP:OD2	1:A:501:THR:HG23	1.93	0.69
1:A:779:ASP:CB	1:A:782:ALA:HB3	2.23	0.69
1:A:293:LEU:HD12	1:A:316:LEU:HD22	1.75	0.69
1:A:624:PHE:CZ	1:A:639:GLU:HG3	2.28	0.69



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
2:B:2977:ANP:O2G	2:B:2977:ANP:O1A	2.11	0.68
1:A:624:PHE:CE1	1:A:639:GLU:HG3	2.28	0.68
1:B:420:PHE:CZ	1:B:621:LYS:HB2	2.27	0.68
1:A:824:LYS:HB3	1:B:306:ARG:HH12	1.58	0.68
1:A:41:ILE:HD12	1:A:46:PRO:HD3	1.76	0.68
1:A:947:ILE:HG21	1:A:954:PHE:HE2	1.59	0.68
1:A:67:MET:HE1	1:A:94:ILE:HG23	1.77	0.67
1:A:140:ASN:OD1	1:A:141:LYS:HD2	1.94	0.67
1:B:50:PHE:HZ	1:B:83:VAL:HG13	1.60	0.67
1:B:699:ILE:HG22	1:B:700:GLY:N	2.10	0.67
1:B:486:GLN:HB3	1:B:490:ARG:HH12	1.60	0.66
1:B:747:LEU:HB3	1:B:894:ARG:HB2	1.77	0.66
1:A:669:THR:HA	1:A:687:ASN:OD1	1.96	0.66
1:A:750:THR:OG1	1:A:753:GLU:HG3	1.95	0.66
1:B:416:VAL:N	3:B:2981:SO4:O2	2.27	0.66
1:B:803:ARG:HG2	1:B:838:TRP:CZ3	2.30	0.66
1:A:293:LEU:CD1	1:A:316:LEU:HD22	2.25	0.66
1:A:78:ASN:HD21	1:A:736:LYS:HZ1	1.42	0.65
1:A:422:ASP:OD1	1:A:453:LYS:HD3	1.97	0.65
1:A:59:ASP:OD1	1:A:61:LYS:HE2	1.96	0.65
1:B:538:MET:HB2	1:B:539:PRO:HD2	1.77	0.65
1:A:31:GLU:OE2	1:A:676:PRO:HD2	1.97	0.65
1:B:803:ARG:HG3	1:B:810:GLU:CG	2.27	0.65
1:A:449:GLN:NE2	3:A:2975:SO4:O1	2.29	0.64
1:A:67:MET:HE3	1:A:94:ILE:HG23	1.80	0.64
1:A:773:ARG:O	1:A:775:ILE:N	2.23	0.64
1:B:654:TYR:OH	1:B:656:GLU:HG2	1.97	0.64
1:B:532:THR:HG23	1:B:535:MET:H	1.63	0.64
1:A:21:THR:HG22	1:A:24:ASN:ND2	2.13	0.64
1:A:535:MET:O	1:A:538:MET:HG2	1.98	0.63
1:A:757:TRP:CZ2	1:A:765:ARG:HD2	2.33	0.63
1:A:404:ASP:OD1	1:A:408:LYS:HE3	1.99	0.63
1:A:256:GLU:HG3	1:A:257:ARG:H	1.63	0.63
1:B:17:LEU:CA	1:B:28:ILE:HD13	2.28	0.63
1:A:603:ASP:HA	1:A:623:ASN:HB2	1.81	0.62
1:A:294:LYS:HE2	1:A:326:ASP:OD2	1.99	0.62
1:A:710:ILE:HD12	1:A:948:ILE:CD1	2.29	0.62
1:A:709:LEU:HD22	1:A:970:MET:SD	2.39	0.62
1:A:299:THR:HG22	1:A:299:THR:O	1.98	0.62
1:B:815:PHE:HB2	1:B:831:MET:HE1	1.82	0.62
1:A:494:VAL:HG12	1:A:495:GLU:HG3	1.82	0.62



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:814:SER:HA	1:B:836:ASN:OD1	2.00	0.62
1:A:212:LEU:HD13	1:A:245:ILE:HG22	1.80	0.62
1:B:775:ILE:O	1:B:775:ILE:HG22	2.00	0.62
1:A:423:GLU:HG2	1:A:451:ARG:HH12	1.66	0.61
1:A:538:MET:CE	1:A:542:ALA:CB	2.78	0.61
1:B:538:MET:HE2	1:B:542:ALA:HB3	1.82	0.61
1:B:277:GLU:HG2	1:B:420:PHE:HE1	1.64	0.61
1:A:763:GLU:HB3	1:A:768:MET:HG3	1.80	0.61
1:A:848:HIS:O	1:A:852:VAL:HG23	2.00	0.61
1:B:658:VAL:HG23	1:B:658:VAL:O	2.01	0.61
1:B:776:ASN:HB3	1:B:779:ASP:HB2	1.81	0.61
1:A:262:LYS:CD	1:A:300:ILE:HD11	2.30	0.61
1:A:486:GLN:HB3	1:A:490:ARG:HH11	1.65	0.61
1:B:881:LEU:HD13	1:B:907:ALA:HA	1.82	0.61
1:B:317:ARG:HG2	1:B:322:VAL:HG21	1.82	0.60
1:A:78:ASN:ND2	1:A:736:LYS:NZ	2.49	0.60
1:A:641:SER:HA	1:A:887:ILE:CD1	2.30	0.60
1:B:544:SER:O	1:B:548:LYS:HG3	2.02	0.60
1:A:430:LEU:HD11	1:A:454:ARG:HA	1.82	0.60
1:A:776:ASN:HB3	1:A:779:ASP:OD2	2.01	0.60
1:B:800:HIS:NE2	1:B:814:SER:HB3	2.17	0.60
1:B:821:ILE:HA	1:B:826:GLU:HG3	1.84	0.60
1:A:435:PHE:CD1	1:A:480:VAL:HG13	2.37	0.60
1:B:674:GLN:HB2	1:B:681:PRO:HA	1.84	0.60
1:B:420:PHE:HZ	1:B:621:LYS:HD2	1.67	0.60
1:A:78:ASN:HD21	1:A:736:LYS:NZ	2.00	0.59
1:A:881:LEU:HD13	1:A:907:ALA:HA	1.83	0.59
1:A:647:PHE:HB2	1:A:881:LEU:HA	1.84	0.59
1:A:227:HIS:CE1	1:A:264:LYS:HZ1	2.19	0.59
1:A:526:LEU:O	1:A:531:PHE:HB2	2.02	0.59
1:A:278:ASP:HB3	1:A:281:VAL:HG23	1.85	0.59
1:B:718:LEU:HD11	1:B:806:LYS:HD2	1.83	0.59
1:A:624:PHE:O	1:A:627:PHE:HB3	2.03	0.59
1:B:223:PRO:HB3	1:B:261:ILE:CD1	2.32	0.59
1:A:816:LEU:HD23	1:A:830:PRO:HA	1.83	0.59
1:B:435:PHE:CD1	1:B:480:VAL:HG13	2.37	0.58
1:A:726:THR:CG2	1:A:730:CYS:HB3	2.33	0.58
1:B:222:VAL:HB	1:B:223:PRO:HD3	1.84	0.58
1:B:699:ILE:HG22	1:B:700:GLY:H	1.66	0.58
1:B:789:ILE:HD12	1:B:815:PHE:CZ	2.38	0.58
1:B:892:ARG:NH1	3:B:2984:SO4:O1	2.37	0.58



	1	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:B:779:ASP:OD1	1:B:782:ALA:HB3	2.03	0.58
1:B:233:THR:O	1:B:235:VAL:HG23	2.03	0.58
1:B:420:PHE:CZ	1:B:621:LYS:HD2	2.39	0.58
1:B:816:LEU:CD2	1:B:830:PRO:HA	2.30	0.58
1:B:223:PRO:HB3	1:B:261:ILE:HD13	1.86	0.58
1:A:182:LYS:HD2	1:A:184:GLU:OE1	2.04	0.58
1:A:547:TRP:NE1	3:A:2974:SO4:O4	2.36	0.58
1:A:654:TYR:CE2	1:B:521:ALA:HB2	2.38	0.58
1:B:67:MET:HE3	1:B:94:ILE:HG23	1.85	0.58
1:A:919:LEU:HD12	1:A:919:LEU:N	2.18	0.58
1:B:799:ILE:HG22	1:B:855:VAL:HG21	1.84	0.57
1:A:422:ASP:CG	1:A:453:LYS:HD3	2.24	0.57
1:B:256:GLU:O	1:B:262:LYS:HE3	2.04	0.57
1:B:654:TYR:CZ	1:B:656:GLU:HG2	2.39	0.57
1:A:259:THR:HG23	1:A:300:ILE:HG21	1.86	0.57
1:A:440:GLY:O	1:A:441:ALA:HB3	2.04	0.57
1:A:774:GLN:C	1:A:776:ASN:H	2.07	0.57
1:B:219:PRO:HB3	1:B:252:ARG:HH11	1.70	0.57
1:B:798:GLY:HA2	1:B:851:MET:HE3	1.85	0.57
1:B:788:LYS:HE3	1:B:791:GLY:HA2	1.87	0.57
1:A:234:PHE:HB3	1:A:275:LEU:HD12	1.87	0.57
1:A:726:THR:HG22	1:A:730:CYS:HB3	1.87	0.56
1:A:779:ASP:HB3	1:A:782:ALA:CB	2.33	0.56
1:A:674:GLN:HB2	1:A:681:PRO:HB3	1.87	0.56
1:B:16:LYS:HB3	1:B:28:ILE:HD12	1.86	0.56
1:B:317:ARG:HA	1:B:322:VAL:HG13	1.86	0.56
1:B:538:MET:CE	1:B:542:ALA:CB	2.83	0.56
1:B:17:LEU:HA	1:B:28:ILE:HD13	1.86	0.56
1:A:321:ASN:O	1:A:321:ASN:OD1	2.24	0.56
1:B:815:PHE:HB2	1:B:831:MET:CE	2.35	0.56
1:B:956:LYS:O	1:B:957:ASN:HB2	2.05	0.56
1:B:339:THR:O	1:B:343:VAL:HG23	2.06	0.56
1:A:423:GLU:HG2	1:A:451:ARG:NH1	2.21	0.56
1:A:824:LYS:CB	1:B:306:ARG:HH12	2.19	0.56
1:B:642:ASN:HD22	1:B:645:LEU:HD12	1.71	0.56
1:A:947:ILE:HG21	1:A:954:PHE:CE2	2.40	0.56
1:B:657:GLY:N	3:B:2982:SO4:O1	2.31	0.56
1:A:40:ILE:HG13	1:A:41:ILE:HG13	1.88	0.55
1:B:36:LEU:HD23	1:B:73:ILE:HD13	1.88	0.55
1:B:727:HIS:ND1	1:B:728:GLU:N	2.54	0.55
1:B:535:MET:HA	1:B:538:MET:SD	2.46	0.55



		Interatomic	Clash
Atom-1	Atom-2	$distance (m \AA)$	overlap (Å)
1:B:58:LYS:HG2	1:B:58:LYS:O	2.06	0.55
1:A:16:LYS:CG	1:A:28:ILE:HD12	2.35	0.55
1:A:802:ARG:HB3	1:A:859:GLU:HG3	1.89	0.55
1:B:227:HIS:ND1	1:B:264:LYS:HE3	2.18	0.55
1:B:817:LEU:HB2	1:B:831:MET:SD	2.46	0.55
1:A:340:THR:HG21	1:A:369:ALA:CA	2.36	0.55
1:A:814:SER:HA	1:A:836:ASN:OD1	2.07	0.55
1:A:231:ALA:CB	1:B:778:ASN:OD1	2.47	0.55
1:B:13:LEU:O	1:B:28:ILE:HD11	2.07	0.54
1:B:801:SER:H	1:B:812:GLU:HB3	1.72	0.54
1:A:183:LYS:HD2	1:B:218:ASP:OD2	2.07	0.54
1:A:716:GLU:HG3	1:A:771:ALA:HB2	1.89	0.54
1:A:731:ARG:N	1:A:915:HIS:HD2	1.99	0.54
1:B:45:VAL:HG11	1:B:86:TYR:CZ	2.42	0.54
1:B:420:PHE:CE1	1:B:621:LYS:HB2	2.42	0.54
1:A:302:ASP:O	1:A:306:ARG:HG3	2.08	0.54
1:B:166:ARG:NH2	1:B:373:ASP:OD2	2.40	0.54
1:B:757:TRP:CH2	1:B:765:ARG:HD2	2.43	0.54
1:A:538:MET:HB2	1:A:539:PRO:HD2	1.88	0.54
1:A:257:ARG:HG3	1:A:258:GLU:HG3	1.90	0.54
1:A:121:ASN:ND2	1:A:741:ALA:HB1	2.23	0.54
1:B:928:ARG:HH11	1:B:928:ARG:HB3	1.72	0.54
1:A:263:ARG:O	1:A:267:VAL:HG23	2.06	0.54
1:A:788:LYS:HD2	1:A:788:LYS:N	2.22	0.54
1:B:538:MET:HE3	1:B:542:ALA:HB3	1.89	0.54
1:A:456:ARG:O	1:A:591:THR:HG23	2.08	0.54
1:A:727:HIS:CE1	1:A:728:GLU:HG2	2.43	0.54
1:B:815:PHE:CB	1:B:831:MET:CE	2.86	0.54
1:A:222:VAL:O	1:A:226:VAL:HG23	2.08	0.54
1:A:764:ASP:OD1	1:A:766:GLU:HB2	2.08	0.53
1:B:294:LYS:HE2	1:B:326:ASP:OD2	2.08	0.53
1:B:671:MET:HB3	1:B:686:ILE:HB	1.90	0.53
1:B:697:ALA:HB1	1:B:699:ILE:HD11	1.90	0.53
1:A:710:ILE:HD12	1:A:948:ILE:HD11	1.91	0.53
1:A:13:LEU:O	1:A:28:ILE:HD11	2.08	0.53
1:A:265:SER:O	1:A:269:ILE:HG13	2.09	0.53
1:A:465:GLY:N	3:A:2977:SO4:O2	2.41	0.53
1:B:129:LEU:HB3	1:B:130:PRO:HD3	1.90	0.53
1:B:276:VAL:HB	1:B:319:VAL:HG11	1.91	0.53
1:B:238:VAL:HG21	1:B:272:MET:O	2.09	0.53
1:B:42:GLU:OE1	1:B:950:HIS:HE1	1.92	0.53



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:797:ALA:HB2	1:B:816:LEU:CG	2.33	0.53
1:A:17:LEU:CA	1:A:28:ILE:HD13	2.39	0.53
1:A:420:PHE:CG	1:A:421:ASP:N	2.76	0.53
1:B:811:TYR:HE2	1:B:841:ARG:HB2	1.74	0.53
1:B:50:PHE:CZ	1:B:83:VAL:HG13	2.41	0.53
1:A:223:PRO:HB3	1:A:261:ILE:CD1	2.39	0.53
1:A:219:PRO:O	1:A:222:VAL:HG23	2.09	0.53
1:A:668:VAL:CG1	1:A:671:MET:HB2	2.39	0.53
1:B:207:ARG:HH11	1:B:207:ARG:HG2	1.73	0.53
1:B:654:TYR:CE2	1:B:656:GLU:HG2	2.44	0.53
1:B:258:GLU:HG2	1:B:260:GLY:H	1.73	0.52
1:B:175:SER:HA	1:B:178:MET:HE3	1.91	0.52
1:B:229:LEU:HD23	1:B:268:ILE:HD13	1.90	0.52
1:B:726:THR:HG22	1:B:727:HIS:N	2.23	0.52
1:B:815:PHE:CB	1:B:831:MET:HE1	2.39	0.52
1:B:730:CYS:HA	1:B:915:HIS:CD2	2.44	0.52
1:B:803:ARG:CG	1:B:810:GLU:HG3	2.39	0.52
1:A:293:LEU:HB3	1:A:313:LEU:HD13	1.89	0.52
1:B:277:GLU:HG2	1:B:420:PHE:CE1	2.44	0.52
1:B:0:HIS:CD2	1:B:42:GLU:HG2	2.45	0.52
1:B:794:ARG:HD3	1:B:831:MET:HE2	1.90	0.52
1:B:779:ASP:OD2	1:B:782:ALA:HB3	2.07	0.52
1:A:346:GLU:OE1	1:A:349:LYS:HD3	2.09	0.52
1:A:335:GLY:O	1:A:369:ALA:HB1	2.10	0.52
1:B:655:LEU:O	1:B:658:VAL:HG22	2.09	0.52
1:A:17:LEU:HA	1:A:28:ILE:HD13	1.92	0.51
1:A:420:PHE:CE2	1:A:421:ASP:O	2.63	0.51
1:A:653:GLY:O	1:A:915:HIS:HE1	1.93	0.51
1:A:697:ALA:HB2	1:A:959:THR:HG21	1.91	0.51
1:B:17:LEU:N	1:B:28:ILE:HD13	2.26	0.51
1:A:733:ALA:HB2	1:A:914:PRO:HG3	1.93	0.51
1:A:734:TYR:CE2	1:A:736:LYS:HD2	2.46	0.51
1:B:180:ASP:O	1:B:186:LYS:CE	2.58	0.51
1:B:532:THR:HG22	1:B:535:MET:CE	2.40	0.51
1:A:320:GLY:O	1:A:321:ASN:HB3	2.11	0.51
1:A:775:ILE:O	1:A:775:ILE:HG22	2.11	0.51
1:B:445:LEU:HD21	1:B:612:TYR:CE2	2.45	0.51
1:A:372:ILE:HD11	1:A:410:ALA:CB	2.32	0.51
1:A:949:THR:OG1	1:A:950:HIS:N	2.44	0.51
1:B:422:ASP:OD1	1:B:453:LYS:HD3	2.10	0.51
1:B:494:VAL:HG12	1:B:495:GLU:HG3	1.92	0.51



		Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlap (Å)
1:B:729:ASN:CB	1:B:865:GLN:NE2	2.73	0.51
1:B:746:HIS:ND1	1:B:749:LYS:NZ	2.50	0.50
1:B:600:VAL:CB	1:B:886:GLU:HG3	2.42	0.50
1:A:197:THR:O	1:A:200:VAL:HG23	2.12	0.50
1:A:398:LYS:O	1:A:402:ILE:HG13	2.12	0.50
1:A:78:ASN:ND2	1:A:736:LYS:HZ3	2.09	0.50
1:A:651:GLU:OE2	1:A:942:GLU:HG3	2.11	0.50
1:B:17:LEU:N	1:B:28:ILE:CD1	2.75	0.50
1:A:263:ARG:NH1	1:B:781:GLU:HB2	2.26	0.50
1:A:364:ILE:HG23	1:A:386:ILE:CG2	2.42	0.50
1:A:850:LYS:O	1:A:854:GLU:HG3	2.11	0.50
1:B:532:THR:CG2	1:B:535:MET:H	2.25	0.50
1:B:731:ARG:NH1	1:B:865:GLN:NE2	2.60	0.50
1:A:698:VAL:HG11	1:A:710:ILE:HD11	1.92	0.50
1:B:2:ASP:OD2	1:B:703:GLY:HA3	2.12	0.50
1:B:83:VAL:HG12	1:B:87:ILE:HG12	1.93	0.50
1:A:574:ASP:O	1:A:578:VAL:HG23	2.12	0.49
1:B:335:GLY:O	1:B:369:ALA:HB1	2.12	0.49
1:A:21:THR:HG22	1:A:24:ASN:HD21	1.77	0.49
1:A:727:HIS:ND1	1:A:729:ASN:N	2.47	0.49
1:B:600:VAL:HG21	1:B:886:GLU:HG3	1.93	0.49
1:A:877:HIS:HE1	1:A:907:ALA:O	1.94	0.49
1:B:740:PHE:HA	1:B:905:VAL:HG21	1.95	0.49
1:B:731:ARG:HH12	1:B:865:GLN:NE2	2.10	0.49
1:A:407:ARG:O	1:A:411:VAL:HG23	2.12	0.49
1:A:719:PRO:HG2	1:A:806:LYS:HD3	1.94	0.49
1:B:178:MET:CE	1:B:216:ILE:HG21	2.43	0.49
1:B:-3:HIS:NE2	1:B:395:HIS:CE1	2.80	0.49
1:A:239:THR:HB	1:A:240:PRO:CD	2.43	0.49
1:A:668:VAL:HG11	1:A:671:MET:SD	2.52	0.49
1:A:686:ILE:CD1	1:A:970:MET:HG2	2.43	0.49
1:B:294:LYS:CE	1:B:326:ASP:OD2	2.61	0.49
1:A:210:PRO:O	1:A:214:GLN:HG2	2.13	0.49
1:A:916:LEU:HD23	1:A:944:GLY:HA3	1.95	0.49
1:A:387:THR:N	1:A:388:PRO:HD2	2.28	0.48
1:A:422:ASP:HB3	1:A:451:ARG:HD2	1.94	0.48
1:B:603:ASP:HA	1:B:623:ASN:HB2	1.94	0.48
1:A:17:LEU:N	1:A:28:ILE:HD13	2.28	0.48
1:B:48:HIS:O	1:B:52:GLU:HG3	2.13	0.48
1:A:263:ARG:NE	1:A:308:VAL:HG21	2.28	0.48
1:B:468:LYS:NZ	3:B:2980:SO4:O1	2.29	0.48



		Interatomic	Clash	
Atom-1	Atom-2	distance $(Å)$	overlap (Å)	
1:A:160:LYS:HG3	1:A:199:THR:HG22	1.95	0.48	
1:A:751:PRO:HB3	1:A:904:LEU:HD13	1.96	0.48	
1:B:727:HIS:ND1	1:B:729:ASN:N	2.44	0.48	
1:B:733:ALA:HB2	1:B:914:PRO:HG3	1.95	0.48	
1:B:811:TYR:HE2	1:B:841:ARG:CB	2.27	0.48	
1:B:815:PHE:HZ	1:B:839:ILE:HD11	1.78	0.48	
1:B:41:ILE:O	2:B:2977:ANP:N6	2.47	0.48	
1:A:372:ILE:CD1	1:A:410:ALA:HB1	2.35	0.48	
1:B:0:HIS:O	1:B:3:SER:HB3	2.14	0.48	
1:B:669:THR:HA	1:B:687:ASN:OD1	2.14	0.48	
1:B:123:VAL:HG12	1:B:367:ILE:HG23	1.96	0.48	
1:B:419:ASN:ND2	1:B:618:ARG:CD	2.73	0.48	
1:B:781:GLU:HA	1:B:784:ASN:ND2	2.28	0.48	
1:A:344:VAL:CG1	1:A:406:PHE:CZ	2.97	0.47	
1:B:387:THR:N	1:B:388:PRO:HD2	2.28	0.47	
1:B:183:LYS:HG3	1:B:184:GLU:OE1	2.14	0.47	
1:A:521:ALA:HB2	1:B:654:TYR:CE2	2.49	0.47	
1:B:850:LYS:O	1:B:854:GLU:HG3	2.14	0.47	
1:B:67:MET:HE1	1:B:94:ILE:HG23	1.92	0.47	
1:A:76:GLN:CB	1:A:774:GLN:HE21	2.06	0.47	
1:A:458:TYR:CD1	1:A:608:TYR:HB2	2.50	0.47	
1:B:666:VAL:HB	1:B:690:CYS:HB2	1.97	0.47	
1:B:798:GLY:CA	1:B:851:MET:HE1	2.42	0.47	
1:B:783:MET:C	1:B:785:LYS:H	2.17	0.47	
1:B:67:MET:HE1	1:B:109:ALA:CB	2.44	0.47	
1:B:466:CYS:SG	1:B:468:LYS:HG3	2.55	0.47	
1:A:698:VAL:HG12	1:A:706:LYS:HE3	1.96	0.47	
3:A:2976:SO4:O2	1:B:871:ARG:NH2	2.43	0.47	
1:A:299:THR:CG2	1:A:299:THR:O	2.62	0.47	
1:B:800:HIS:NE2	1:B:814:SER:CB	2.78	0.47	
1:A:200:VAL:CG2	1:A:245:ILE:CD1	2.93	0.46	
1:A:293:LEU:CB	1:A:313:LEU:HD13	2.45	0.46	
1:A:393:PHE:CD1	1:A:394:LEU:HG	2.50	0.46	
1:B:178:MET:HE1	1:B:216:ILE:HG21	1.96	0.46	
1:B:372:ILE:HD11	1:B:410:ALA:CB	2.40	0.46	
1:A:405:GLU:OE2	1:A:409:ARG:NE	2.42	0.46	
1:B:773:ARG:O	1:B:775:ILE:N	2.49	0.46	
1:A:645:LEU:H	1:A:903:LYS:NZ	2.14	0.46	
1:B:183:LYS:CG	1:B:184:GLU:OE1	2.63	0.46	
1:B:634:ALA:HA	1:B:637:TYR:CD1	2.50	0.46	
1:A:194:THR:OG1	1:B:210:PRO:HG3	2.16	0.46	



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:39:ASN:O	1:B:702:ASN:HB3	2.15	0.46
1:A:16:LYS:HB3	1:A:28:ILE:HD12	1.98	0.46
1:B:440:GLY:O	1:B:441:ALA:HB3	2.16	0.46
1:B:532:THR:HG22	1:B:535:MET:CG	2.42	0.46
1:A:16:LYS:HB3	1:A:28:ILE:CD1	2.46	0.46
1:A:600:VAL:HG21	1:A:886:GLU:HB3	1.97	0.46
1:B:647:PHE:HB2	1:B:881:LEU:HA	1.98	0.46
1:B:803:ARG:CG	1:B:810:GLU:CG	2.93	0.46
1:B:668:VAL:O	1:B:687:ASN:HA	2.15	0.46
1:B:732:ILE:HG12	1:B:916:LEU:HB2	1.98	0.46
1:A:104:GLU:O	1:A:108:VAL:HG23	2.16	0.45
1:A:174:LEU:O	1:A:178:MET:HG3	2.16	0.45
1:B:227:HIS:CE1	1:B:264:LYS:CE	2.74	0.45
1:B:-3:HIS:NE2	1:B:395:HIS:HE1	2.13	0.45
1:B:781:GLU:HA	1:B:784:ASN:HD22	1.82	0.45
1:B:803:ARG:HD2	1:B:838:TRP:CH2	2.50	0.45
1:A:102:ASP:OD2	1:A:105:ILE:HG13	2.15	0.45
1:A:379:GLN:NE2	1:A:404:ASP:OD2	2.50	0.45
1:B:549:MET:HE3	1:B:581:LEU:HD13	1.98	0.45
1:B:674:GLN:HB2	1:B:681:PRO:CA	2.45	0.45
1:B:568:GLU:OE1	1:B:597:HIS:ND1	2.47	0.45
1:B:597:HIS:HD1	1:B:597:HIS:H	1.64	0.45
1:A:45:VAL:HG11	1:A:86:TYR:CE2	2.52	0.45
1:A:899:GLY:O	1:A:902:VAL:HB	2.16	0.45
1:A:222:VAL:N	1:A:223:PRO:HD2	2.31	0.45
1:A:747:LEU:HB3	1:A:894:ARG:HB2	1.97	0.45
1:A:924:ASN:O	1:A:924:ASN:OD1	2.35	0.45
1:A:924:ASN:ND2	2:A:2973:ANP:O3'	2.50	0.45
1:A:829:VAL:CG1	1:A:830:PRO:HD2	2.47	0.45
1:A:851:MET:O	1:A:855:VAL:HG23	2.17	0.45
1:B:16:LYS:CB	1:B:28:ILE:HD12	2.47	0.45
1:B:699:ILE:CG2	1:B:700:GLY:N	2.80	0.45
1:B:774:GLN:O	1:B:774:GLN:HG2	2.16	0.45
1:A:159:ALA:HB1	1:A:162:GLN:HB2	1.99	0.45
1:A:16:LYS:HG2	1:A:28:ILE:HD12	1.99	0.45
1:B:11:GLU:O	1:B:15:GLN:HG3	2.17	0.45
1:B:818:GLY:HA3	1:B:821:ILE:HD11	1.98	0.45
1:B:16:LYS:HB3	1:B:28:ILE:CD1	2.47	0.45
1:B:634:ALA:HA	1:B:637:TYR:HE1	1.75	0.45
1:B:750:THR:OG1	1:B:753:GLU:HG3	2.16	0.45
1:A:41:ILE:O	2:A:2973:ANP:N6	2.47	0.45



		Interatomic	Clash
Atom-1	Atom-2	distance $(Å)$	overlan (Å)
1:B:136:ILE:HB	1:B:148:ILE:HG21	1 99	0.45
1:B:718:LEU:HD12	1:B:719:PRO:HD2	1.97	0.45
1:B:789:ILE:CD1	1:B:815:PHE:CZ	3.00	0.45
1:B:125:ILE:HG23	1:B:126:LYS:N	2.32	0.44
1:B:568:GLU:N	1:B:569:PRO:CD	2.80	0.44
1:B:647:PHE:C	1:B:648:LYS:HD3	2.37	0.44
1:B:963:TRP:HB3	1:B:970:MET:SD	2.57	0.44
1:B:276:VAL:HB	1:B:319:VAL:CG1	2.46	0.44
1:B:719:PRO:HG2	1:B:806:LYS:HD3	1.99	0.44
1:A:262:LYS:HD3	1:A:296:ASN:CG	2.38	0.44
1:A:640:LEU:HD21	1:A:886:GLU:HB2	1.99	0.44
1:A:538:MET:HE3	1:A:542:ALA:HB3	1.94	0.44
1:A:916:LEU:CD2	1:A:944:GLY:HA3	2.47	0.44
1:A:586:ASN:ND2	3:A:2976:SO4:O3	2.51	0.44
1:A:917:ILE:HG22	1:A:919:LEU:HD11	2.00	0.44
1:B:207:ARG:HG2	1:B:207:ARG:NH1	2.33	0.44
1:B:555:ARG:HH21	1:B:559:ARG:NH2	2.15	0.44
1:B:709:LEU:CD2	1:B:970:MET:CE	2.92	0.44
1:A:486:GLN:HB3	1:A:490:ARG:NH1	2.33	0.44
1:B:740:PHE:CE1	1:B:905:VAL:HB	2.53	0.44
1:B:370:ASP:OD2	1:B:374:GLU:OE1	2.36	0.44
1:B:594:THR:HG21	1:B:601:PHE:HE2	1.83	0.44
1:B:532:THR:CG2	1:B:535:MET:HG3	2.44	0.44
1:B:538:MET:HE3	1:B:542:ALA:CB	2.47	0.44
1:B:36:LEU:CD2	1:B:73:ILE:HD13	2.48	0.44
1:A:333:HIS:HB3	1:A:339:THR:HG1	1.82	0.43
1:A:420:PHE:O	1:A:421:ASP:OD1	2.36	0.43
1:A:868:PRO:HG2	1:A:873:GLU:OE1	2.17	0.43
1:A:868:PRO:CG	1:A:873:GLU:OE1	2.66	0.43
1:B:302:ASP:O	1:B:306:ARG:HG3	2.18	0.43
1:A:705:GLY:HA3	1:A:965:VAL:HG11	2.01	0.43
1:A:858:LYS:HD3	1:B:428:GLU:OE2	2.17	0.43
1:B:184:GLU:OE1	1:B:184:GLU:N	2.41	0.43
1:A:180:ASP:O	1:A:186:LYS:HE3	2.19	0.43
1:A:282:ILE:O	1:A:282:ILE:HG13	2.17	0.43
1:B:803:ARG:HG2	1:B:810:GLU:HG3	1.99	0.43
1:B:877:HIS:HE1	1:B:907:ALA:O	2.01	0.43
1:A:42:GLU:OE2	1:A:43:HIS:CD2	2.72	0.43
1:A:749:LYS:O	1:A:893:ILE:HG13	2.18	0.43
1:B:11:GLU:OE2	1:B:52:GLU:OE2	2.37	0.43
1:B:639:GLU:O	1:B:641:SER:N	2.52	0.43



	to ac pagem	Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:709:LEU:CD2	1:A:970:MET:SD	3.05	0.43	
1:A:69:ALA:O	1:A:73:ILE:HG13	2.19	0.43	
1:A:867:ARG:HG3	1:A:867:ARG:HH11	1.83	0.43	
1:A:671:MET:SD	1:A:712:VAL:HG11	2.59	0.43	
1:A:917:ILE:HG22	1:A:919:LEU:CD1	2.48	0.43	
1:B:774:GLN:C	1:B:776:ASN:H	2.22	0.43	
1:B:815:PHE:HB3	1:B:831:MET:CE	2.49	0.43	
1:A:125:ILE:HG21	1:A:162:GLN:HB3	2.01	0.43	
1:A:53:LEU:O	1:A:57:ILE:HG13	2.18	0.43	
1:B:773:ARG:HH11	1:B:773:ARG:HB3	1.83	0.43	
1:B:550:LYS:HE2	1:B:580:TRP:CD2	2.54	0.43	
1:B:290:LEU:N	1:B:291:PRO:HD2	2.35	0.42	
1:A:301:ALA:O	1:A:302:ASP:C	2.57	0.42	
1:B:803:ARG:HD3	1:B:838:TRP:CD2	2.54	0.42	
1:B:710:ILE:CD1	1:B:948:ILE:HD13	2.40	0.42	
1:A:358:LYS:O	1:A:362:GLU:HG3	2.19	0.42	
1:A:364:ILE:HG23	1:A:386:ILE:HG21	2.01	0.42	
1:A:737:GLN:HE21	1:A:737:GLN:HB2	1.70	0.42	
1:B:826:GLU:O	1:B:827:ARG:HD3	2.19	0.42	
1:A:234:PHE:CB	1:A:275:LEU:HD12	2.50	0.42	
1:A:391:THR:HB	2:A:2973:ANP:O4'	2.20	0.42	
1:A:430:LEU:CD1	1:A:454:ARG:HA	2.49	0.42	
1:A:654:TYR:OH	1:A:656:GLU:HB2	2.19	0.42	
1:A:773:ARG:C	1:A:775:ILE:H	2.08	0.42	
1:A:730:CYS:HA	1:A:915:HIS:CD2	2.55	0.42	
1:B:642:ASN:ND2	1:B:645:LEU:HD12	2.33	0.42	
1:B:815:PHE:CZ	1:B:839:ILE:HD11	2.53	0.42	
1:A:133:THR:O	1:A:137:VAL:HG23	2.19	0.42	
1:A:166:ARG:NH2	1:A:373:ASP:OD2	2.53	0.42	
1:A:666:VAL:HB	1:A:690:CYS:HB2	2.01	0.42	
1:B:773:ARG:C	1:B:775:ILE:H	2.23	0.42	
1:B:816:LEU:CD2	1:B:830:PRO:CA	2.98	0.42	
1:A:382:TRP:CD2	1:A:407:ARG:HB2	2.55	0.42	
1:A:485:THR:OG1	1:A:488:GLU:HG3	2.20	0.42	
1:A:757:TRP:CE3	1:A:758:ARG:HG3	2.55	0.42	
1:B:16:LYS:CG	1:B:28:ILE:HD12	2.49	0.42	
1:B:76:GLN:OE1	1:B:775:ILE:HG23	2.19	0.42	
1:A:194:THR:OG1	1:B:210:PRO:CG	2.67	0.42	
1:A:221:GLU:OE2	1:A:224:GLU:HB3	2.20	0.42	
1:A:340:THR:OG1	1:A:369:ALA:HB2	2.20	0.42	
1:A:532:THR:HG23	1:A:535:MET:H	1.85	0.42	



Interatomic Clash			Clash
Atom-1	Atom-2	distance $(Å)$	overlan (Å)
1:B:525:LYS:NZ	1:B:528:GLU:OE2	2.48	0.42
1:B:726:THR:CG2	1:B:727:HIS:N	2.82	0.42
1:B:752:SEB:O	1:B:756:GLN:HG3	2.20	0.42
1:B:77:SEB:HA	1:B:738:HIS:CE1	2 55	0.42
1:A:737:GLN:HB3	1:A:925:TYR:CD2	2.55	0.42
1:B:223:PRO:HB3	1:B:261:ILE:HD11	2.01	0.42
1:A:260:GLY:O	1:A:264:LYS:HG3	2.20	0.41
1:A:781:GLU:C	1:A:783:MET:H	2.23	0.41
1:B:283:ALA:N	1:B:284:PRO:HD2	2.35	0.41
1:B:427:GLY:HA3	1:B:453:LYS:CG	2.50	0.41
1:A:259:THR:CG2	1:A:300:ILE:HG21	2.49	0.41
1:A:347:LEU:HD11	1:A:406:PHE:HA	2.02	0.41
1:A:749:LYS:HB3	1:A:753:GLU:HB2	2.01	0.41
1:B:658:VAL:O	1:B:658:VAL:CG2	2.66	0.41
1:A:644:ASP:O	1:A:645:LEU:HD23	2.21	0.41
1:A:67:MET:HE2	1:A:109:ALA:CA	2.29	0.41
1:A:847:SER:OG	1:A:848:HIS:HD2	2.04	0.41
1:B:420:PHE:CG	1:B:421:ASP:N	2.89	0.41
1:A:200:VAL:HG21	1:A:245:ILE:CD1	2.45	0.41
1:A:256:GLU:HG3	1:A:257:ARG:N	2.33	0.41
1:A:283:ALA:HB3	1:A:284:PRO:CD	2.50	0.41
1:A:310:LEU:HD21	1:A:314:LYS:HE3	2.02	0.41
1:A:430:LEU:O	1:A:484:PRO:HG2	2.20	0.41
1:A:808:THR:OG1	1:A:809:TYR:N	2.52	0.41
1:A:227:HIS:HE1	1:A:264:LYS:HZ1	1.64	0.41
1:A:710:ILE:HD12	1:A:948:ILE:HD13	2.01	0.41
1:B:879:SER:HA	1:B:883:LEU:O	2.20	0.41
1:A:389:TYR:O	1:A:392:ILE:HG13	2.21	0.41
1:A:66:ALA:O	1:A:69:ALA:HB3	2.20	0.41
1:A:776:ASN:HB3	1:A:779:ASP:CG	2.41	0.41
1:B:229:LEU:HB3	1:B:268:ILE:HD11	2.03	0.41
1:B:743:ILE:HG12	1:B:743:ILE:O	2.21	0.41
1:A:427:GLY:HA3	1:A:453:LYS:HG3	2.02	0.41
1:A:466:CYS:SG	1:A:468:LYS:HG3	2.60	0.41
1:B:795:ARG:HG3	1:B:828:TRP:CZ3	2.56	0.41
1:A:341:LEU:O	1:A:344:VAL:HG22	2.20	0.41
1:A:493:TYR:HA	1:A:565:LEU:HB2	2.03	0.41
1:A:568:GLU:N	1:A:569:PRO:CD	2.84	0.41
1:A:172:PRO:O	1:A:176:GLU:HG3	2.21	0.41
1:A:956:LYS:O	1:A:957:ASN:HB2	2.21	0.41
1:B:275:LEU:HA	1:B:275:LEU:HD23	1.92	0.40



Atom-1	Atom-2	Interatomic	Clash
		distance (A)	overlap (A)
1:B:757:TRP:CZ2	1:B:765:ARG:HD2	2.56	0.40
1:B:825:SER:O	1:B:826:GLU:C	2.59	0.40
1:A:276:VAL:HB	1:A:319:VAL:CG1	2.47	0.40
1:A:324:GLU:O	1:A:325:ASP:CB	2.69	0.40
1:B:21:THR:HG23	1:B:23:ASP:H	1.87	0.40
1:B:84:GLU:HB3	1:B:85:PRO:CD	2.51	0.40
1:B:957:ASN:HA	1:B:957:ASN:HD22	1.65	0.40
1:A:17:LEU:N	1:A:28:ILE:CD1	2.84	0.40
1:A:263:ARG:NH2	1:A:304:GLU:OE1	2.27	0.40
1:A:68:GLN:O	1:A:72:HIS:HD2	2.03	0.40
1:B:658:VAL:O	3:B:2983:SO4:O2	2.39	0.40
1:A:321:ASN:O	1:A:322:VAL:C	2.59	0.40
1:A:430:LEU:HD21	1:A:454:ARG:CZ	2.51	0.40
1:A:797:ALA:HB2	1:A:816:LEU:HG	2.03	0.40
1:B:821:ILE:HD13	1:B:828:TRP:CH2	2.56	0.40
1:B:857:MET:CE	1:B:866:PHE:CZ	3.04	0.40
1:B:870:THR:OG1	1:B:873:GLU:HG3	2.22	0.40
1:A:395:HIS:ND1	2:A:2973:ANP:O2A	2.54	0.40
1:B:67:MET:HE1	1:B:109:ALA:HA	2.02	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	Perce	entiles
1	А	971/986~(98%)	909 (94%)	58~(6%)	4 (0%)	34	72
1	В	979/986~(99%)	936 (96%)	38 (4%)	5(0%)	29	68
All	All	1950/1972~(99%)	1845~(95%)	96~(5%)	9 (0%)	29	68

All (9) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
1	А	774	GLN
1	А	775	ILE
1	В	232	THR
1	В	640	LEU
1	А	545	GLY
1	В	229	LEU
1	В	774	GLN
1	А	972	PRO
1	В	775	ILE

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	А	831/843~(99%)	813 (98%)	18 (2%)	52 81
1	В	838/843~(99%)	817~(98%)	21 (2%)	47 79
All	All	1669/1686~(99%)	1630 (98%)	39 (2%)	50 80

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	101	LYS
1	А	166	ARG
1	А	169	GLU
1	А	215	CYS
1	А	224	GLU
1	А	432	ASN
1	А	449	GLN
1	А	493	TYR
1	А	573	LEU
1	А	659	LYS
1	А	701	PRO
1	А	737	GLN
1	А	748	ASP
1	A	779	ASP
1	А	876	GLU



Mol	Chain	Res	Type
1	А	881	LEU
1	А	929	ASP
1	А	958	LEU
1	В	-3	HIS
1	В	215	CYS
1	В	257	ARG
1	В	322	VAL
1	В	342	GLN
1	В	387	THR
1	В	432	ASN
1	В	490	ARG
1	В	493	TYR
1	В	529	PHE
1	В	534	GLU
1	В	583	ASN
1	В	737	GLN
1	В	748	ASP
1	В	773	ARG
1	В	859	GLU
1	В	872	LYS
1	В	876	GLU
1	В	881	LEU
1	В	956	LYS
1	В	958	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	76	GLN
1	А	78	ASN
1	А	97	ASN
1	А	271	ASN
1	А	345	ASN
1	А	379	GLN
1	А	413	ASN
1	А	432	ASN
1	А	496	HIS
1	А	597	HIS
1	А	604	ASN
1	А	674	GLN
1	А	711	ASN
1	А	729	ASN



Mol	Chain	Res	Type
1	А	737	GLN
1	А	756	GLN
1	А	774	GLN
1	А	848	HIS
1	А	865	GLN
1	А	877	HIS
1	А	915	HIS
1	А	924	ASN
1	В	97	ASN
1	В	271	ASN
1	В	321	ASN
1	В	342	GLN
1	В	395	HIS
1	В	413	ASN
1	В	496	HIS
1	В	604	ASN
1	В	642	ASN
1	В	711	ASN
1	В	729	ASN
1	В	737	GLN
1	В	756	GLN
1	В	784	ASN
1	В	820	ASN
1	В	848	HIS
1	В	865	GLN
1	В	877	HIS
1	В	915	HIS
1	В	924	ASN
1	В	950	HIS
1	В	957	ASN

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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)

14 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).

Mal	Type	Chain	Bos	Link	Bo	ond leng	ths	B	ond ang	gles
	туре	Unain	1105		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	В	2983	-	4,4,4	0.64	0	6,6,6	0.54	0
3	SO4	В	2984	-	4,4,4	0.64	0	6,6,6	0.54	0
2	ANP	А	2973	-	29,33,33	2.91	7 (24%)	$31,\!52,\!52$	1.90	8 (25%)
3	SO4	А	2975	-	4,4,4	0.63	0	6,6,6	0.54	0
3	SO4	А	2976	-	4,4,4	0.63	0	6,6,6	0.53	0
3	SO4	В	2978	-	4, 4, 4	0.61	0	$6,\!6,\!6$	0.06	0
3	SO4	А	2978	-	4, 4, 4	0.65	0	$6,\!6,\!6$	0.56	0
3	SO4	В	2979	-	4,4,4	0.62	0	6,6,6	0.05	0
2	ANP	В	2977	-	29,33,33	2.88	7 (24%)	31,52,52	1.90	8 (25%)
3	SO4	А	2974	-	4,4,4	0.63	0	6,6,6	0.53	0
3	SO4	В	2981	-	4,4,4	0.61	0	6,6,6	0.07	0
3	SO4	В	2980	-	4,4,4	0.63	0	6,6,6	0.53	0
3	SO4	A	2977	-	4,4,4	0.62	0	6,6,6	0.52	0
3	SO4	В	2982	-	4,4,4	0.64	0	6,6,6	0.56	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ANP	В	2977	-	-	2/14/38/38	0/3/3/3
2	ANP	А	2973	-	-	2/14/38/38	0/3/3/3

All (14) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	$\operatorname{Ideal}(\operatorname{\AA})$
2	А	2973	ANP	PG-01G	9.92	1.61	1.46
2	А	2973	ANP	PB-O1B	9.81	1.61	1.46
2	В	2977	ANP	PB-O1B	9.79	1.61	1.46
2	В	2977	ANP	PG-01G	9.76	1.61	1.46
2	А	2973	ANP	PB-O2B	-3.05	1.48	1.56
2	А	2973	ANP	PG-O3G	-3.05	1.48	1.56
2	В	2977	ANP	PB-O2B	-3.02	1.48	1.56
2	В	2977	ANP	PG-O3G	-3.02	1.48	1.56
2	А	2973	ANP	PA-O1A	3.02	1.61	1.50
2	В	2977	ANP	PA-O1A	2.93	1.61	1.50
2	А	2973	ANP	O4'-C1'	2.42	1.44	1.41
2	В	2977	ANP	O4'-C1'	2.24	1.44	1.41
2	В	2977	ANP	PB-O3A	2.16	1.61	1.59
2	A	2973	ANP	PB-O3A	2.09	1.61	1.59

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms		$Observed(^{o})$	$Ideal(^{o})$
2	В	2977	ANP	O1G-PG-N3B	-5.36	103.88	111.77
2	А	2973	ANP	O1G-PG-N3B	-5.36	103.88	111.77
2	А	2973	ANP	N3-C2-N1	-4.51	121.63	128.68
2	В	2977	ANP	N3-C2-N1	-4.38	121.83	128.68
2	А	2973	ANP	PA-O3A-PB	-3.33	120.88	132.62
2	А	2973	ANP	O1B-PB-N3B	-3.13	107.16	111.77
2	В	2977	ANP	PA-O3A-PB	-3.10	121.69	132.62
2	В	2977	ANP	O2G-PG-O1G	-3.01	105.88	113.45
2	В	2977	ANP	O1B-PB-N3B	-2.83	107.61	111.77
2	В	2977	ANP	O2B-PB-O3A	2.52	113.04	104.64
2	А	2973	ANP	C4-C5-N7	-2.50	106.80	109.40
2	В	2977	ANP	O4'-C1'-C2'	-2.48	103.30	106.93
2	А	2973	ANP	C5'-C4'-C3'	-2.38	106.27	115.18
2	А	2973	ANP	C3'-C2'-C1'	-2.37	97.41	100.98
2	В	2977	ANP	C5'-C4'-C3'	-2.18	107.02	115.18
2	A	2973	ANP	O2B-PB-O3A	2.03	111.41	104.64

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	А	2973	ANP	O4'-C4'-C5'-O5'
2	В	2977	ANP	O4'-C4'-C5'-O5'
2	А	2973	ANP	C3'-C4'-C5'-O5'
2	В	2977	ANP	C3'-C4'-C5'-O5'



There are no ring outliers.

Mol	Chain	\mathbf{Res}	Type	Clashes	Symm-Clashes
3	В	2983	SO4	1	0
3	В	2984	SO4	1	0
2	А	2973	ANP	4	0
3	А	2975	SO4	1	0
3	А	2976	SO4	2	0
3	А	2978	SO4	1	0
2	В	2977	ANP	2	0
3	А	2974	SO4	1	0
3	В	2981	SO4	1	0
3	В	2980	SO4	1	0
3	А	2977	SO4	1	0
3	В	2982	SO4	1	0

12 monomers are involved in 17 short contacts:

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.









5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	В	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	В	726:THR	С	727:HIS	Ν	1.10



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, 95^{th} 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	А	973/986~(98%)	0.09	35 (3%) 42 17	19, 41, 78, 105	0
1	В	981/986~(99%)	-0.20	14 (1%) 75 49	15, 30, 60, 102	0
All	All	1954/1972~(99%)	-0.06	49 (2%) 57 29	15, 35, 72, 105	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ	
1	А	641	SER	11.2	
1	А	643	THR	6.7	
1	А	778	ASN	6.4	
1	В	778	ASN	6.3	
1	А	973	SER	5.1	
1	А	642	ASN	5.0	
1	А	972	PRO	4.8	
1	А	644	ASP	4.8	
1	В	640	LEU	4.7	
1	В	639	GLU	4.4	
1	А	426	GLU	4.3	
1	А	779	ASP	4.2	
1	А	424	GLU	4.0	
1	А	422	ASP	3.9	
1	А	645	LEU	3.9	
1	А	777	GLU	3.8	
1	А	637	TYR	3.6	
1	А	640	LEU	3.6	
1	А	638	GLU	3.5	
1	A	423	GLU	3.4	
1	В	642	ASN	3.3	
1	A	639	GLU	3.3	
1	A	970	MET	3.3	
1	A	$\overline{971}$	THR	3.1	



Mol	Chain	Res	Type	RSRZ
1	А	421	ASP	3.1
1	А	967	ASP	3.0
1	В	774	GLN	2.8
1	А	958	LEU	2.8
1	А	417	GLY	2.8
1	А	425	ASP	2.7
1	В	976	ASN	2.7
1	А	678	THR	2.7
1	В	232	THR	2.6
1	В	775	ILE	2.6
1	А	418	PRO	2.6
1	В	641	SER	2.5
1	А	427	GLY	2.5
1	А	416	VAL	2.4
1	В	-2	HIS	2.3
1	А	2	ASP	2.2
1	А	776	ASN	2.2
1	А	615	LEU	2.2
1	В	423	GLU	2.2
1	В	233	THR	2.1
1	А	671	MET	2.1
1	А	646	GLU	2.1
1	В	-1	HIS	2.1
1	В	975	HIS	2.0
1	А	727	HIS	2.0

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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^{th} 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	${f B} ext{-factors}({f A}^2)$	Q<0.9
3	SO4	А	2978	5/5	0.80	0.37	87,87,88,89	0
3	SO4	В	2981	5/5	0.80	0.33	90,92,92,92	0
2	ANP	В	2977	31/31	0.84	0.26	33,34,37,40	0
3	SO4	А	2975	5/5	0.84	0.32	88,89,89,90	0
2	ANP	А	2973	31/31	0.85	0.28	$34,\!35,\!39,\!41$	0
3	SO4	В	2982	5/5	0.85	0.35	82,82,83,85	0
3	SO4	А	2974	5/5	0.86	0.28	84,85,85,86	0
3	SO4	В	2983	5/5	0.87	0.39	87,87,88,89	0
3	SO4	В	2984	5/5	0.93	0.21	$62,\!65,\!66,\!69$	0
3	SO4	В	2979	5/5	0.94	0.22	79,79,80,81	0
3	SO4	А	2976	5/5	0.95	0.15	$62,\!63,\!63,\!63$	0
3	SO4	В	2978	5/5	0.95	0.15	42,43,44,46	0
3	SO4	A	2977	5/5	0.98	0.13	43,44,44,44	0
3	SO4	В	2980	5/5	0.98	0.13	26,28,32,36	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.

